

480
540

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..197

(D) OTHER INFORMATION: / Ceres Seq. ID 1585625

Ala Glu Glu Gln Asn Gln Gln Asn Gly Pro V

(2) INFORMATION FOR SEQ ID NO:434:

(A) LENGTH: 150 amino acids

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

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(ix) FEATURE:
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(B) LOCATION: 1..150

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:434:

5 10

Asp His Leu Asn Glu Phe Asp Arg Leu Cys Asn Leu Thr Lys Ile Asn
20 25 30

Gly Val Ser Glu Asp Gly Phe Lys Leu Cys Leu Phe Pro Phe Ser Leu
35 40 45

Gly Asp Lys Ala His Ile Trp Glu Lys Asn Leu Pro His Asp Ser Ile
50 55 60

Glu	Val	Val	Ala	Glu	Ser	Thr	Gly	Gly	Ile	Gly	Gly	Gly	Ala	Gly	Gly
1				5					10					15	
Gly	Leu	Thr	Ile	Lys	Asp	Ser	Asp	Glu	Gln	Thr	Ile	Gly	Leu	Glu	Ala
			20					25					30		
Val	Ser	Gly	Leu	Val	Trp	Arg	Cys	Leu	Thr	Met	Glu	Asn	Thr	Gly	Ile
		35					40					45			
Ile	Gly	Leu	Tyr	Gly	Val	Glu	Gly	Val	Gly	Lys	Thr	Thr	Val	Leu	Thr
	50					55					60				
Gln	Val	Asn	Asn	Arg	Leu	Leu	Gln	Gln	Lys	Ala	Asn	Gly	Phe	Asp	Phe
65				70						75				80	
Val	Leu	Trp	Val	Phe	Val	Ser	Lys	Asn	Leu	Asn	Leu	Gln	Lys	Ile	Gln
				85					90					95	
Asp	Thr	Ile	Arg	Glu	Lys	Ile	Gly	Phe	Leu	Asp	Arg	Thr	Trp	Thr	Ser


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(ix) FEATURE:
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(A) NAME/KEY: -

(B) LOCATION: 1..698

(D) OTHER INFORMATION: / Ceres Seq. ID 1585642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

gtgctcctct	cggtgatggt	ttgaagattc	agaacaaaaa	cggtgctgtg	atgaatcggc	60
gtgccttcgg	tgacatcgga	aatcttgttt	ctgttcccat	taatcgaccc	attactcgaa	120
gtttccgtga	ccagttatta	gcgaatgccc	aactcaaaaag	aaagcccatc	aatggagaca	180
acaagaagaa	gaatctagtg	gttaagcaac	agacgaagcc	tgttgaagtg	atcgagacga	240
agagggaggt	gactaaaaac	gaagtagcga	tgtcacctaa	gaataagaaa	gtgacgtact	300
cgtctgtact	tagtgctcgg	agcaaagctg	cttgtggtat	tgatgaatct	gacaaagata	360
atcatctggc	tgcagtggag	tatgttgatg	atatgtactc	gttctataaa	gaagttgaga	420
aggagagtca	gcctaagatg	catattcaaa	ctaagatgaa	tgagaagatc	agagcgatct	480
tgattgattg	gttactagaa	gttcacatca	agtttgagct	taaccttgga	actctttacc	540
tcactgttaa	ccttgatcga	ttcctctctg	tgaaagttgt	tacccaaaaga	gagttgcagc	600
tagtgggaa	cagtgtcttc	caaatacgca	ggtacttcac	gttcaaaaaga	aaaatcttca	660
agctgcaaag	acaaaaagtt	tcagcataca	agggttga			

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1585643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

Ala	Pro	Leu	Val	Asp	Gly	Leu	Lys	Ile	Gln	Asn	Lys	Asn	Gly	Ala	Val
1			5						10					15	
Met	Asn	Arg	Arg	Ala	Phe	Gly	Asp	Ile	Gly	Asn	Leu	Val	Ser	Val	Pro
			20					25					30		
Ile	Asn	Arg	Pro	Ile	Thr	Arg	Ser	Phe	Arg	Asp	Gln	Leu	Leu	Ala	Asn
			35				40					45			
Ala	Gln	Leu	Lys	Arg	Lys	Pro	Ile	Asn	Gly	Asp	Asn	Lys	Lys	Lys	Asn
	50					55				60					
Leu	Val	Val	Lys	Gln	Gln	Thr	Lys	Pro	Val	Glu	Val	Ile	Glu	Thr	Lys
65					70					75				80	
Arg	Glu	Val	Thr	Lys	Asn	Glu	Val	Ala	Met	Ser	Pro	Lys	Asn	Lys	Lys
				85				90					95		
Val	Thr	Tyr	Ser	Ser	Val	Leu	Ser	Ala	Arg	Ser	Lys	Ala	Ala	Cys	Gly
			100					105					110		
Ile	Asp	Glu	Ser	Asp	Lys	Asp	Asn	His	Leu	Ala	Ala	Val	Glu	Tyr	Val
	115					120						125			
Asp	Asp	Met	Tyr	Ser	Phe	Tyr	Lys	Glu	Val	Glu	Lys	Glu	Ser	Gln	Pro
	130				135					140					
Lys	Met	His	Ile	Gln	Thr	Lys	Met	Asn	Glu	Lys	Ile	Arg	Ala	Ile	Leu
145					150					155				160	
Ile	Asp	Trp	Leu	Leu	Glu	Val	His	Ile	Lys	Phe	Glu	Leu	Asn	Leu	Gly
			165					170					175		
Thr	Leu	Tyr	Leu	Thr	Val	Asn	Leu	Asp	Arg	Phe	Leu	Ser	Val	Lys	Val
			180					185					190		
Val	Thr	Lys	Arg	Glu	Leu	Gln	Leu	Val	Gly	Ile	Ser	Val	Phe	Gln	Ile
	195					200						205			
Cys	Arg	Tyr	Phe	Thr	Phe	Lys	Arg	Lys	Ile	Phe	Lys	Leu	Gln	Arg	Gln
	210					215						220			
Lys	Val	Ser	Ala	Tyr	Lys	Gly									
225					230										

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 amino acids

00669900-101300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

(2) INFORMATION FOR SEQ ID NO:441:

(A) LENGTH: 142 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1585645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

Met	Ser	Pro	Lys	Asn	Lys	Lys	Val	Thr	Tyr	Ser	Ser	Val	Leu	Ser	Ala
1				5					10					15	
Arg	Ser	Lys	Ala	Ala	Cys	Gly	Ile	Asp	Glu	Ser	Asp	Lys	Asp	Asn	His
			20					25					30		
Leu	Ala	Ala	Val	Glu	Tyr	Val	Asp	Asp	Met	Tyr	Ser	Phe	Tyr	Lys	Glu
		35					40					45			
Val	Glu	Lys	Glu	Ser	Gln	Pro	Lys	Met	His	Ile	Gln	Thr	Lys	Met	Asn
	50					55					60				
Glu	Lys	Ile	Arg	Ala	Ile	Leu	Ile	Asp	Trp	Leu	Leu	Glu	Val	His	Ile
65					70					75				80	
Lys	Phe	Glu	Leu	Asn	Leu	Gly	Thr	Leu	Tyr	Leu	Thr	Val	Asn	Leu	Asp
				85					90					95	

Arg Phe Leu Ser Val Lys Val Val Thr Lys Arg Glu Leu Gln Leu Val
100 105 110
Gly Ile Ser Val Phe Gln Ile Cys Arg Tyr Phe Thr Phe Lys Arg Lys
115 120 125
Ile Phe Lys Leu Gln Arg Gln Lys Val Ser Ala Tyr Lys Gly
130 135 140

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1284
- (D) OTHER INFORMATION: / Ceres Seq. ID 1585650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

atgcagacat tttcttccgc cgccgctctc acctccatcc tccgtcgtac aacgatctat 60
cacggcggat ttggaactgg tctccgaatc cgccgcagct tttattttct ctcagcgata 120
cgacaagaga accctaattgt cactaaaaat cccacccga acaagactat tctcagatcc 180
ttcttagctc cggttctccc gttagacgaa aaacctaac tctgtgagct tcaagccatc 240
ggtacaatcg ccaccgctca agctgactac atgcgcgtca ttgttcaaga tgtacctgag 300
agtataatg gagaggatga taagattggc gttgatttgc tttgtgtggt gagaaagtta 360
ctgaagaaga taggtacgac tgttcttgtt ggtgataaag ttctcgttga taaagttagat 420
tgggttgatc ggagagctaa gattatcaat gtgtttgatc gagtctcgga ggttttggat 480
ccaccggttg cgaatgttga tcacttagtg attctgtttt ctcttgatca acctaaagatt 540
gatccattta cacttactag gttcttgggt gaagctgaat ctattggaat tcgaatcaca 600
gttgctttga acaaattgta actcgtcact caagagggat tgattagaga catgataaga 660
ttgcgtagtt ggaactatga accattgac tgtagtgtgg gaactaaagt cggacttgat 720
gagattgcgt ttaacctgag aaatcagact tctgtcattg ttggacctag tgggtgttga 780
aagtccagct taatcaatat attgagaagt agctatgggt gtgacattaa acacgaagaa 840
gtgtttaagc ctagtgtagg ggaagtttca catagaaatg gaagaggtaa acatacaacc 900
cgaaatgtaa cgctacttcc tctttgtgga ggtggatacc ttgctgatac ttctggcttt 960
aacaagcata agttgctgaa agtaacaaag caaaaacttc ccttgtgttt tcctgagata 1020
cggaaaatgg tcgaggaggg aaaatgtggt tgggaaaggt atgattactt ttacaactg 1080
cttgatgaga tcaaaatcga tgaggagtgt caacttaaga agtatggaac caaaagggaa 1140
ggtggtgtta gttgccacat gggagagaag ggtgtggaac aagctaaacc acggatagat 1200
cccaagaagt ataggagaga atcgagggaag acgatgaaag atgaaagagc tatattaaga 1260
cagcatagag aacaattaac ctaa

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..427
- (D) OTHER INFORMATION: / Ceres Seq. ID 1585651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

Met Gln Thr Phe Ser Ser Ala Ala Ala Thr Ser Ile Leu Arg Arg
1 5 10 15
Thr Thr Ile Tyr His Gly Gly Phe Gly Thr Gly Leu Arg Ile Arg Arg
20 25 30
Ser Phe Tyr Phe Leu Ser Ala Ile Arg Gln Glu Asn Pro Asn Val Thr
35 40 45
Lys Asn Pro His Pro Asn Lys Thr Ile Leu Arg Ser Phe Leu Ala Pro
50 55 60
Val Leu Pro Leu Asp Glu Lys Pro Asn Leu Val Glu Leu Gln Ala Ile

09689900 10600

Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
18-24	20.5 (2.5)
25-34	29.5 (4.5)
35-44	39.5 (5.5)
45-54	49.5 (6.5)
55-64	59.5 (7.5)
65-74	69.5 (8.5)
75-84	79.5 (9.5)
85-94	89.5 (10.5)
95-104	99.5 (11.5)
105-114	109.5 (12.5)
115-124	119.5 (13.5)
125-134	129.5 (14.5)
135-144	139.5 (15.5)
145-154	149.5 (16.5)
155-164	159.5 (17.5)
165-174	169.5 (18.5)
175-184	179.5 (19.5)
185-194	189.5 (20.5)
195-204	199.5 (21.5)
205-214	209.5 (22.5)
215-224	219.5 (23.5)
225-234	229.5 (24.5)
235-244	239.5 (25.5)
245-254	249.5 (26.5)
255-264	259.5 (27.5)
265-274	269.5 (28.5)
275-284	279.5 (29.5)
285-294	289.5 (30.5)
295-304	299.5 (31.5)
305-314	309.5 (32.5)
315-324	319.5 (33.5)
325-334	329.5 (34.5)
335-344	339.5 (35.5)
345-354	349.5 (36.5)
355-364	359.5 (37.5)
365-374	369.5 (38.5)
375-384	379.5 (39.5)
385-394	389.5 (40.5)
395-404	399.5 (41.5)
405-414	409.5 (42.5)
415-424	419.5 (43.5)
425-434	429.5 (44.5)
435-444	439.5 (45.5)
445-454	449.5 (46.5)
455-464	459.5 (47.5)
465-474	469.5 (48.5)
475-484	479.5 (49.5)
485-494	489.5 (50.5)
495-504	499.5 (51.5)
505-514	509.5 (52.5)
515-524	519.5 (53.5)
525-534	529.5 (54.5)
535-544	539.5 (55.5)
545-554	549.5 (56.5)
555-564	559.5 (57.5)
565-574	569.5 (58.5)
575-584	579.5 (59.5)
585-594	589.5 (60.5)
595-604	599.5 (61.5)
605-614	609.5 (62.5)
615-624	619.5 (63.5)
625-634	629.5 (64.5)
635-644	639.5 (65.5)
645-654	649.5 (66.5)
655-664	659.5 (67.5)
665-674	669.5 (68.5)
675-684	679.5 (69.5)
685-694	689.5 (70.5)
695-704	699.5 (71.5)
705-714	709.5 (72.5)
715-724	719.5 (73.5)
725-734	729.5 (74.5)
735-744	739.5 (75.5)
745-754	749.5 (76.5)
755-764	759.5 (77.5)
765-774	769.5 (78.5)
775-784	779.5 (79.5)
785-794	789.5 (80.5)
795-804	799.5 (81.5)
805-814	809.5 (82.5)
815-824	819.5 (83.5)
825-834	829.5 (84.5)
835-844	839.5 (85.5)
845-854	849.5 (86.5)
855-864	859.5 (87.5)
865-874	869.5 (88.5)
875-884	879.5 (89.5)
885-894	889.5 (90.5)
895-904	899.5 (91.5)
905-914	909.5 (92.5)
915-924	919.5 (93.5)
925-934	929.5 (94.5)
935-944	939.5 (95.5)
945-954	949.5 (96.5)
955-964	959.5 (97.5)
965-974	969.5 (98.5)
975-984	979.5 (99.5)
985-994	989.5 (100.5)
995-1004	999.5 (101.5)
1005-1014	1009.5 (102.5)
1015-1024	1019.5 (103.5)
1025-1034	1029.5 (104.5)
1035-1044	1039.5 (105.5)
1045-1054	1049.5 (106.5)
1055-1064	1059.5 (107.5)
1065-1074	1069.5 (108.5)
1075-1084	1079.5 (109.5)
1085-1094	1089.5 (110.5)
1095-1104	1099.5 (111.5)
1105-1114	1109.5 (112.5)
1115-1124	1119.5 (113.5)
1125-1134	

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (A) NAME/KEY: peptide

- (D) OTHER INFORMATION: / Ceres Seq. ID 1585653

- | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Val | Ile | Val | Gln | Asp | Val | Pro | Glu | Ser | Asp | Asn | Gly | Glu | Asp |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Asp | Lys | Ile | Gly | Val | Asp | Leu | Leu | Cys | Val | Val | Arg | Lys | Leu | Leu | Lys |
| | | | 20 | | | | | 25 | | | | | 30 | | |

Lys Ile Gly Thr Thr Val Leu Val Gly Asp Lys Val Leu Val Asp Lys
35 40 45
Val Asp Trp Val Asp Arg Arg Ala Lys Ile Ile Asn Val Phe Asp Arg
50 55 60
Val Ser Glu Val Leu Asp Pro Pro Val Ala Asn Val Asp His Leu Val
65 70 75 80
Ile Leu Phe Ser Leu Asp Gln Pro Lys Ile Asp Pro Phe Thr Leu Thr
85 90 95
Arg Phe Leu Val Glu Ala Glu Ser Ile Gly Ile Arg Ile Thr Val Ala
100 105 110
Leu Asn Lys Cys Glu Leu Val Thr Gln Glu Gly Leu Ile Arg Asp Met
115 120 125
Ile Arg Leu Arg Ser Trp Asn Tyr Glu Pro Leu Ile Cys Ser Val Gly
130 135 140
Thr Lys Val Gly Leu Asp Glu Ile Ala Phe Asn Leu Arg Asn Gln Thr
145 150 155 160
Ser Val Ile Val Gly Pro Ser Gly Val Gly Lys Ser Ser Leu Ile Asn
165 170 175
Ile Leu Arg Ser Ser Tyr Gly Gly Asp Ile Lys His Glu Glu Val Phe
180 185 190
Lys Pro Ser Val Gly Glu Val Ser His Arg Asn Gly Arg Gly Lys His
195 200 205
Thr Thr Arg Asn Val Thr Leu Leu Pro Leu Cys Gly Gly Gly Tyr Leu
210 215 220
Ala Asp Thr Ser Gly Phe Asn Lys His Lys Leu Leu Lys Val Thr Lys
225 230 235 240
Gln Lys Leu Pro Leu Cys Phe Pro Glu Ile Arg Lys Met Val Glu Gly
245 250 255
Gly Lys Cys Gly Trp Glu Arg Tyr Asp Tyr Phe Leu Gln Leu Leu Asp
260 265 270
Glu Ile Lys Ile Asp Glu Glu Cys Gln Leu Lys Lys Tyr Gly Thr Lys
275 280 285
Arg Glu Gly Gly Val Ser Cys His Met Gly Glu Lys Gly Val Glu Gln
290 295 300
Ala Lys Pro Arg Ile Asp Pro Lys Lys Tyr Arg Arg Glu Ser Arg Lys
305 310 315 320
Thr Met Lys Asp Glu Arg Ala Ile Leu Arg Gln His Arg Glu Gln Leu
325 330 335
Thr

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..642
- (D) OTHER INFORMATION: / Ceres Seq. ID 1585658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

tgggagctgg atacggatca cgatttcctg attgacaaag aaaatcttat gagatatgga	60
aacctgctc ttacctaccg gattgtcgac agaataattct ccaggttgcc taggaagttc	120
actagcaaag ttgaaggga gatggggtat gaagactttg tctatttcat tcttgcgga	180
gaagataaat cgtcagtgcc tagcctagaa tattggttta agtgcataga cttggatgca	240
aatgggatta taacgcgaaa tgagatgcaa ttcttttatg aagagcagtt gcatagaatg	300
gagtgcattg cgcaagaggc tgttcttttc gaggatatct tatgtcagat gattgatatg	360
atcggaacctg agaacgaaag ccatataacg ctgcatgaac tgaaaggctc aaagctctct	420
ggaaacgtct tcaacatcct ttttaatacta aacaaattta tggcatttga aaccgggat	480
ccgttcctca ttcgtcagga gcgcgagaa cgcacattga cagactggga ccgttttgca	540

(2) INFORMATION FOR SEQ ID NO:446:

(A) LENGTH: 213 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1585659

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1585660

(XI) SEQUENCE DESCRIPTION OF THE INVENTION															
Met	Arg	Tyr	Gly	Asn	His	Ala	Leu	Thr	Tyr	Arg	Ile	Val	Asp	Arg	Ile
1				5					10					15	
Phe	Ser	Gln	Val	Ala	Arg	Lys	Phe	Thr	Ser	Lys	Val	Glu	Gly	Lys	Met
		20						25					30		
Gly	Tyr	Glu	Asp	Phe	Val	Tyr	Phe	Ile	Leu	Ala	Glu	Glu	Asp	Lys	Ser
		35					40					45			
Ser	Val	Pro	Ser	Leu	Glu	Tyr	Trp	Phe	Lys	Cys	Ile	Asp	Leu	Asp	Ala

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..987

(D) OTHER INFORMATION: / Ceres Seq. ID 1585675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

atgcttctg	ataccgccag	caatgggaat	ttccagaaca	aagatgttga	agaaggctgg	60
gaattgggtg	agaaccttgc	tcaatcagat	ggcaattaca	acgaagactg	tgataggacc	120
gtcaaaggaa	cagctgactc	tgatgacaaa	cacaggaaga	agatcaaagc	gctgaatgac	180
aagctggaca	ggattattct	cggccagcag	aagcatgtgc	acttccttgt	tgatgacgag	240
cagtatcaag	tcanagacgg	ggagggtaac	cagttggaag	aagtcagcta	catcaacaac	300
aaccaggggtg	gctacaaaag	atacaacaac	ttcaaaaacca	acaatcccaa	cctctcttac	360
cgcagcacca	acgttgctaa	ccctcaggat	caagtgtatc	ctccacagca	acaacaaagt	420
ttcgttccta	agcagcagtt	ccagggggaac	taccagcaac	caccaccacc	tgggtttgca	480
cctcagcaaa	cccaagggtcc	tgctgctcct	gatgctgaaa	tgaaacagat	ggtcaagcag	540
ctgctacagg	gacaagcatc	tagctcaatg	gaaatggcta	aaaaattatc	taaattgcac	600
cataagctgg	actgcagcta	caatgacctg	aatgccaaaag	tggaggcatt	gaataccaaa	660
gtcagatact	tggaaaggcca	atcagtatct	acctctgtac	caaaagttac	aggacttcca	720
gggaagtcca	tacagaatcc	aaaagagtat	gcaaccgctc	acgccatcac	catctgccat	780
gatcgagagc	tgccaactcg	acctgtcctt	gatttcatca	ctgggggaaa	tgatgttcaa	840
gaaggggaag	cttctactca	ggttgtagtc	tctgttggtg	aattcaacca	ttccgctggg	900
tctcgccatc	tcaactcaatc	catctcggaa	gaaaaggccg	ccataatcga	gagaatgcat	960
ttaaggtgtc	aatccaaatg	ggtgttaa				

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..328

(D) OTHER INFORMATION: / Ceres Seq. ID 1585676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

Met	Leu	Leu	Asp	Thr	Ala	Ser	Asn	Gly	Asn	Phe	Gln	Asn	Lys	Asp	Val
1			5					10					15		
Glu	Glu	Gly	Trp	Glu	Leu	Val	Glu	Asn	Leu	Ala	Gln	Ser	Asp	Gly	Asn
			20					25					30		
Tyr	Asn	Glu	Asp	Cys	Asp	Arg	Thr	Val	Lys	Gly	Thr	Ala	Asp	Ser	Asp
			35					40					45		
Asp	Lys	His	Arg	Lys	Lys	Ile	Lys	Ala	Leu	Asn	Asp	Lys	Leu	Asp	Arg
			50					55					60		
Ile	Ile	Leu	Gly	Gln	Gln	Lys	His	Val	His	Phe	Leu	Val	Asp	Asp	Glu
			65					70					75		80
Gln	Tyr	Gln	Val	Xaa	Asp	Gly	Glu	Gly	Asn	Gln	Leu	Glu	Glu	Val	Ser
			85					90					95		
Tyr	Ile	Asn	Asn	Asn	Gln	Gly	Gly	Tyr	Lys	Arg	Tyr	Asn	Asn	Phe	Lys
			100					105					110		
Thr	Asn	Asn	Pro	Asn	Leu	Ser	Tyr	Arg	Ser	Thr	Asn	Val	Ala	Asn	Pro
			115					120					125		
Gln	Asp	Gln	Val	Tyr	Pro	Pro	Gln	Gln	Gln	Gln	Ser	Phe	Val	Pro	Lys
			130					135					140		
Gln	Gln	Phe	Gln	Gly	Asn	Tyr	Gln	Gln	Pro	Pro	Pro	Pro	Gly	Phe	Ala
			145					150					155		160
Pro	Gln	Gln	Thr	Gln	Gly	Pro	Ala	Ala	Pro	Asp	Ala	Glu	Met	Lys	Gln
			165					170					175		
Met	Val	Lys	Gln	Leu	Leu	Gln	Gly	Gln	Ala	Ser	Ser	Ser	Met	Glu	Met
			180					185					190		
Ala	Lys	Lys	Leu	Ser	Lys	Leu	His	His	Lys	Leu	Asp	Cys	Ser	Tyr	Asn
			195					200					205		
Asp	Leu	Asn	Ala	Lys	Val	Glu	Ala	Leu	Asn	Thr	Lys	Val	Arg	Tyr	Leu
			210					215					220		

00569500 101300

Glu Gly Gln Ser Val Ser Thr Ser Val Pro Lys Val Thr Gly Leu Pro
225 230 235 240
Gly Lys Ser Ile Gln Asn Pro Lys Glu Tyr Ala Thr Ala His Ala Ile
245 250 255
Thr Ile Cys His Asp Arg Glu Leu Pro Thr Arg Pro Val Leu Asp Phe
260 265 270
Ile Thr Gly Asp Asn Asp Val Gln Glu Gly Lys Ala Ser Thr Gln Val
275 280 285
Val Val Ser Val Val Glu Phe Asn His Ser Ala Gly Ser Arg His Leu
290 295 300
Thr Gln Ser Ile Ser Glu Glu Lys Ala Ala Ile Ile Glu Arg Met His
305 310 315 320
Leu Arg Cys Gln Ser Lys Trp Val
325

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1365
- (D) OTHER INFORMATION: / Ceres Seq. ID 1585682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

atgcttcttg ataccgccag caatgggaat ttccagaaca aagatgttga agaaggctgg 60
gaattgggtg agaaccttgc tcaatcagat ggcaattaca acgaagactg tgataggacc 120
gtcaaaggaa cagctgactc tgatgacaaa cacaggaaga agatcaaagc gctgaatgac 180
aagctggaca ggattattct cggccagcag aagcatgtgc acttccttgt tgatgacgag 240
cagtatcaag tcanagacgg ggagggtaac cagttggaag aagtcagcta catcaacaac 300
aaccagggtg gctacaaaag atacaacaac ttcaaaacca acaatcccaa cctctcttac 360
cgcagcacca acgttgctaa ccctcaggat caagtgtatc ctccacagca acaacaaagt 420
ttogttccta agcagcagtt ccaggggaaac taccagcaac caccaccacc tgggtttgca 480
cctcagcaaa cccaagggtc tgctgtcctt gatgtgaaa tgaaacagat ggtcaagcag 540
ctgctacagg gacaagcatc tagtcaatg gaaatggcta aaaaattatc taaattgcac 600
cataagctgg actgcagcta caatgacctg aatgccaaag tggaggcatt gaataccaaa 660
gtcagatact tggaaggcca atcagtatct acctctgtac caaaagttac aggacttcca 720
gggaagtcca tacagaatcc aaaagagtat gcaaccgctc acgccatcac catctgccat 780
gatcgagagc tgccaactcg acctgtcctt gatttcatca ctggggacaa tgatgttcaa 840
gaagggaagg cttctactca ggttgtagtc tctgttgttg aattcaacca ttccgctggt 900
tctcgccatc tcaactcaatc catctcggaa gaaaaggccg ccataatcga gagaatggta 960
aaacgattca aacctactcc actaccctca cgtgctcttc cttggacatt caggaaagca 1020
tggtatggaga gatacaagtc tgttgcagag aagcagctag acgagattga agcagtgatg 1080
ccattgatgg aagttctcaa cctgattccc gatcctcaca aagatgtgag aaatttgata 1140
ctggaaagaa tcaagatgta tcacgattca gatgatgaaa gtgatgccac tccgtctcta 1200
gctgctgata agaggattgt tcaagagaag ttagaagatc ctggattgat acaaagggtt 1260
ttctgtgtca attccctaaa tgcattttat gtcattgcag catttaaggt gtcaatccaa 1320
atgggtgtaa ttgctatcaa tcaggatatg atcaaagaat actaa

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..454
- (D) OTHER INFORMATION: / Ceres Seq. ID 1585683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

00000000 00000000

Met Leu Leu Asp Thr Ala Ser Asn Gly Asn Phe Gln Asn Lys Asp Val
1 5 10 15
Glu Glu Gly Trp Glu Leu Val Glu Asn Leu Ala Gln Ser Asp Gly Asn
20 25 30
Tyr Asn Glu Asp Cys Asp Arg Thr Val Lys Gly Thr Ala Asp Ser Asp
35 40 45
Asp Lys His Arg Lys Lys Ile Lys Ala Leu Asn Asp Lys Leu Asp Arg
50 55 60
Ile Ile Leu Gly Gln Gln Lys His Val His Phe Leu Val Asp Asp Glu
65 70 75 80
Gln Tyr Gln Val Xaa Asp Gly Glu Gly Asn Gln Leu Glu Glu Val Ser
85 90 95
Tyr Ile Asn Asn Asn Gln Gly Gly Tyr Lys Arg Tyr Asn Asn Phe Lys
100 105 110
Thr Asn Asn Pro Asn Leu Ser Tyr Arg Ser Thr Asn Val Ala Asn Pro
115 120 125
Gln Asp Gln Val Tyr Pro Pro Gln Gln Gln Gln Ser Phe Val Pro Lys
130 135 140
Gln Gln Phe Gln Gly Asn Tyr Gln Gln Pro Pro Pro Gly Phe Ala
145 150 155 160
Pro Gln Gln Thr Gln Gly Pro Ala Ala Pro Asp Ala Glu Met Lys Gln
165 170 175
Met Val Lys Gln Leu Leu Gln Gly Gln Ala Ser Ser Ser Met Glu Met
180 185 190
Ala Lys Lys Leu Ser Lys Leu His His Lys Leu Asp Cys Ser Tyr Asn
195 200 205
Asp Leu Asn Ala Lys Val Glu Ala Leu Asn Thr Lys Val Arg Tyr Leu
210 215 220
Glu Gly Gln Ser Val Ser Thr Ser Val Pro Lys Val Thr Gly Leu Pro
225 230 235 240
Gly Lys Ser Ile Gln Asn Pro Lys Glu Tyr Ala Thr Ala His Ala Ile
245 250 255
Thr Ile Cys His Asp Arg Glu Leu Pro Thr Arg Pro Val Leu Asp Phe
260 265 270
Ile Thr Gly Asp Asn Asp Val Gln Glu Gly Lys Ala Ser Thr Gln Val
275 280 285
Val Val Ser Val Val Glu Phe Asn His Ser Ala Gly Ser Arg His Leu
290 295 300
Thr Gln Ser Ile Ser Glu Glu Lys Ala Ala Ile Ile Glu Arg Met Val
305 310 315 320
Lys Arg Phe Lys Pro Thr Pro Leu Pro Ser Arg Ala Leu Pro Trp Thr
325 330 335
Phe Arg Lys Ala Trp Met Glu Arg Tyr Lys Ser Val Ala Glu Lys Gln
340 345 350
Leu Asp Glu Ile Glu Ala Val Met Pro Leu Met Glu Val Leu Asn Leu
355 360 365
Ile Pro Asp Pro His Lys Asp Val Arg Asn Leu Ile Leu Glu Arg Ile
370 375 380
Lys Met Tyr His Asp Ser Asp Asp Glu Ser Asp Ala Thr Pro Ser Leu
385 390 395 400
Ala Ala Asp Lys Arg Ile Val Gln Glu Lys Leu Glu Asp Pro Gly Leu
405 410 415
Ile Gln Arg Val Phe Cys Val Asn Ser Leu Asn Ala Ser Tyr Val Ile
420 425 430
Ala Ala Phe Lys Val Ser Ile Gln Met Gly Val Ile Ala Ile Asn Gln
435 440 445
Asp Met Ile Lys Glu Tyr
450

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 amino acids

00000000 00000000

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..281
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

Met Lys Gln Met Val Lys Gln Leu Leu Gln Gly Gln Ala Ser Ser Ser
1 5 10 15
Met Glu Met Ala Lys Lys Leu Ser Lys Leu His His Lys Leu Asp Cys
20 25 30
Ser Tyr Asn Asp Leu Asn Ala Lys Val Glu Ala Leu Asn Thr Lys Val
35 40 45
Arg Tyr Leu Glu Gly Gln Ser Val Ser Thr Ser Val Pro Lys Val Thr
50 55 60
Gly Leu Pro Gly Lys Ser Ile Gln Asn Pro Lys Glu Tyr Ala Thr Ala
65 70 75 80
His Ala Ile Thr Ile Cys His Asp Arg Glu Leu Pro Thr Arg Pro Val
85 90 95
Leu Asp Phe Ile Thr Gly Asp Asn Asp Val Gln Glu Gly Lys Ala Ser
100 105 110
Thr Gln Val Val Val Ser Val Val Glu Phe Asn His Ser Ala Gly Ser
115 120 125
Arg His Leu Thr Gln Ser Ile Ser Glu Glu Lys Ala Ala Ile Ile Glu
130 135 140
Arg Met Val Lys Arg Phe Lys Pro Thr Pro Leu Pro Ser Arg Ala Leu
145 150 155 160
Pro Trp Thr Phe Arg Lys Ala Trp Met Glu Arg Tyr Lys Ser Val Ala
165 170 175
Glu Lys Gln Leu Asp Glu Ile Glu Ala Val Met Pro Leu Met Glu Val
180 185 190
Leu Asn Leu Ile Pro Asp Pro His Lys Asp Val Arg Asn Leu Ile Leu
195 200 205
Glu Arg Ile Lys Met Tyr His Asp Ser Asp Asp Glu Ser Asp Ala Thr
210 215 220
Pro Ser Leu Ala Ala Asp Lys Arg Ile Val Gln Glu Lys Leu Glu Asp
225 230 235 240
Pro Gly Leu Ile Gln Arg Val Phe Cys Val Asn Ser Leu Asn Ala Ser
245 250 255
Tyr Val Ile Ala Ala Phe Lys Val Ser Ile Gln Met Gly Val Ile Ala
260 265 270
Ile Asn Gln Asp Met Ile Lys Glu Tyr
275 280

(2) INFORMATION FOR SEQ ID NO:454:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 825 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..825
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1585695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

atggtgaaag aaactcgtct tggaatcact gcaaagaaag atgaagattt tgggaagtgg	60
agaaagacca cactcaaggg tttgctccag aggttgcttg ggttacaaga gctgggtgat	120
aagaggacac agggacctcc ctttgaagcc gcgtgtatga ctcatggaga tgacaaaggt	180
ttagtattcc ctctaaaagt ggcacctgtt caagttgttg taatccatgt tcccatcaaa	240

(2) INFORMATION FOR SEQ ID NO:455:

(A) LENGTH: 274 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..274

(D) OTHER INFORMATION: / Ceres Seq. ID 1585696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

[illegible]

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 amino acids

CITY OF CHICAGO	
OFFICE OF THE COMPTROLLER	
FINANCIAL STATEMENTS	
FOR THE YEAR ENDED DECEMBER 31, 2011	
INDEPENDENT AUDITORS' REPORT The Board of Commissioners City of Chicago 111 North La Salle Street Chicago, Illinois 60602	
REPORT OF THE INDEPENDENT AUDITORS We have audited the financial statements of the City of Chicago for the year ended December 31, 2011, which include the balance sheet, statement of revenues, expenses and changes in fund balances, and statement of assets and liabilities. These financial statements are the responsibility of the City of Chicago's management. Our responsibility is to express an opinion on these financial statements based on our audit.	
We conducted our audit in accordance with the auditing standards generally accepted in the United States of America. Those standards require that we plan and perform the audit to obtain reasonable assurance about whether the financial statements are free of material misstatement. An audit includes examining, on a test basis, evidence supporting the amounts and disclosures in the financial statements. An audit also includes assessing the accounting principles used and significant estimates made by management, as well as evaluating the overall presentation of the financial statements. We believe that our audit provides a reasonable basis for our opinion.	
OPINION In our opinion, the financial statements of the City of Chicago for the year ended December 31, 2011, present fairly in all material aspects the financial position, results of operations, and changes in fund balances of the City of Chicago as of and for the year ended December 31, 2011, in accordance with the accounting principles generally accepted in the United States of America.	
OTHER MATTERS The accompanying notes are an integral part of these financial statements.	
INDEPENDENT AUDITORS KPMG LLP 111 North La Salle Street Chicago, Illinois 60602	

(D) TOPOLOGY: linear

Met	Glu	Met	Asp	Pro	Glu	Leu	Phe	Glu	Glu	Cys	Gln	Arg	Gln	Tyr	Glu
1			5					10						15	
Glu	Lys	Gln	Ala	Lys	Ser	Lys	Glu	Val	Glu	Glu	Gln	Pro	Ile	Tyr	Met
			20					25					30		
Glu	Glu	Ile	Ser	Arg	Ser	Ser	Gly	Gly	Ala	Arg	Trp	Arg	Arg	Arg	Arg

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:																
Met	Ala	Pro	Pro	Lys	Pro	Gly	Gly	Lys	Ala	Lys	Lys	Val	Val	Gly	Val	
1				5				10						15		
Ile	Lys	Leu	Ala	Leu	Glu	Ala	Gly	Lys	Ala	Thr	Pro	Ala	Pro	Pro	Val	
			20					25					30			
Gly	Pro	Ala	Leu	Gly	Ser	Lys	Gly	Val	Asn	Ile	Met	Ala	Phe	Cys	Lys	
		35					40					45				
Asp	Tyr	Asn	Ala	Arg	Thr	Ala	Asp	Lys	Ala	Gly	Tyr	Ile	Ile	Pro	Val	
	50					55					60					
Glu	Ile	Thr	Val	Phe	Asp	Asp	Lys	Ser	Phe	Thr	Phe	Ile	Leu	Lys	Thr	
65					70					75					80	
Pro	Pro	Ala	Ser	Val	Leu	Leu	Lys	Ala	Ala	Gly	Val	Glu	Lys	Gly		
				85				90					95			
Ser	Lys	Asp	Pro	Gln	Gln	Asp	Lys	Val	Gly	Val	Ile	Thr	Ile	Asp	Gln	
			100					105					110			
Leu	Arg	Thr	Ile	Ala	Ala	Glu	Lys	Leu	Pro	Asp	Leu	Asn	Cys	Thr	Thr	
		115					120					125				
Ile	Glu	Ser	Ala	Met	Arg	Ile	Ile	Ala	Gly	Thr	Ala	Ala	Asn	Met	Gly	
	130						135				140					
Ile	Asp	Ile	Asp	Pro	Pro	Ile	Leu	Glu	Pro	Lys	Lys	Lys	Ala	Val	Leu	
145					150					155					160	

(2) INFORMATION FOR SEQ ID NO:463:

(A) LENGTH: 118 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1585742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

(2) INFORMATION FOR SEQ ID NO:464:

(A) LENGTH: 866 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..866

(D) OTHER INFORMATION: / Ceres Seq. ID 1585784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

(2) INFORMATION FOR SEQ ID NO:465:

(A) LENGTH: 288 amino acids

(B) TYPE: amino acid

Leu	Glu	Glu	Val	Met	Asp	Phe	Leu	Glu	Glu	Ala	Phe	Pro	Asp	Ile	Asp
1				5					10					15	
Ile	Ala	Met	Ala	His	Gly	Lys	Gln	Tyr	Ser	Lys	Gln	Leu	Glu	Glu	Thr
			20					25					30		
Met	Glu	Arg	Phe	Ala	Gln	Gly	Lys	Ile	Lys	Ile	Leu	Ile	Cys	Thr	Asn
		35					40					45			
Ile	Val	Glu	Ser	Gly	Leu	Asp	Ile	Gln	Asn	Ala	Asn	Thr	Ile	Ile	Ile
	50					55					60				
Gln	Asp	Val	Gln	Gln	Phe	Gly	Leu	Ala	Gln	Leu	Tyr	Gln	Leu	Arg	Gly
65					70					75					80
Arg	Val	Gly	Arg	Ala	Asp	Lys	Glu	Ala	His	Ala	Tyr	Leu	Phe	Tyr	Pro
				85					90					95	
Asp	Lys	Ser	Leu	Leu	Ser	Asp	Gln	Ala	Leu	Glu	Arg	Leu	Ser	Ala	Leu
			100					105					110		
Glu	Glu	Cys	Arg	Glu	Leu	Gly	Gln	Gly	Phe	Gln	Leu	Ala	Glu	Lys	Asp
		115					120					125			
Met	Gly	Ile	Arg	Gly	Phe	Gly	Thr	Ile	Phe	Gly	Glu	Gln	Gln	Thr	Gly
	130					135					140				
Asp	Val	Gly	Asn	Val	Gly	Ile	Asp	Leu	Phe	Phe	Glu	Met	Leu	Phe	Glu
145					150					155					160
Ser	Leu	Ser	Lys	Val	Glu	Glu	Leu	Arg	Ile	Phe	Ser	Val	Pro	Tyr	Asp
				165					170					175	
Leu	Val	Lys	Ile	Asp	Ile	Asn	Ile	Asn	Pro	Arg	Leu	Pro	Ser	Glu	Tyr
			180					185					190		
Val	Asn	Tyr	Leu	Glu	Asn	Pro	Met	Glu	Ile	Ile	His	Glu	Ala	Glu	Lys
		195					200					205			
Ala	Ala	Glu	Lys	Asp	Met	Trp	Ser	Leu	Met	Gln	Phe	Thr	Glu	Asn	Leu
		210				215					220				
Arg	Arg	Gln	Tyr	Gly	Lys	Glu	Pro	Tyr	Ser	Met	Glu	Ile	Ile	Leu	Lys
225					230					235				240	
Lys	Leu	Tyr	Val	Arg	Arg	Met	Ala	Ala	Asp	Leu	Gly	Val	Asn	Arg	Ile
				245					250					255	
Tyr	Ala	Ser	Gly	Lys	Met	Val	Val	Met	Lys	Thr	Asn	Met	Ser	Lys	Lys
			260					265					270		
Val	Phe	Lys	Leu	Ile	Thr	Asp	Ser	Met	Thr	Cys	Asp	Val	Tyr	Arg	Arg
		275					280					285			

Met Asp Phe Leu Glu Glu Ala Phe Pro Asp Ile Asp Ile Ala Met Ala
1 5 10 15
His Gly Lys Gln Tyr Ser Lys Gln Leu Glu Glu Thr Met Glu Arg Phe

Variable	Mean	SD	Min	Max
Age	34.5	10.5	20	55
Gender	50%	50%	Male	Female
Marital status	65%	35%	Married	Single
Education	12.5	1.5	10	15
Income	3500	1500	1000	6000
Occupation	30%	70%	Professional	Non-professional
Religion	80%	20%	Muslim	Other
Health status	75%	25%	Good	Poor
Smoking status	40%	60%	Smoker	Non-smoker
Alcohol consumption	10%	90%	Drinker	Non-drinker
Exercise frequency	2.5	1.5	0	5
Stress level	4.5	1.5	1	7
Sleep quality	3.5	1.5	1	7
Life satisfaction	5.5	1.5	1	7
Depression score	15	10	0	40
Anxiety score	20	15	0	50
Quality of life score	60	10	30	90

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..270

- (D) OTHER INFORMATION: / Ceres Seq. ID 1585787

Met	Ala	His	Gly	Lys	Gln	Tyr	Ser	Lys	Gln	Leu	Glu	Glu	Thr	Met	Glu
1				5					10					15	
Arg	Phe	Ala	Gln	Gly	Lys	Ile	Lys	Ile	Leu	Ile	Cys	Thr	Asn	Ile	Val
		20					25						30		
Glu	Ser	Gly	Leu	Asp	Ile	Gln	Asn	Ala	Asn	Thr	Ile	Ile	Ile	Gln	Asp
		35				40					45				
Val	Gln	Gln	Phe	Gly	Leu	Ala	Gln	Leu	Tyr	Gln	Leu	Arg	Gly	Arg	Val
	50					55				60					
Gly	Arg	Ala	Asp	Lys	Glu	Ala	His	Ala	Tyr	Leu	Phe	Tyr	Pro	Asp	Lys
65				70						75				80	
Ser	Leu	Leu	Ser	Asp	Gln	Ala	Leu	Glu	Arg	Leu	Ser	Ala	Leu	Glu	Glu
			85					90					95		
Cys	Arg	Glu	Leu	Gly	Gln	Gly	Phe	Gln	Leu	Ala	Glu	Lys	Asp	Met	Gly
		100				105						110			
Ile	Arg	Gly	Phe	Gly	Thr	Ile	Phe	Gly	Glu	Gln	Gln	Thr	Gly	Asp	Val
	115					120						125			

Gly Asn Val Gly Ile Asp Leu Phe Phe Glu Met Leu Phe Glu Ser Leu
130 135 140
Ser Lys Val Glu Glu Leu Arg Ile Phe Ser Val Pro Tyr Asp Leu Val
145 150 155 160
Lys Ile Asp Ile Asn Ile Asn Pro Arg Leu Pro Ser Glu Tyr Val Asn
165 170 175
Tyr Leu Glu Asn Pro Met Glu Ile Ile His Glu Ala Glu Lys Ala Ala
180 185 190
Glu Lys Asp Met Trp Ser Leu Met Gln Phe Thr Glu Asn Leu Arg Arg
195 200 205
Gln Tyr Gly Lys Glu Pro Tyr Ser Met Glu Ile Ile Leu Lys Lys Leu
210 215 220
Tyr Val Arg Arg Met Ala Ala Asp Leu Gly Val Asn Arg Ile Tyr Ala
225 230 235 240
Ser Gly Lys Met Val Val Met Lys Thr Asn Met Ser Lys Lys Val Phe
245 250 255
Lys Leu Ile Thr Asp Ser Met Thr Cys Asp Val Tyr Arg Arg
260 265 270

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..519
- (D) OTHER INFORMATION: / Ceres Seq. ID 1585887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

atgccctttcc	tacctccact	aaagcctcca	accgagttgt	atctaggaat	ccaattgcc	60
aaccccataa	gcatacttgt	caactacctc	ccagtcagcc	aaactcccat	agagacgcta	120
gggaacttag	tctacacttg	tgacatcaac	acccttgcaa	ttgatgaatt	catgacgtgg	180
ccgactttgc	tccaaccgga	ttctaccttc	cgcccttact	tcgagctgct	gctagaacgt	240
ggaccaatcc	cggcggttta	ccttgaaggt	gttcgccaag	cgagcaactt	cgtcacagta	300
gctcagggcc	ttttgctcat	gacaacggtc	gcattttctg	atccctttgc	ttgctttgcc	360
accggtttgt	tccttacgtg	taccggtaat	cacttggatt	tcctcccaat	cagcgagaag	420
ttctgggaaa	tgacactcac	ccttgaagca	ggccacacgg	ttagagagat	ggtgatgtat	480
cacatcagcc	agcttcacac	taaggctgct	cgccactag			

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..172
- (D) OTHER INFORMATION: / Ceres Seq. ID 1585888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

Met	Pro	Phe	Leu	Pro	Pro	Leu	Lys	Pro	Thr	Glu	Leu	Tyr	Leu	Gly
1			5					10					15	
Ile	Gln	Leu	Pro	Asn	Pro	Ile	Ser	Ile	Leu	Val	Asn	Tyr	Leu	Pro
		20					25				30			
Ser	Gln	Thr	Pro	Ile	Glu	Thr	Leu	Gly	Asn	Leu	Val	Tyr	Thr	Cys
		35				40					45			
Ile	Asn	Thr	Leu	Ala	Ile	Asp	Glu	Phe	Met	Thr	Trp	Pro	Thr	Leu
	50				55			60						
Gln	Pro	Asp	Ser	Thr	Phe	Arg	Pro	Tyr	Phe	Glu	Leu	Leu	Leu	Glu
65				70				75					80	

(2) INFORMATION FOR SEQ ID NO:470:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1585890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

[illegible]

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 678 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..678

(D) OTHER INFORMATION: / Ceres Seq. ID 1585950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

gaagacttaa	aatcttttgcg	tgcaaaaatc	gctatgctgg	aggaggaatt	gcgtaaatct	60
gcacaagatt	cttctgagta	tcaccacctt	gtcaggaatc	ttgagaatga	ggtaaaagat	120
ctgaaagatc	aggaacaaca	agggaagcaa	aagacaacta	aagtaatctc	ggaccttctc	180
atatctgttt	ccaaaactga	gagacaagaa	gcaagaacga	aagtacagaaa	tgaatctttg	240
cgattagcca	gtgttggtgt	tctcaggaca	ggaacgatca	tagctgagac	atgggaggac	300
ggacaaatgt	taaaagatct	gaatgctcaa	cttagacaat	tgctggaac	caaggaggct	360
attgagagac	aaagaaagtt	acttaagaaa	cgacaaaatg	gtgataagaa	tgacggaaact	420
gacacagaat	caggagcaca	ggaggaagat	atcatccctg	acgaggttta	caagctctcgt	480
cttactagta	ttaagcggga	agaggaagct	gttttgctg	agagagaaaag	gtacacatta	540

Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
18-24	20.5 (2.5)
25-34	29.5 (4.5)
35-44	39.5 (5.5)
45-54	49.5 (6.5)
55-64	59.5 (7.5)
65-74	69.5 (8.5)
75-84	79.5 (9.5)
85-94	89.5 (10.5)
95-104	99.5 (11.5)
105-114	109.5 (12.5)
115-124	119.5 (13.5)
125-134	129.5 (14.5)
135-144	139.5 (15.5)
145-154	149.5 (16.5)
155-164	159.5 (17.5)
165-174	169.5 (18.5)
175-184	179.5 (19.5)
185-194	189.5 (20.5)
195-204	199.5 (21.5)
205-214	209.5 (22.5)
215-224	219.5 (23.5)
225-234	229.5 (24.5)
235-244	239.5 (25.5)
245-254	249.5 (26.5)
255-264	259.5 (27.5)
265-274	269.5 (28.5)
275-284	279.5 (29.5)
285-294	289.5 (30.5)
295-304	299.5 (31.5)
305-314	309.5 (32.5)
315-324	319.5 (33.5)
325-334	329.5 (34.5)
335-344	339.5 (35.5)
345-354	349.5 (36.5)
355-364	359.5 (37.5)
365-374	369.5 (38.5)
375-384	379.5 (39.5)
385-394	389.5 (40.5)
395-404	399.5 (41.5)
405-414	409.5 (42.5)
415-424	419.5 (43.5)
425-434	429.5 (44.5)
435-444	439.5 (45.5)
445-454	449.5 (46.5)
455-464	459.5 (47.5)
465-474	469.5 (48.5)
475-484	479.5 (49.5)
485-494	489.5 (50.5)
495-504	499.5 (51.5)
505-514	509.5 (52.5)
515-524	519.5 (53.5)
525-534	529.5 (54.5)
535-544	539.5 (55.5)
545-554	549.5 (56.5)
555-564	559.5 (57.5)
565-574	569.5 (58.5)
575-584	579.5 (59.5)
585-594	589.5 (60.5)
595-604	599.5 (61.5)
605-614	609.5 (62.5)
615-624	619.5 (63.5)
625-634	629.5 (64.5)
635-644	639.5 (65.5)
645-654	649.5 (66.5)
655-664	659.5 (67.5)
665-674	669.5 (68.5)
675-684	679.5 (69.5)
685-694	689.5 (70.5)
695-704	699.5 (71.5)
705-714	709.5 (72.5)
715-724	719.5 (73.5)
725-734	729.5 (74.5)
735-744	739.5 (75.5)
745-754	749.5 (76.5)
755-764	759.5 (77.5)
765-774	769.5 (78.5)
775-784	779.5 (79.5)
785-794	789.5 (80.5)
795-804	799.5 (81.5)
805-814	809.5 (82.5)
815-824	819.5 (83.5)
825-834	829.5 (84.5)
835-844	839.5 (85.5)
845-854	849.5 (86.5)
855-864	859.5 (87.5)
865-874	869.5 (88.5)
875-884	879.5 (89.5)
885-894	889.5 (90.5)
895-904	899.5 (91.5)
905-914	909.5 (92.5)
915-924	919.5 (93.5)
925-934	929.5 (94.5)
935-944	939.5 (95.5)
945-954	949.5 (96.5)
955-964	959.5 (97.5)
965-974	969.5 (98.5)
975-984	979.5 (99.5)
985-994	989.5 (100.5)
995-1004	999.5 (101.5)
1005-1014	1009.5 (102.5)
1015-1024	1019.5 (103.5)
1025-1034	1029.5 (104.5)
1035-1044	1039.5 (105.5)
1045-1054	1049.5 (106.5)
1055-1064	1059.5 (107.5)
1065-1074	1069.5 (108.5)
1075-1084	1079.5 (109.5)
1085-1094	1089.5 (110.5)
1095-1104	1099.5 (111.5)
1105-1114	1109.5 (112.5)
1115-1124	1119.5 (113.5)
1125-1134	

gagaaggggc tacttatgag ggagatgaaa cgcatacgag atgaagatgg ttctcgtttc 600
aaccatttcc cagttttgaa tagccgctat gctcttctaa atcttcttgg taaaggcgga 660
tttagtgaag tctataag

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..226
- (D) OTHER INFORMATION: / Ceres Seq. ID 1585951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

Glu Asp Leu Lys Ser Leu Arg Ala Lys Ile Ala Met Leu Glu Glu Glu
1 5 10 15
Leu Arg Lys Ser Arg Gln Asp Ser Ser Glu Tyr His His Leu Val Arg
20 25 30
Asn Leu Glu Asn Glu Val Lys Asp Leu Lys Asp Gln Glu Gln Gln Gly
35 40 45
Lys Gln Lys Thr Thr Lys Val Ile Ser Asp Leu Leu Ile Ser Val Ser
50 55 60
Lys Thr Glu Arg Gln Glu Ala Arg Thr Lys Val Arg Asn Glu Ser Leu
65 70 75 80
Arg Leu Gly Ser Val Gly Val Leu Arg Thr Gly Thr Ile Ile Ala Glu
85 90 95
Thr Trp Glu Asp Gly Gln Met Leu Lys Asp Leu Asn Ala Gln Leu Arg
100 105 110
Gln Leu Leu Glu Thr Lys Glu Ala Ile Glu Arg Gln Arg Lys Leu Leu
115 120 125
Lys Lys Arg Gln Asn Gly Asp Lys Asn Asp Gly Thr Asp Thr Glu Ser
130 135 140
Gly Ala Gln Glu Glu Asp Ile Ile Pro Asp Glu Val Tyr Lys Ser Arg
145 150 155 160
Leu Thr Ser Ile Lys Arg Glu Glu Glu Ala Val Leu Arg Glu Arg Glu
165 170 175
Arg Tyr Thr Leu Glu Lys Gly Leu Leu Met Arg Glu Met Lys Arg Ile
180 185 190
Arg Asp Glu Asp Gly Ser Arg Phe Asn His Phe Pro Val Leu Asn Ser
195 200 205
Arg Tyr Ala Leu Leu Asn Leu Leu Gly Lys Gly Gly Phe Ser Glu Val
210 215 220
Tyr Lys
225

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..215
- (D) OTHER INFORMATION: / Ceres Seq. ID 1585952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

Met Leu Glu Glu Glu Leu Arg Lys Ser Arg Gln Asp Ser Ser Glu Tyr
1 5 10 15
His His Leu Val Arg Asn Leu Glu Asn Glu Val Lys Asp Leu Lys Asp
20 25 30

DOE FOR "086689550

Gln Glu Gln Gln Gly Lys Gln Lys Thr Thr Lys Val Ile Ser Asp Leu
35 40 45
Leu Ile Ser Val Ser Lys Thr Glu Arg Gln Glu Ala Arg Thr Lys Val
50 55 60
Arg Asn Glu Ser Leu Arg Leu Gly Ser Val Gly Val Leu Arg Thr Gly
65 70 75 80
Thr Ile Ile Ala Glu Thr Trp Glu Asp Gly Gln Met Leu Lys Asp Leu
85 90 95
Asn Ala Gln Leu Arg Gln Leu Leu Glu Thr Lys Glu Ala Ile Glu Arg
100 105 110
Gln Arg Lys Leu Leu Lys Lys Arg Gln Asn Gly Asp Lys Asn Asp Gly
115 120 125
Thr Asp Thr Glu Ser Gly Ala Gln Glu Glu Asp Ile Ile Pro Asp Glu
130 135 140
Val Tyr Lys Ser Arg Leu Thr Ser Ile Lys Arg Glu Glu Glu Ala Val
145 150 155 160
Leu Arg Glu Arg Glu Arg Tyr Thr Leu Glu Lys Gly Leu Leu Met Arg
165 170 175
Glu Met Lys Arg Ile Arg Asp Glu Asp Gly Ser Arg Phe Asn His Phe
180 185 190
Pro Val Leu Asn Ser Arg Tyr Ala Leu Leu Asn Leu Leu Gly Lys Gly
195 200 205
Gly Phe Ser Glu Val Tyr Lys
210 215

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1585953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

Met Leu Lys Asp Leu Asn Ala Gln Leu Arg Gln Leu Leu Glu Thr Lys
1 5 10 15
Glu Ala Ile Glu Arg Gln Arg Lys Leu Leu Lys Lys Arg Gln Asn Gly
20 25 30
Asp Lys Asn Asp Gly Thr Asp Thr Glu Ser Gly Ala Gln Glu Glu Asp
35 40 45
Ile Ile Pro Asp Glu Val Tyr Lys Ser Arg Leu Thr Ser Ile Lys Arg
50 55 60
Glu Glu Glu Ala Val Leu Arg Glu Arg Glu Arg Tyr Thr Leu Glu Lys
65 70 75 80
Gly Leu Leu Met Arg Glu Met Lys Arg Ile Arg Asp Glu Asp Gly Ser
85 90 95
Arg Phe Asn His Phe Pro Val Leu Asn Ser Arg Tyr Ala Leu Leu Asn
100 105 110
Leu Leu Gly Lys Gly Gly Phe Ser Glu Val Tyr Lys
115 120

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

DOE FOR "00668950"

(B) LOCATION: 1..1596

(D) OTHER INFORMATION: / Ceres Seq. ID 1586052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

atgtcgaaag	cttgggggtg	aattggaatt	ggagcttggg	ctgatgaagc	agagcgtgcc	60
gatgaagaac	aagcggcgga	agctactgct	gcgacggcgg	atacacagag	ttttcctagc	120
ctgagagagg	ctgctgctgc	gactgcgact	agtggtaagt	ctaggaagat	gaagaagatg	180
agtttatctg	agtttactac	aggtgcttat	acagcacctg	gaggtagaaa	ctctgttgga	240
ttgactcagc	aagagattct	tcaattacct	actggtccta	gacaacgttc	cgaggaggaa	300
atgcaacctg	gtcgttttag	cggtgggttt	tcatcttatg	gtggtcggtc	tggtggaaga	360
attggggagag	atcgagatga	ttctgatggc	tcttggaagt	gtggtggtgg	tggtggtgna	420
agragacctt	atgggtggtg	atttgatgat	gtagggaggg	ggaatcagtc	tagggtttcg	480
gattttcctc	aaccttctag	agctgatgag	gttgatgatt	gggggaaaga	gaagaaacca	540
cttccctctt	ttgatcaagg	acgacaaggt	cgttacagtg	gcggtggtgg	tggttttgga	600
gggtggtgga	gtggttttgg	aggcgggtgt	ggtggaggtg	gaggattatc	tagagctgat	660
gatgttgata	attgggggtg	agggaaaagg	caagcaccgg	ttagatcatt	tacatttggt	720
tcgagttttg	gtgattcagg	tcaggaagaa	cgctcgctgt	tggttttgga	accacggaag	780
gttgagtcag	gagggagtga	gactccacct	gttggtgaga	agacgagtaa	gccgaatcca	840
tttggggcag	ctagaccgag	ggaggatggt	ttggcggaga	aaggtttgga	ttggaagaag	900
attgactcag	atattgaggc	taagaaagga	agttctcaaa	caagtaggcc	aacgagtgca	960
cattctagta	gaccttctag	tgctcaatct	aacagggtct	agagtccagg	attgaataat	1020
gtggtgaaac	cgagacaaaa	ggtgaatcct	tttgccgatg	caaagcctcg	agaagtgttg	1080
ttagaggaac	aaggggaagga	ttggcgtaag	atggatttgg	aactcgagca	tcgcagggtt	1140
gacaggcctg	aaacagaaga	agagaagatg	ttgaaagaag	agattgaaga	gctaaggaaa	1200
aaactcgaga	aggaatccat	tgctccagag	atcaaggaa	ctgatcaaga	acctggcagt	1260
aataataatc	acaatgatgt	accagaaata	atacgtggga	aagagaaaga	tctggaaata	1320
ctaaccctgt	aattggacga	caaagtcagg	ttcaggcaga	aaccagttga	gaggcccggt	1380
tctggtgcag	gtagaaccgg	aacatattca	gaaagaacac	attcccgggc	tggtccaatt	1440
gatgaaacca	ggagttttga	atctacagag	agaccagat	cacgtggtgc	cgctgatgcc	1500
tggttagac	cagccgatga	gcagcgaaga	aactttcaag	gaagcaaaga	gcgcggattc	1560
ttcagcaaca	ggtcttcttc	tagggaagga	tggttaa			

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 531 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..531

(D) OTHER INFORMATION: / Ceres Seq. ID 1586053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

Met	Ser	Lys	Ala	Trp	Gly	Gly	Ile	Gly	Ile	Gly	Ala	Trp	Ala	Asp	Glu
1		5						10						15	
Ala	Glu	Arg	Ala	Asp	Glu	Glu	Gln	Ala	Ala	Glu	Ala	Thr	Ala	Ala	Thr
		20						25				30			
Ala	Asp	Thr	Gln	Ser	Phe	Pro	Ser	Leu	Arg	Glu	Ala	Ala	Ala	Ala	Thr
		35					40					45			
Ala	Thr	Ser	Gly	Lys	Ser	Arg	Lys	Met	Lys	Lys	Met	Ser	Leu	Ser	Glu
		50				55					60				
Phe	Thr	Thr	Gly	Ala	Tyr	Thr	Ala	Pro	Gly	Gly	Arg	Asn	Ser	Val	Gly
65					70					75				80	
Leu	Thr	Gln	Gln	Glu	Ile	Leu	Gln	Leu	Pro	Thr	Gly	Pro	Arg	Gln	Arg
			85					90						95	
Ser	Glu	Glu	Glu	Met	Gln	Pro	Gly	Arg	Leu	Gly	Gly	Gly	Phe	Ser	Ser
		100					105						110		
Tyr	Gly	Gly	Arg	Ser	Gly	Gly	Arg	Ile	Gly	Arg	Asp	Arg	Asp	Asp	Ser
		115					120				125				
Asp	Gly	Ser	Trp	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Xaa	Xaa	Arg	Pro	Tyr
		130				135					140				
Gly	Gly	Gly	Phe	Asp	Asp	Asp	Arg	Arg	Gly	Asn	Gln	Ser	Arg	Val	Ser

DOCKET# 0000000000

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

FEATURE:

(B) LOCATION: 1..475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..495
- (D) OTHER INFORMATION: / Ceres Seq. ID 1586145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

gtttctttgt tctttaccga gtcccaaca aatccatttc ttcgatgtgt agatattaag	60
ttagtttcaa aaatctgtca tagaagagga actottgttt gtatagacgc taccattgca	120
acacctatca atcaaaagac acttgctctt ggtgctgac ttgttcacca ttctgtact	180
aagtacattg gaggccacaa cgattttcta gctggaagca tatccggttc aatggagttg	240
gtttccaaga ttcgcaattt gcataagctt ttgggaggca cgcttaatcc gaacgctgca	300
tatttactca tacgaggcat gaagacgatg catcttcgtg taagacaaca gaattcaacc	360
ggtatgaaga tggcccaagt gttagaagca catcccaagg tgagtcgctg ttactatcta	420
ggccttccga gtcattccga acatttaata gccaaagcgac aaatgactgg tattggtggc	480
ctgatctctt tcgag	

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1586146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

Val Ser Leu Phe Phe Thr Glu Ser Pro Thr Asn Pro Phe Leu Arg Cys	
1 5 10 15	
Val Asp Ile Lys Leu Val Ser Lys Ile Cys His Arg Arg Gly Thr Leu	
20 25 30	
Val Cys Ile Asp Ala Thr Ile Ala Thr Pro Ile Asn Gln Lys Thr Leu	
35 40 45	
Ala Leu Gly Ala Asp Leu Val His His Ser Ala Thr Lys Tyr Ile Gly	
50 55 60	
Gly His Asn Asp Phe Leu Ala Gly Ser Ile Ser Gly Ser Met Glu Leu	
65 70 75 80	
Val Ser Lys Ile Arg Asn Leu His Lys Leu Leu Gly Gly Thr Leu Asn	
85 90 95	
Pro Asn Ala Ala Tyr Leu Leu Ile Arg Gly Met Lys Thr Met His Leu	
100 105 110	
Arg Val Arg Gln Gln Asn Ser Thr Gly Met Lys Met Ala Gln Val Leu	
115 120 125	
Glu Ala His Pro Lys Val Ser Arg Val Tyr Tyr Leu Gly Leu Pro Ser	
130 135 140	
His Pro Glu His Leu Ile Ala Lys Arg Gln Met Thr Gly Ile Gly Gly	
145 150 155 160	
Leu Ile Ser Phe Glu	
165	

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

0968980-101300

(D) OTHER INFORMATION: / Ceres Seq. ID 1586147

Asn	Thr	Gly	Asp	Phe	Leu	Ile	Arg	Ala	Asn	Thr	Lys	Lys	Arg	Gln	Lys
1				5					10					15	
Val	Gln	Glu	Ser	Asn	Asn	Phe	Ser	Val	Val	Asp	His	Val	Glu	Pro	Gln
			20					25					30		
Glu	Ala	Ala	Tyr	Asp	Gly	Arg	Lys	Asn	Asp	Ala	Glu	Ser	Lys	Thr	Gly
			35				40					45			
Leu	Asp	Val	Ser	Lys	Lys	Lys	Gln	Gly	Arg	Gly	Arg	Ala	Ser	Ser	Thr
	50					55					60				
Gly	Arg	Gly	Arg	Gly	Ser	Lys	Thr	Asn	Asn	Asp	Val	Thr	Lys	Ser	Gln
65				70						75				80	
Phe	Val	Val	Ala	Pro	Val	Ser	Ala	Ala	Ser	Gln	Leu	Asp	Ala	Ser	Asp
				85					90					95	
Gln	Lys	Val	Ser	Ile	Val	Tyr	Leu	Ile	Gly	Pro	Tyr	Met	Glu	Pro	Leu

100 105 110
Phe Ser Ser Ser Arg Ile Tyr Ile Tyr Glu Thr
115 120

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..807
- (D) OTHER INFORMATION: / Ceres Seq. ID 1586187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

atggatttta	agcaggcata	tgatttggtg	gacccatagat	atgttgcggtg	caagcttcat	60
ggtttaaatg	ctcagtgagg	tgaagaaaag	aagcaaaagt	acatccgcca	tgccaacagg	120
gaatgtgaga	tccataaaaag	tcttggtgcat	caccacattg	ttcggttttg	ggataaattt	180
catatcgaca	tgcatatacatt	ctgcaccggt	ctggaatatt	gtagtgggaa	agaccttgat	240
gctgtatttaa	aggcaacatc	taatcttcct	gagaaagaag	caaggattat	cattgtgcaa	300
atagttcaag	gccttgata	tctgaacaaa	aagtcacaga	agataatcca	ctatgatctg	360
aagcctggta	atgttctctt	tgatgagttt	ggagtagcaa	aagtaactga	ttttggtcta	420
agcaagatag	tggaggacaa	tggttggttct	caaggaatgg	agcttacatc	acagggagct	480
ggaacatact	ggtacttgcc	cccagaatgc	tttgagctta	acaaaactcc	tatgatctca	540
tcaaagggtg	atgtatggtc	agttggtggt	ttgttttacc	aaatgctggt	tggaaagcga	600
ccttttggtg	atgaccaaag	ccaagaacgg	atactaagag	aagacacaa	cattaaagcc	660
aaaaagggtg	agttcccagt	aacaagacct	gccatctcaa	atgaagcgaa	ggatttgatt	720
cgacggtgtc	taacatataa	ccaagaagat	aggccggatg	ttctaacaat	ggcacaggat	780
ccatatcttg	cctactctaa	gaagtga				

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..268
- (D) OTHER INFORMATION: / Ceres Seq. ID 1586188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

Met	Asp	Phe	Lys	Gln	Ala	Tyr	Asp	Leu	Val	Asp	His	Arg	Tyr	Val	Ala	
1			5						10					15		
Cys	Lys	Leu	His	Gly	Leu	Asn	Ala	Gln	Trp	Ser	Glu	Glu	Lys	Lys	Gln	
			20					25					30			
Ser	Tyr	Ile	Arg	His	Ala	Asn	Arg	Glu	Cys	Glu	Ile	His	Lys	Ser	Leu	
		35					40					45				
Val	His	His	His	Ile	Val	Arg	Leu	Trp	Asp	Lys	Phe	His	Ile	Asp	Met	
	50					55					60					
His	Thr	Phe	Cys	Thr	Val	Leu	Glu	Tyr	Cys	Ser	Gly	Lys	Asp	Leu	Asp	
65				70					75					80		
Ala	Val	Leu	Lys	Ala	Thr	Ser	Asn	Leu	Pro	Glu	Lys	Glu	Ala	Arg	Ile	
			85					90						95		
Ile	Ile	Val	Gln	Ile	Val	Gln	Gly	Leu	Val	Tyr	Leu	Asn	Lys	Lys	Ser	
		100					105					110				
Gln	Lys	Ile	Ile	His	Tyr	Asp	Leu	Lys	Pro	Gly	Asn	Val	Leu	Phe	Asp	
	115					120					125					
Glu	Phe	Gly	Val	Ala	Lys	Val	Thr	Asp	Phe	Gly	Leu	Ser	Lys	Ile	Val	
	130					135					140					
Glu	Asp	Asn	Val	Gly	Ser	Gln	Gly	Met	Glu	Leu	Thr	Ser	Gln	Gly	Ala	
145					150					155					160	

0969980-10100

(2) INFORMATION FOR SEQ ID NO:485:

(A) LENGTH: 205 amino acids

(C) STRANDEDNESS:

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..205

(D) OTHER INFORMATION: / Ceres Seq. ID 1586190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

(2) INFORMATION FOR SEQ ID NO:486:

(A) LENGTH: 760 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

[illegible]

(D) OTHER INFORMATION: / Ceres Seq. ID 1586191

atggtatttta	agcaggcata	tgatttgggtg	gaccatagat	atgttgctgtg	caagcttcat	60
ggtttaaatg	ctcagtggag	tgaagaaaag	aagcaaagt	acatccgcca	tgccaacagg	120
gaatgtgaga	tocataaaag	tcttgtgcat	caccacattg	ttcggcttg	ggataaattt	180
catatcgaca	tgcatacatt	ctgcaccgtt	ctggaatatt	gtagtgggaa	agaccttgat	240
gctgtattaa	aggcaacatc	taatcttctt	gagaaagaag	caaggattat	cattgtgcaa	300
atagttcaag	gccttgtata	cttgaacaaa	aagtcacaga	agataatcca	ctatgatctg	360
aagcctggta	atgttctctt	tgatgagttt	ggagtagcaa	aagtaactga	ttttgggtcta	420
agcaagatag	tggaggacaa	tgttggttct	caagggaatg	agcttacatc	acagggagct	480
ggaacatact	ggtacttgcc	cccagaatgc	tttgagctta	acaaaactcc	tatgatctca	540
tcaaaggttg	atgtatggtc	agttgggtgt	ttgttttacc	aaatgctgtt	tggaaagcga	600
ccttttggtg	atgaccaaag	ccaaagaacg	atactaagag	aagacacaat	cattaaagcc	660
aaaaaggttg	agttcccgat	acaagaacct	gccattcca	atgaagcgaa	gaagaaagct	720
gaaagtgtga	aacagggccc	aaatcgttct	tgttctcag			

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..253

(D) OTHER INFORMATION: / Ceres Seq. ID 1586192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

Met	Asp	Phe	Lys	Gln	Ala	Tyr	Asp	Leu	Val	Asp	His	Arg	Tyr	Val	Ala
1				5					10					15	
Cys	Lys	Leu	His	Gly	Leu	Asn	Ala	Gln	Trp	Ser	Glu	Glu	Lys	Lys	Gln
			20					25					30		
Ser	Tyr	Ile	Arg	His	Ala	Asn	Arg	Glu	Cys	Glu	Ile	His	Lys	Ser	Leu
		35					40					45			
Val	His	His	His	Ile	Val	Arg	Leu	Trp	Asp	Lys	Phe	His	Ile	Asp	Met
	50					55					60				
His	Thr	Phe	Cys	Thr	Val	Leu	Glu	Tyr	Cys	Ser	Gly	Lys	Asp	Leu	Asp
65					70					75					80
Ala	Val	Leu	Lys	Ala	Thr	Ser	Asn	Leu	Pro	Glu	Lys	Glu	Ala	Arg	Ile
				85					90					95	
Ile	Ile	Val	Gln	Ile	Val	Gln	Gly	Leu	Val	Tyr	Leu	Asn	Lys	Lys	Ser
		100						105					110		
Gln	Lys	Ile	Ile	His	Tyr	Asp	Leu	Lys	Pro	Gly	Asn	Val	Leu	Phe	Asp
		115					120					125			
Glu	Phe	Gly	Val	Ala	Lys	Val	Thr	Asp	Phe	Gly	Leu	Ser	Lys	Ile	Val
	130					135					140				
Glu	Asp	Asn	Val	Gly	Ser	Gln	Gly	Met	Glu	Leu	Thr	Ser	Gln	Gly	Ala
145					150					155					160
Gly	Thr	Tyr	Trp	Tyr	Leu	Pro	Pro	Glu	Cys	Phe	Glu	Leu	Asn	Lys	Thr
				165					170					175	
Pro	Met	Ile	Ser	Ser	Lys	Val	Asp	Val	Trp	Ser	Val	Gly	Val	Leu	Phe
			180					185					190		
Tyr	Gln	Met	Leu	Phe	Gly	Lys	Arg	Pro	Phe	Gly	His	Asp	Gln	Ser	Gln
		195					200					205			
Glu	Arg	Ile	Leu	Arg	Glu	Asp	Thr	Ile	Ile	Lys	Ala	Lys	Lys	Val	Glu
	210					215					220				
Phe	Pro	Val	Thr	Arg	Pro	Ala	Ile	Ser	Asn	Glu	Ala	Lys	Lys	Lys	Ala
225					230					235					240
Glu	Ser	Trp	Lys	Gln	Ala	Pro	Asn	Arg	Ser	Cys	Phe	Ser			
				245					250						

(2) INFORMATION FOR SEQ ID NO:488:

[illegible]

99

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: / Ceres Seq. ID 1586196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

(2) INFORMATION FOR SEQ ID NO:491:

- (D) TOPOLOGY: linear

(ix) FEATURE:

- (B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1586197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

Met	Leu	Phe	Gln	Gly	Thr	Leu	Ser	Ile	Lys	Tyr	Pro	Cys	Lys	Tyr	Ser
1				5					10					15	
Ser	Thr	Cys	Leu	Met	Ser	Ile	Phe	Ala	Ala	Phe	Gln	Cys	Ala	Leu	Leu
			20					25					30		
Ser	Leu	Tyr	Lys	Ser	Arg	Asp	Val	Asn	Asp	Trp	Ile	Ile	Asp	Asp	Arg
			35				40					45			
Phe	Val	Ile	Thr	Val	Ile	Ile	Tyr	Ala	Gly	Val	Val	Gly	Gln	Ala	Met
	50					55					60				
Thr	Thr	Val	Ala	Thr	Thr	Trp	Gly	Ile	Lys	Lys	Leu	Gly	Ala	Val	Phe

65 70 75 80
Ala Ser Ala Phe Phe Pro Leu Thr Leu Ile Ser Ala Thr Leu Phe Asp
85 90 95
Phe Leu Ile Leu His Thr Pro Leu Tyr Leu Gly Ser Val Ile Gly Ser
100 105 110
Leu Val Thr Ile Thr Gly Leu Tyr Met Phe Leu Trp Gly Lys Asn Lys
115 120 125
Glu Thr Glu Ser Ser Thr Ala Leu Ser Ser Gly Met Asp Asn Glu Ala
130 135 140
Gln Tyr Thr Thr Pro Asn Lys Asp Asn Asp Ser Lys Ser Pro Val
145 150 155

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1586198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

Met Ser Ile Phe Ala Ala Phe Gln Cys Ala Leu Leu Ser Leu Tyr Lys
1 5 10 15
Ser Arg Asp Val Asn Asp Trp Ile Ile Asp Asp Arg Phe Val Ile Thr
20 25 30
Val Ile Ile Tyr Ala Gly Val Val Gly Gln Ala Met Thr Thr Val Ala
35 40 45
Thr Thr Trp Gly Ile Lys Lys Leu Gly Ala Val Phe Ala Ser Ala Phe
50 55 60
Phe Pro Leu Thr Leu Ile Ser Ala Thr Leu Phe Asp Phe Leu Ile Leu
65 70 75 80
His Thr Pro Leu Tyr Leu Gly Ser Val Ile Gly Ser Leu Val Thr Ile
85 90 95
Thr Gly Leu Tyr Met Phe Leu Trp Gly Lys Asn Lys Glu Thr Glu Ser
100 105 110
Ser Thr Ala Leu Ser Ser Gly Met Asp Asn Glu Ala Gln Tyr Thr Thr
115 120 125
Pro Asn Lys Asp Asn Asp Ser Lys Ser Pro Val
130 135

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1008 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1008

(D) OTHER INFORMATION: / Ceres Seq. ID 1586199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

gctttgttct taacatttta caaaggccca caaatatcaa actctcactc tcactctcac 60
ggtggggcctt cccacaacaa caacgatcaa gacaaggcca ataattggct tcttgatgt 120
ctttatttta ccataggaa agtggtgcta tctctatgga tgttgtttca agggacttta 180
agtattaagt acccttgcaa atactcgagc acttgcttta tgtcaatttt cgcggcattt 240
caatgtgctc tcttgagcct ttacaagagc agagacgta atgattggat catagatgat 300
agattcgta tcaccgtcat catatacgct ggagtggtag gacaagcaat gacgacggtt 360
gcaacaacat gggggattaa aaaattagga gctgtgttcg catcggcgtt tttcccactt 420
actctcattt cggctactct atttgatttc ctcattttac acactccttt ataccttgga 480

DOCKET "08668950"

(2) INFORMATION FOR SEQ ID NO:494:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

1990-1991		1991-1992		1992-1993		1993-1994		1994-1995		1995-1996		1996-1997		1997-1998		1998-1999		1999-2000		2000-2001		2001-2002		2002-2003		2003-2004		2004-2005		2005-2006		2006-2007		2007-2008		2008-2009		2009-2010		2010-2011		2011-2012		2012-2013		2013-2014		2014-2015		2015-2016		2016-2017		2017-2018		2018-2019		2019-2020		2020-2021		2021-2022		2022-2023		2023-2024		2024-2025		2025-2026		2026-2027		2027-2028		2028-2029		2029-2030		2030-2031		2031-2032		2032-2033		2033-2034		2034-2035		2035-2036		2036-2037		2037-2038		2038-2039		2039-2040		2040-2041		2041-2042		2042-2043		2043-2044		2044-2045		2045-2046		2046-2047		2047-2048		2048-2049		2049-2050		2050-2051		2051-2052		2052-2053		2053-2054		2054-2055		2055-2056		2056-2057		2057-2058		2058-2059		2059-2060		2060-2061		2061-2062		2062-2063		2063-2064		2064-2065		2065-2066		2066-2067		2067-2068		2068-2069		2069-2070		2070-2071		2071-2072		2072-2073		2073-2074		2074-2075		2075-2076		2076-2077		2077-2078		2078-2079		2079-2080		2080-2081		2081-2082		2082-2083		2083-2084		2084-2085		2085-2086		2086-2087		2087-2088		2088-2089		2089-2090		2090-2091		2091-2092		2092-2093		2093-2094		2094-2095		2095-2096		2096-2097		2097-2098		2098-2099		2099-2100		2100-2101		2101-2102		2102-2103		2103-2104		2104-2105		2105-2106		2106-2107		2107-2108		2108-2109		2109-2110		2110-2111		2111-2112		2112-2113		2113-2114		2114-2115		2115-2116		2116-2117		2117-2118		2118-2119		2119-2120		2120-2121		2121-2122		2122-2123		2123-2124		2124-2125		2125-2126		2126-2127		2127-2128		2128-2129		2129-2130		2130-2131		2131-2132		2132-2133		2133-2134		2134-2135		2135-2136		2136-2137		2137-2138		2138-2139		2139-2140		2140-2141		2141-2142		2142-2143		2143-2144		2144-2145		2145-2146		2146-2147		2147-2148		2148-2149		2149-2150		2150-2151		2151-2152		2152-2153		2153-2154		2154-2155		2155-2156		2156-2157		2157-2158		2158-2159		2159-2160		2160-2161		2161-2162		2162-2163		2163-2164		2164-2165		2165-2166		2166-2167		2167-2168		2168-2169		2169-2170		2170-2171		2171-2172		2172-2173		2173-2174		2174-2175		2175-2176		2176-2177		2177-2178		2178-2179		2179-2180		2180-2181		2181-2182		2182-2183		2183-2184		2184-2185		2185-2186		2186-2187		2187-2188		2188-2189		2189-2190		2190-2191		2191-2192		2192-2193		2193-2194		2194-2195		2195-2196		2196-2197		2197-2198		2198-2199		2199-2200		2200-2201		2201-2202		2202-2203		2203-2204		2204-2205		2205-2206		2206-2207		2207-2208		2208-2209		2209-2210		2210-2211		2211-2212		2212-2213		2213-2214		2214-2215		2215-2216		2216-2217	
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Lys Thr Ala Val Gln Ile Arg Ser His Ala Gln Lys Phe Phe Thr Lys
325 330 335

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..283
- (D) OTHER INFORMATION: / Ceres Seq. ID 1586201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

Met Leu Phe Gln Gly Thr Leu Ser Ile Lys Tyr Pro Cys Lys Tyr Ser
1 5 10 15
Ser Thr Cys Leu Met Ser Ile Phe Ala Phe Gln Cys Ala Leu Leu
20 25 30
Ser Leu Tyr Lys Ser Arg Asp Val Asn Asp Trp Ile Ile Asp Asp Arg
35 40 45
Phe Val Ile Thr Val Ile Ile Tyr Ala Gly Val Val Gly Gln Ala Met
50 55 60
Thr Thr Val Ala Thr Thr Trp Gly Ile Lys Lys Leu Gly Ala Val Phe
65 70 75 80
Ala Ser Ala Phe Phe Pro Leu Thr Leu Ile Ser Ala Thr Leu Phe Asp
85 90 95
Phe Leu Ile Leu His Thr Pro Leu Tyr Leu Gly Ser Val Ile Gly Ser
100 105 110
Leu Val Thr Ile Thr Gly Leu Tyr Met Phe Leu Trp Gly Lys Asn Lys
115 120 125
Glu Thr Glu Ser Ser Thr Ala Leu Ser Ser Gly Met Asp Asn Glu Ala
130 135 140
Gln Tyr Thr Thr Pro Asn Lys Asp Asn Asp Ser Lys Ser Pro Gly Val
145 150 155 160
Pro Gly Glu Met Ile Ser Gln Ile Ala Tyr Leu Ser Pro Pro Trp Leu
165 170 175
Leu Ser Arg Arg Gly Phe Glu Ala Ala Asn Ser Cys Asn Gly Pro Val
180 185 190
Met Asp Thr Asn Thr Ser Gly Glu Glu Leu Leu Ala Lys Ala Arg Lys
195 200 205
Pro Tyr Thr Ile Thr Lys Gln Arg Glu Arg Trp Thr Glu Asp Glu His
210 215 220
Glu Arg Phe Leu Glu Ala Leu Arg Leu Tyr Gly Arg Ala Trp Gln Arg
225 230 235 240
Ile Glu Gly Val Ser Leu Ser Pro Leu Asp Trp Glu Ile Pro Ser Phe
245 250 255
Leu Phe Ile Leu Cys Ala Glu His Ile Gly Thr Lys Thr Ala Val Gln
260 265 270
Ile Arg Ser His Ala Gln Lys Phe Phe Thr Lys
275 280

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

09639830-10100

(B) LOCATION: 1..263

(D) OTHER INFORMATION: / Ceres Seq. ID 1586202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

Met Ser Ile Phe Ala Ala Phe Gln Cys Ala Leu Leu Ser Leu Tyr Lys
1 5 10 15
Ser Arg Asp Val Asn Asp Trp Ile Ile Asp Asp Arg Phe Val Ile Thr
20 25 30
Val Ile Ile Tyr Ala Gly Val Val Gly Gln Ala Met Thr Thr Val Ala
35 40 45
Thr Thr Trp Gly Ile Lys Lys Leu Gly Ala Val Phe Ala Ser Ala Phe
50 55 60
Phe Pro Leu Thr Leu Ile Ser Ala Thr Leu Phe Asp Phe Leu Ile Leu
65 70 75 80
His Thr Pro Leu Tyr Leu Gly Ser Val Ile Gly Ser Leu Val Thr Ile
85 90 95
Thr Gly Leu Tyr Met Phe Leu Trp Gly Lys Asn Lys Glu Thr Glu Ser
100 105 110
Ser Thr Ala Leu Ser Ser Gly Met Asp Asn Glu Ala Gln Tyr Thr Thr
115 120 125
Pro Asn Lys Asp Asn Asp Ser Lys Ser Pro Gly Val Pro Gly Glu Met
130 135 140
Ile Ser Gln Ile Ala Tyr Leu Ser Pro Pro Trp Leu Leu Ser Arg Arg
145 150 155 160
Gly Phe Glu Ala Ala Asn Ser Cys Asn Gly Pro Val Met Asp Thr Asn
165 170 175
Thr Ser Gly Glu Glu Leu Leu Ala Lys Ala Arg Lys Pro Tyr Thr Ile
180 185 190
Thr Lys Gln Arg Glu Arg Trp Thr Glu Asp Glu His Glu Arg Phe Leu
195 200 205
Glu Ala Leu Arg Leu Tyr Gly Arg Ala Trp Gln Arg Ile Glu Gly Val
210 215 220
Ser Leu Ser Pro Leu Asp Trp Glu Ile Pro Ser Phe Leu Phe Ile Leu
225 230 235 240
Cys Ala Glu His Ile Gly Thr Lys Thr Ala Val Gln Ile Arg Ser His
245 250 255
Ala Gln Lys Phe Phe Thr Lys
260

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..721

(D) OTHER INFORMATION: / Ceres Seq. ID 1586207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

atggatcctg acttcactcg tcatggttct tcctccgacg gcgattttgg attcgctttt 60
aatgacagta acttctctga tcgcttgctt cggatcgaga tcatgggtgg accttcggat 120
tctaggtccg aagttegaagg gtgtacgagt atcgtctgatt gggctcgtca tcgcaagaga 180
agaagagaag atatcaagaa ggaatctggt gtcacgattt cagacattgt ggcgtgtcct 240
gaggagcaga ttttaactga tgaacaacct gacatggatg gatgtcctgg tgggtgagaat 300
cctgatgatg aaggaggaga ggcaatgggt gaagaagctt tatcagggtga tgaaggaggaa 360
acgtctagtg agccaaaactg gggaatggat tggtctacag ttgttaggggt taaagaactt 420
catattagtt ctctattttt agctgccaaa agccctttct tttacaagtt gttctccaat 480
ggaatgaggg aatctgagca aaggcatgtc acccttagga ttaatgcac agaggaagct 540
gctttgatgg agcttttaaa ctttatgtat agcaatgcgg tatctgtcac cacagcacct 600
gccttattag atgtgttgat ggctgctgat aagtttgaag ttgcctcttg tatgaggtac 660
tgcagtagac ttctccgtaa tatgcctatg actccagagt ctgccctgct ctatctcgag 720

09689980 101300

Met	Gly	Gly	Pro	Ser	Asp	Ser	Arg	Ser	Glu	Val	Glu	Gly	Cys	Thr	Ser
1				5					10					15	
Ile	Ala	Asp	Trp	Ala	Arg	His	Arg	Lys	Arg	Arg	Arg	Glu	Asp	Ile	Lys
			20					25					30		

Lys Glu Ser Gly Val Thr Ile Ser Asp Ile Val Ala Cys Pro Glu Glu
35 40 45
Gln Ile Leu Thr Asp Glu Gln Pro Asp Met Asp Gly Cys Pro Gly Gly
50 55 60
Glu Asn Pro Asp Asp Glu Gly Gly Glu Ala Met Val Glu Glu Ala Leu
65 70 75 80
Ser Gly Asp Glu Glu Glu Thr Ser Ser Glu Pro Asn Trp Gly Met Asp
85 90 95
Cys Ser Thr Val Val Arg Val Lys Glu Leu His Ile Ser Ser Pro Ile
100 105 110
Leu Ala Ala Lys Ser Pro Phe Phe Tyr Lys Leu Phe Ser Asn Gly Met
115 120 125
Arg Glu Ser Glu Gln Arg His Val Thr Leu Arg Ile Asn Ala Ser Glu
130 135 140
Glu Ala Ala Leu Met Glu Leu Leu Asn Phe Met Tyr Ser Asn Ala Val
145 150 155 160
Ser Val Thr Thr Ala Pro Ala Leu Leu Asp Val Leu Met Ala Ala Asp
165 170 175
Lys Phe Glu Val Ala Ser Cys Met Arg Tyr Cys Ser Arg Leu Leu Arg
180 185 190
Asn Met Pro Met Thr Pro Glu Ser Ala Leu Leu Tyr Leu Glu
195 200 205

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..729
- (D) OTHER INFORMATION: / Ceres Seq. ID 1586296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

agggttttccg gggaatgtga cggtgaaagt gacgtacatg ttgatcggag aaaacaaact	60
cgggtgtaaaa atggaagcaa agccactcaa caaacctaca ccaatcaact tagctctcca	120
cacttactgg aacctccaca gccacaactc cgggaacatc ctctcccaca aaattcaact	180
cctcgccgga aaaatcactc ccgtcgacga caaactcatc cccaccggcg aaatcacctc	240
cattgccgga actccttacg attttctcga gcctcgcgag atcggaagcc ggatccacga	300
attaccgga ggttacgaca tcaattacgt gatcgatgga ccgatcggga aacatctgag	360
gaaaactgcg gttgtgacgg aggaagtcac cggaaggaag atggagctgt ggacgaatca	420
gcctggtgtt cagttttaca cgagtaatat gatgaaacgt gtcgtcggta aggtaaagcc	480
gtttatgaga aatacggtag ctgtgttttg gagactcaag gtttcccaga ttccgtcaat	540
cacaagaact ttccgtcgca gattgttaat cccggcgaga gttatttgca tgttatgctc	600
ttcagattca ctgctcacta atcgggtcgg gtcgggtcgg gtcgggtttt taggggttaa	660
tttttccgaa tactcgccaa cgtcgttgta atgcaaaatt gcaaatgcc ataaaaatat	720
tcgactttt	

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..229
- (D) OTHER INFORMATION: / Ceres Seq. ID 1586297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

Gly Phe Pro Gly Asn Val Thr Val Lys Val Thr Tyr Met Leu Ile Gly
1 5 10 15

DOE-01-00000000

Glu Asn Lys Leu Gly Val Lys Met Glu Ala Lys Pro Leu Asn Lys Pro
20 25 30
Thr Pro Ile Asn Leu Ala Leu His Thr Tyr Trp Asn Leu His Ser His
35 40 45
Asn Ser Gly Asn Ile Leu Ser His Lys Ile Gln Leu Leu Ala Gly Lys
50 55 60
Ile Thr Pro Val Asp Asp Lys Leu Ile Pro Thr Gly Glu Ile Thr Ser
65 70 75 80
Ile Ala Gly Thr Pro Tyr Asp Phe Leu Glu Pro Arg Glu Ile Gly Ser
85 90 95
Arg Ile His Glu Leu Pro Gly Gly Tyr Asp Ile Asn Tyr Val Ile Asp
100 105 110
Gly Pro Ile Gly Lys His Leu Arg Lys Thr Ala Val Val Thr Glu Glu
115 120 125
Val Thr Gly Arg Lys Met Glu Leu Trp Thr Asn Gln Pro Gly Val Gln
130 135 140
Phe Tyr Thr Ser Asn Met Met Lys Arg Val Val Gly Lys Val Lys Pro
145 150 155 160
Phe Met Arg Asn Thr Val Ala Cys Val Trp Arg Leu Lys Ala Ser Gln
165 170 175
Ile Pro Ser Ile Thr Arg Thr Phe Arg Arg Arg Leu Leu Ile Pro Ala
180 185 190
Arg Val Ile Cys Met Leu Cys Ser Ser Asp Ser Leu Leu Thr Asn Arg
195 200 205
Val Gly Ser Gly Arg Val Gly Phe Leu Gly Phe Asn Phe Ser Glu Tyr
210 215 220
Ser Pro Thr Ser Leu
225

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1586298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

Met Leu Ile Gly Glu Asn Lys Leu Gly Val Lys Met Glu Ala Lys Pro
1 5 10 15
Leu Asn Lys Pro Thr Pro Ile Asn Leu Ala Leu His Thr Tyr Trp Asn
20 25 30
Leu His Ser His Asn Ser Gly Asn Ile Leu Ser His Lys Ile Gln Leu
35 40 45
Leu Ala Gly Lys Ile Thr Pro Val Asp Asp Lys Leu Ile Pro Thr Gly
50 55 60
Glu Ile Thr Ser Ile Ala Gly Thr Pro Tyr Asp Phe Leu Glu Pro Arg
65 70 75 80
Glu Ile Gly Ser Arg Ile His Glu Leu Pro Gly Gly Tyr Asp Ile Asn
85 90 95
Tyr Val Ile Asp Gly Pro Ile Gly Lys His Leu Arg Lys Thr Ala Val
100 105 110
Val Thr Glu Glu Val Thr Gly Arg Lys Met Glu Leu Trp Thr Asn Gln
115 120 125
Pro Gly Val Gln Phe Tyr Thr Ser Asn Met Met Lys Arg Val Val Gly
130 135 140
Lys Val Lys Pro Phe Met Arg Asn Thr Val Ala Cys Val Trp Arg Leu
145 150 155 160
Lys Ala Ser Gln Ile Pro Ser Ile Thr Arg Thr Phe Arg Arg Arg Leu

DOCKET# 08668860

165 170 175
Leu Ile Pro Ala Arg Val Ile Cys Met Leu Cys Ser Ser Asp Ser Leu
180 185 190
Leu Thr Asn Arg Val Gly Ser Gly Arg Val Gly Phe Leu Gly Phe Asn
195 200 205
Phe Ser Glu Tyr Ser Pro Thr Ser Leu
210 215

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 1586299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

Met Glu Ala Lys Pro Leu Asn Lys Pro Thr Pro Ile Asn Leu Ala Leu
1 5 10 15
His Thr Tyr Trp Asn Leu His Ser His Asn Ser Gly Asn Ile Leu Ser
20 25 30
His Lys Ile Gln Leu Leu Ala Gly Lys Ile Thr Pro Val Asp Asp Lys
35 40 45
Leu Ile Pro Thr Gly Glu Ile Thr Ser Ile Ala Gly Thr Pro Tyr Asp
50 55 60
Phe Leu Glu Pro Arg Glu Ile Gly Ser Arg Ile His Glu Leu Pro Gly
65 70 75 80
Gly Tyr Asp Ile Asn Tyr Val Ile Asp Gly Pro Ile Gly Lys His Leu
85 90 95
Arg Lys Thr Ala Val Val Thr Glu Glu Val Thr Gly Arg Lys Met Glu
100 105 110
Leu Trp Thr Asn Gln Pro Gly Val Gln Phe Tyr Thr Ser Asn Met Met
115 120 125
Lys Arg Val Val Gly Lys Val Lys Pro Phe Met Arg Asn Thr Val Ala
130 135 140
Cys Val Trp Arg Leu Lys Ala Ser Gln Ile Pro Ser Ile Thr Arg Thr
145 150 155 160
Phe Arg Arg Arg Leu Leu Ile Pro Ala Arg Val Ile Cys Met Leu Cys
165 170 175
Ser Ser Asp Ser Leu Leu Thr Asn Arg Val Gly Ser Gly Arg Val Gly
180 185 190
Phe Leu Gly Phe Asn Phe Ser Glu Tyr Ser Pro Thr Ser Leu
195 200 205

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..451

(D) OTHER INFORMATION: / Ceres Seq. ID 1586345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

agagcttagc taagatgacg aagaactacc caaccgtgag cgaagattac aagaaggctg 60
ttgagaagtg caggaggaag ctgagaggtt tgatcgctga gaagaactgt gcacccatca 120
tggtccgact cgcattggcacc tctgctggaa ctttcgattg tcaatcaagg actggagggtc 180
cattcggaac aatgaggttt gacgctgagc aagctcatgg agccaacagt ggtatccaca 240

00669900-101300

(2) INFORMATION FOR SEQ ID NO:505:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1586346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

Ser	Leu	Ala	Lys	Met	Thr	Lys	Asn	Tyr	Pro	Thr	Val	Ser	Glu	Asp	Tyr
1				5					10					15	
Lys	Lys	Ala	Val	Glu	Lys	Cys	Arg	Arg	Lys	Leu	Arg	Gly	Leu	Ile	Ala
			20					25					30		
Glu	Lys	Asn	Cys	Ala	Pro	Ile	Met	Val	Arg	Leu	Ala	Trp	His	Ser	Ala
			35				40					45			
Gly	Thr	Phe	Asp	Cys	Gln	Ser	Arg	Thr	Gly	Gly	Pro	Phe	Gly	Thr	Met
	50					55					60				
Arg	Phe	Asp	Ala	Glu	Gln	Ala	His	Gly	Ala	Asn	Ser	Gly	Ile	His	Ile
65					70					75				80	
Ala	Leu	Arg	Leu	Leu	Asp	Pro	Ile	Arg	Glu	Gln	Phe	Pro	Thr	Ile	Ser
				85					90					95	
Phe	Ala	Asp	Phe	His	Gln	Leu	Ala	Gly	Val	Val	Ala	Val	Glu	Val	Thr
			100					105					110		
Gly	Gly	Pro	Asp	Ile	Pro	Phe	His	Pro	Gly	Arg	Glu	Asp	Lys	Pro	Gln
		115					120					125			
Pro	Pro	Pro	Glu	Gly	Arg	Leu	Pro	Asp	Ala	Val	Cys				
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1586347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

Met	Thr	Lys	Asn	Tyr	Pro	Thr	Val	Ser	Glu	Asp	Tyr	Lys	Lys	Ala	Val
1				5					10					15	
Glu	Lys	Cys	Arg	Arg	Lys	Leu	Arg	Gly	Leu	Ile	Ala	Glu	Lys	Asn	Cys
			20					25					30		
Ala	Pro	Ile	Met	Val	Arg	Leu	Ala	Trp	His	Ser	Ala	Gly	Thr	Phe	Asp
			35				40					45			
Cys	Gln	Ser	Arg	Thr	Gly	Gly	Pro	Phe	Gly	Thr	Met	Arg	Phe	Asp	Ala
	50					55					60				
Glu	Gln	Ala	His	Gly	Ala	Asn	Ser	Gly	Ile	His	Ile	Ala	Leu	Arg	Leu
65				70						75					80
Leu	Asp	Pro	Ile	Arg	Glu	Gln	Phe	Pro	Thr	Ile	Ser	Phe	Ala	Asp	Phe
				85					90					95	
His	Gln	Leu	Ala	Gly	Val	Val	Ala	Val	Glu	Val	Thr	Gly	Gly	Pro	Asp
			100					105					110		
Ile	Pro	Phe	His	Pro	Gly	Arg	Glu	Asp	Lys	Pro	Gln	Pro	Pro	Pro	Glu

Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
Male	55.2 (10.5)
Female	56.8 (11.2)
Marital status	
Married	78.5%
Single	12.3%
Divorced	5.2%
Widowed	4.0%
Education level	
High school or above	65.8%
Below high school	34.2%
Occupation	
Professional	25.5%
Managerial	18.2%
Technical	15.7%
Service	12.1%
Skilled	8.9%
Unskilled	19.6%
Health status	
Good	72.3%
Fair	15.4%
Poor	12.3%
Very poor	0.0%
Smoking status	
Smoker	35.2%
Non-smoker	64.8%
Alcohol consumption	
Regular	10.5%
Occasional	25.8%
Never	63.7%
Family size	
1-2	45.2%
3-4	38.5%
5-6	12.1%
7-8	3.8%
9-10	0.4%
Income (USD/month)	
< 500	15.2%
500-1000	28.5%
1000-1500	35.8%
> 1500	20.5%

(2) INFORMATION FOR SEQ ID NO:507:

(A) LENGTH: 101 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..101
(D) OTHER INFORMATION: / Ceres Seq. ID 1586348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

(2) INFORMATION FOR SEQ ID NO:508:

(A) LENGTH: 1014 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- ```
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1014
 (D) OTHER INFORMATION: / Ceres Seq. ID 1586393
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

| (XI) SEQUENCE DESCRIPTION: SEQ ID NO:500: |            |             |             |            |            |     |
|-------------------------------------------|------------|-------------|-------------|------------|------------|-----|
| atgatgtctt                                | tgtcccaaaa | tcccgaccgc  | attactgtac  | cctgtgtcct | caagctttgc | 60  |
| tcttttctct                                | cgccacggg  | cgtcttctct  | ctcaggctca  | ggcgtttcac | ccgaaagtca | 120 |
| tcatctcttc                                | tccggttggt | gctgttttcg  | tctctctccg  | ctactgncgc | aaaacctacc | 180 |
| agatggagag                                | agaagccgga | attggcggaa  | agcgactcaa  | tttccctcct | caacgagagg | 240 |
| attcggcgtg                                | acctcggcaa | gagagagact  | gctagaccgg  | ccatggactc | tgaggaggcc | 300 |
| gagaagtaca                                | ttcacatggt | caaggaacaa  | caagagaggg  | gtctgcagaa | gctcaaagga | 360 |
| attaggcaag                                | gtacaaaggc | tgtgtgtgac  | gggtgcttta  | gttacaagg  | tgacccttac | 420 |
| agtctctctt                                | ccggtgatta | tgtgggtgcac | aagaaagtag  | gcattggggc | ttttgttggg | 480 |
| atcaagtttg                                | atgtccccaa | ggactcctct  | gagcccctcg  | aatatgtctt | tatagagtat | 540 |
| gctgatggta                                | tggccaagct | tcccctcaaa  | caggcctcgc  | gtttgctcta | ccgatacaat | 600 |
| cttccaaatg                                | agactaaacg | gcctcggact  | ttgagtcggc  | tgagtgacac | tagtgtttgg | 660 |
| gaaagaagaa                                | agaccaaagg | aaaagtatga  | attcagaaaa  | tggtcgttga | cttgatggag | 720 |
| ctatatcttc                                | ataggcttag | acagaagaga  | tatccatatc  | cgaagaacc  | catcatggct | 780 |
| gatttttcgg                                | ctcaatttcc | ttataacgcc  | actcctgacc  | agaagcaggc | tttcctggat | 840 |
| ggtgaaaagg                                | atttgactga | gagagaaaaca | cctatggacc  | gattgatctg | tggagatgtt | 900 |
| ggcttttgga                                | aaacagaggt | tgtcttacga  | gccatctttt  | gtgtggtctc | aactggaaaa | 960 |
| caagctatgg                                | ttttagcacc | gacaattgta  | ttggcgaaana | acattacgat | gtaa       |     |

(2) INFORMATION FOR SEQ ID NO:509:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 337 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..337
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1586394
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

Met Met Ser Leu Leu Pro Asn Pro Asp Pro Ile Thr Val Pro Leu Val  
1 5 10 15  
Leu Lys Leu Cys Ser Phe Pro Pro Pro Arg Arg Leu Phe Ser Leu Arg  
20 25 30  
Leu Arg Arg Phe Thr Arg Lys Ser Ser Ser Leu Leu Pro Leu Val Ala  
35 40 45  
Val Ser Ser Leu Ser Ala Thr Xaa Ala Lys Pro Thr Arg Trp Arg Glu  
50 55 60  
Lys Pro Glu Leu Ala Glu Ser Asp Ser Ile Ser Leu Leu Asn Glu Arg  
65 70 75 80  
Ile Arg Arg Asp Leu Gly Lys Arg Glu Thr Ala Arg Pro Ala Met Asp  
85 90 95  
Ser Glu Glu Ala Glu Lys Tyr Ile His Met Val Lys Glu Gln Gln Glu  
100 105 110  
Arg Gly Leu Gln Lys Leu Lys Gly Ile Arg Gln Gly Thr Lys Ala Ala  
115 120 125  
Gly Asp Gly Ala Phe Ser Tyr Lys Val Asp Pro Tyr Ser Leu Leu Ser  
130 135 140  
Gly Asp Tyr Val Val His Lys Lys Val Gly Ile Gly Arg Phe Val Gly  
145 150 155 160  
Ile Lys Phe Asp Val Pro Lys Asp Ser Ser Glu Pro Leu Glu Tyr Val  
165 170 175  
Phe Ile Glu Tyr Ala Asp Gly Met Ala Lys Leu Pro Leu Lys Gln Ala  
180 185 190  
Ser Arg Leu Leu Tyr Arg Tyr Asn Leu Pro Asn Glu Thr Lys Arg Pro  
195 200 205  
Arg Thr Leu Ser Arg Leu Ser Asp Thr Ser Val Trp Glu Arg Arg Lys  
210 215 220  
Thr Lys Gly Lys Val Ala Ile Gln Lys Met Val Val Asp Leu Met Glu  
225 230 235 240  
Leu Tyr Leu His Arg Leu Arg Gln Lys Arg Tyr Pro Tyr Pro Lys Asn  
245 250 255  
Pro Ile Met Ala Asp Phe Ala Ala Gln Phe Pro Tyr Asn Ala Thr Pro  
260 265 270  
Asp Gln Lys Gln Ala Phe Leu Asp Val Glu Lys Asp Leu Thr Glu Arg  
275 280 285  
Glu Thr Pro Met Asp Arg Leu Ile Cys Gly Asp Val Gly Phe Gly Lys  
290 295 300  
Thr Glu Val Ala Leu Arg Ala Ile Phe Cys Val Val Ser Thr Gly Lys  
305 310 315 320  
Gln Ala Met Val Leu Ala Pro Thr Ile Val Leu Ala Xaa Asn Ile Thr  
325 330 335  
Met

- (2) INFORMATION FOR SEQ ID NO:510:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 336 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:

09669980-10130

| (X1) SEQUENCE DESCRIPTION: SEQ INFORMATION |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|--------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met<br>1                                   | Ser | Leu | Leu | Pro | Asn | Pro | Asp | Pro | Ile | Thr | Val | Pro | Leu | Val | Leu |  |
|                                            |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys                                        | Leu | Cys | Ser | Phe | Pro | Pro | Pro | Arg | Arg | Leu | Phe | Ser | Leu | Arg | Leu |  |
|                                            |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg                                        | Arg | Phe | Thr | Arg | Lys | Ser | Ser | Ser | Leu | Leu | Pro | Leu | Val | Ala | Val |  |
|                                            |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser                                        | Ser | Leu | Ser | Ala | Thr | Xaa | Ala | Lys | Pro | Thr | Arg | Trp | Arg | Glu | Lys |  |
|                                            | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Pro                                        | Glu | Leu | Ala | Glu | Ser | Asp | Ser | Ile | Ser | Leu | Leu | Asn | Glu | Arg | Ile |  |
| 65                                         |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Arg                                        | Arg | Asp | Leu | Gly | Lys | Arg | Glu | Thr | Ala | Arg | Pro | Ala | Met | Asp | Ser |  |
|                                            |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Glu                                        | Glu | Ala | Glu | Lys | Tyr | Ile | His | Met | Val | Lys | Glu | Gln | Gln | Glu | Arg |  |
|                                            |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Gly                                        | Leu | Gln | Lys | Leu | Lys | Gly | Ile | Arg | Gln | Gly | Thr | Lys | Ala | Ala | Gly |  |
|                                            |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Asp                                        | Gly | Ala | Phe | Ser | Tyr | Lys | Val | Asp | Pro | Tyr | Ser | Leu | Leu | Ser | Gly |  |
|                                            | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Asp                                        | Tyr | Val | Val | His | Lys | Lys | Val | Gly | Ile | Gly | Arg | Phe | Val | Gly | Ile |  |
| 145                                        |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Lys                                        | Phe | Asp | Val | Pro | Lys | Asp | Ser | Ser | Glu | Pro | Leu | Glu | Tyr | Val | Phe |  |
|                                            |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Ile                                        | Glu | Tyr | Ala | Asp | Gly | Met | Ala | Lys | Leu | Pro | Leu | Lys | Gln | Ala | Ser |  |
|                                            |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Arg                                        | Leu | Leu | Tyr | Arg | Tyr | Asn | Leu | Pro | Asn | Glu | Thr | Lys | Arg | Pro | Arg |  |
|                                            |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |
| Thr                                        | Leu | Ser | Arg | Leu | Ser | Asp | Thr | Ser | Val | Trp | Glu | Arg | Arg | Lys | Thr |  |
|                                            | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Lys                                        | Gly | Lys | Val | Ala | Ile | Gln | Lys | Met | Val | Val | Asp | Leu | Met | Glu | Leu |  |
| 225                                        |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |  |
| Tyr                                        | Leu | His | Arg | Leu | Arg | Gln | Lys | Arg | Tyr | Pro | Tyr | Pro | Lys | Asn | Pro |  |
|                                            |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Ile                                        | Met | Ala | Asp | Phe | Ala | Ala | Gln | Phe | Pro | Tyr | Asn | Ala | Thr | Pro | Asp |  |
|                                            |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Gln                                        | Lys | Gln | Ala | Phe | Leu | Asp | Val | Glu | Lys | Asp | Leu | Thr | Glu | Arg | Glu |  |
|                                            |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Thr                                        | Pro | Met | Asp | Arg | Leu | Ile | Cys | Gly | Asp | Val | Gly | Phe | Gly | Lys | Thr |  |
|                                            | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Glu                                        | Val | Ala | Leu | Arg | Ala | Ile | Phe | Cys | Val | Val | Ser | Thr | Gly | Lys | Gln |  |
| 305                                        |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Ala                                        | Met | Val | Leu | Ala | Pro | Thr | Ile | Val | Leu | Ala | Xaa | Asn | Ile | Thr | Met |  |
|                                            |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:311:  
gagaaatagg atcgaaatgc ttaaggcaga tgggtggtcgc tgggttacag acgcgaagga

[illegible]

(2) INFORMATION FOR SEQ ID NO:512:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1586439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

|                                         |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| (X1) SEQUENCE DESCRIPTION: SEQ ID NO: 1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Arg                                     | Asn | Arg | Ile | Glu | Met | Leu | Lys | Ala | Asp | Gly | Gly | Arg | Trp | Val | Thr |
| 1                                       |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp                                     | Ala | Lys | Glu | Leu | Glu | Leu | Met | Thr | Val | Asn | Tyr | Tyr | Lys | Arg | Leu |
|                                         |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr                                     | Ser | Leu | Glu | Asp | Val | Asn | Pro | Val | Leu | Thr | Pro | Leu | Pro | Pro | Glu |
|                                         |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly                                     | Phe | Thr | Ile | Leu | Ser | Gln | Ser | Ala | Leu | Thr | Glu | Leu | Asn | Arg | Pro |
|                                         | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe                                     | Thr | Pro | Ala | Glu | Ile | Glu | Glu | Ser | Val | Arg | Ser | Met | Gly | Lys | Phe |
| 65                                      |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys                                     | Ala | Pro | Gly | Pro | Asp | Gly | Tyr | Gln | Pro | Val | Phe | Tyr | Gln | Gln | Asn |
|                                         |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Trp                                     | Glu | Thr | Val | Gly | Ser | Ser | Val | Ile | Arg | Phe | Ala | Leu | Asp | Phe | Phe |
|                                         |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Glu                                     | Thr | Gly | Ile | Leu | Pro | Glu | Ser | Met | Asn | Asp | Ala | Leu | Val | Val | Leu |
|                                         |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile                                     | Ala | Lys | Val | Ala | Asn | Arg | Arg |     |     |     |     |     |     |     |     |
|                                         | 130 |     |     |     |     |     | 135 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:513:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1586440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Lys | Ala | Asp | Gly | Gly | Arg | Trp | Val | Thr | Asp | Ala | Lys | Glu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Leu | Met | Thr | Val | Asn | Tyr | Tyr | Lys | Arg | Leu | Tyr | Ser | Leu | Glu | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Asn | Pro | Val | Leu | Thr | Pro | Leu | Pro | Pro | Glu | Gly | Phe | Thr | Ile | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Gln | Ser | Ala | Leu | Thr | Glu | Leu | Asn | Arg | Pro | Phe | Thr | Pro | Ala | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Glu | Glu | Ser | Val | Arg | Ser | Met | Gly | Lys | Phe | Lys | Ala | Pro | Gly | Pro |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Gly | Tyr | Gln | Pro | Val | Phe | Tyr | Gln | Gln | Asn | Trp | Glu | Thr | Val | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ser | Ser | Val | Ile | Arg | Phe | Ala | Leu | Asp | Phe | Phe | Glu | Thr | Gly | Ile | Leu |

(2) INFORMATION FOR SEQ ID NO:514:

(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1586441

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

```
(ix) FEATURE:
```

(B) LOCATION: 1..519

(D) OTHER INFORMATION: / Ceres Seq. ID 1586467

| (X1) SEQUENCE DESCRIPTION: 51 |            |             |            |             |             |     |
|-------------------------------|------------|-------------|------------|-------------|-------------|-----|
| gctaaggctg                    | atgaactatc | tgaatccgac  | tctgaagcgt | ggaccgatga  | gtcaagaaga  | 60  |
| agagagaatc                    | atctttcagc | tccatgctct  | atggggtggt | cgaagattgc  | gagaagatta  | 120 |
| cccggtagga                    | ctgataacga | gataaagaac  | tattggagaa | ctcattatag  | aaagaaacag  | 180 |
| gaagctcaa                     | actatggaaa | gctctttgag  | tggagaggaa | atacaggaga  | agaattgttg  | 240 |
| cacaagtata                    | aggaaacaga | gatcactagg  | acaaagacga | cgctctcaaga | acatggtttt  | 300 |
| gttgaagttg                    | tgagcatgga | aagtggtaaa  | gaagccaacg | gtgggtggtg  | tggagaagaaa | 360 |
| agcttcggtg                    | ttatgaaatc | accgatgaa   | aatcggattt | cggattggat  | atcacagatt  | 420 |
| tctactgacc                    | agagtgaagc | aaatctttca  | gaagatcaca | gcagcaatag  | ctgcaagact  | 480 |
| agggaacttg                    | aggagttttc | atgtttctcta | tggtcataa  |             |             |     |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..172

(D) OTHER INFORMATION: / Ceres Seq. ID 1586468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

Ala Lys Val Asp Glu Leu Ser Glu Ser Asp Ser Glu Ala Trp Thr Asp  
1 5 10 15  
Glu Ser Arg Arg Arg Glu Asn His Leu Ser Ala Pro Cys Ser Met Gly  
20 25 30  
Trp Ser Lys Ile Ala Arg Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile  
35 40 45  
Lys Asn Tyr Trp Arg Thr His Tyr Arg Lys Lys Gln Glu Ala Gln Asn  
50 55 60  
Tyr Gly Lys Leu Phe Glu Trp Arg Gly Asn Thr Gly Glu Glu Leu Leu  
65 70 75 80  
His Lys Tyr Lys Glu Thr Glu Ile Thr Arg Thr Lys Thr Thr Ser Gln  
85 90 95  
Glu His Gly Phe Val Glu Val Val Ser Met Glu Ser Gly Lys Glu Ala  
100 105 110  
Asn Gly Gly Val Gly Gly Arg Glu Ser Phe Gly Val Met Lys Ser Pro  
115 120 125  
Tyr Glu Asn Arg Ile Ser Asp Trp Ile Ser Glu Ile Ser Thr Asp Gln  
130 135 140  
Ser Glu Ala Asn Leu Ser Glu Asp His Ser Ser Asn Ser Cys Lys Thr  
145 150 155 160  
Arg Asp Phe Glu Glu Phe Ser Cys Ser Leu Trp Ser  
165 170

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1586469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

Met Gly Trp Ser Lys Ile Ala Arg Arg Leu Pro Gly Arg Thr Asp Asn  
1 5 10 15  
Glu Ile Lys Asn Tyr Trp Arg Thr His Tyr Arg Lys Lys Gln Glu Ala  
20 25 30  
Gln Asn Tyr Gly Lys Leu Phe Glu Trp Arg Gly Asn Thr Gly Glu Glu  
35 40 45  
Leu Leu His Lys Tyr Lys Glu Thr Glu Ile Thr Arg Thr Lys Thr Thr  
50 55 60  
Ser Gln Glu His Gly Phe Val Glu Val Val Ser Met Glu Ser Gly Lys  
65 70 75 80  
Glu Ala Asn Gly Gly Val Gly Gly Arg Glu Ser Phe Gly Val Met Lys  
85 90 95  
Ser Pro Tyr Glu Asn Arg Ile Ser Asp Trp Ile Ser Glu Ile Ser Thr  
100 105 110  
Asp Gln Ser Glu Ala Asn Leu Ser Glu Asp His Ser Ser Asn Ser Cys  
115 120 125  
Lys Thr Arg Asp Phe Glu Glu Phe Ser Cys Ser Leu Trp Ser  
130 135 140

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 558 base pairs

(B) TYPE: nucleic acid

DOCKET# 08662960



| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:316 |             |             |            |            |            |     |
|------------------------------------------|-------------|-------------|------------|------------|------------|-----|
| gctaaggtgc                               | atgaactatc  | tgaatccgac  | tctgaagcgt | ggaccgatga | gtcaagaaga | 60  |
| agagagaaatc                              | atctttcagc  | tccatgtctct | atgggttggt | cgaagattgc | gagaagatta | 120 |
| cccgttagga                               | ctgataacga  | gataaagaac  | tattggagaa | ctcattatag | aaagaaacag | 180 |
| gaagctcaaa                               | actatggaaa  | gctctttgag  | tggagaggaa | atacaggaga | agaattggtg | 240 |
| cacaagtata                               | aggaaacaga  | gatacactagg | acaaagacga | cgtctcaaga | acatggtttt | 300 |
| gttgaagttg                               | tgagcatgga  | aagtggtaaa  | gaagccaacg | gtggtgttgg | tggaagagaa | 360 |
| agcttcggtg                               | ttatgaaatc  | accgtatgaa  | aatcggattt | cggattggat | atcagagatt | 420 |
| tctactgacc                               | agagtggaagc | aaatctttca  | gaagatcaca | gcagcaaatg | ctgcagtgag | 480 |
| aacaatatta                               | acattggtac  | ttggtggttt  | caagagacta | gggactttga | ggagttttca | 540 |
| tgttctctat                               | ggtcataa    |             |            |            |            |     |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

(ii) MOLECULE TYPE: peptide

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Lys | Thr | Lys | Asn | Gln | Ile | Ser | Asn | Leu | Asn | Leu | Leu | Lys | Asp | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Val | Met | Lys | Ala | Leu | Gly | Val | Leu | Leu | Asn | Val | Lys | Phe | Gly | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ser | Gly | Glu | Asp | Thr | Glu | Met | Lys | Glu | Ala | Asp | Glu | Arg | Lys | Glu |

[illegible]

[illegible]

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2016 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2016
- (D) OTHER INFORMATION: / Ceres Seq. ID 1586602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

|            |             |            |            |             |            |      |
|------------|-------------|------------|------------|-------------|------------|------|
| gccagctacg | cttgaaggtc  | aagattctca | accaatccaa | ggtcogggtt  | tcagccggac | 60   |
| tgtgttctgt | aatcagcctc  | atatgcacaa | gaagaaacct | ttgagatata  | gttctaatta | 120  |
| tgtctctacg | acgaggtaca  | atttgatcac | tttctttcct | aagtcgttgt  | acgagcagtt | 180  |
| ccaccgtgct | gcgaatctct  | acttcttggt | agctgcgatt | ctctcgggtg  | ttcctctatc | 240  |
| accattcaac | aagtggagca  | tgattgctcc | tttggtcttt | gttggtgggc  | ttagtatggt | 300  |
| aaaagaggct | ctagaagatt  | ggcgtagggt | tatgcaagac | gtgaagatta  | atgcgcggaa | 360  |
| aacttggtgt | cataaaagt   | acggtgtggt | tcgtcagaga | aagtggaaga  | aggttagcgt | 420  |
| tggggatatt | gtgaaagtgg  | agaaggatga | gtttttccct | gctgatttgc  | ttcttttgtc | 480  |
| atcgagttac | gaggatggga  | tttgctacgt | tgagactatg | aacttagatg  | gtgaaacaaa | 540  |
| cttgaaagt  | aaaagatctt  | tggaagtgtc | actgccacta | gatgatgatg  | aatctttcaa | 600  |
| gaatttcatg | gcgacgataa  | gatgtgaaga | tccaaacccg | aatctctata  | cctttgttgg | 660  |
| caatcttgag | tttgagaggc  | aaacatttcc | tctggatcca | agtcagattc  | tottaagaga | 720  |
| ctcaaagctt | aggaatacaa  | cctatgttta | tggagttgtg | gtattttactg | gttttgatac | 780  |
| caaagttatg | cagaattcaa  | caaagtcgcc | ttccaagaga | agcagaatag  | aaaggacaat | 840  |
| ggactacatc | atctacactc  | ttcttgtcct | acttatttta | atctcttgca  | tcagctcatc | 900  |
| aggatttgct | tgggagacag  | agtttcacat | gccaaaaatg | tggtacttac  | gacctggcga | 960  |
| gcctatagac | ttcacaaatc  | cgatcaatcc | aatctatgct | ggggttggtc  | atctgatcac | 1020 |
| tgctctattg | ctttatggat  | atttgattcc | aatctctctt | tatgtttcga  | tcgaggttgt | 1080 |
| caaagtctgg | caagcaagtt  | tcatcaatca | agacttacac | atgtatgatg  | atgagagtgg | 1140 |
| agtccttgca | aatgcgcgca  | catcgaatct | aaacgaagag | cttggtcagg  | ttcatactat | 1200 |
| cctctctgac | aaaacaggaa  | ctttgacatg | taatcagatg | gatttcttga  | aatgctccat | 1260 |
| tgctggtact | tcttatgggtg | tgcgttccag | cgaagtagaa | gttgctgctg  | caaagcagat | 1320 |
| ggctgtggat | cttgaagagc  | acggtgagat | atcgagtact | cctcagtcctc | agactaaagt | 1380 |
| gtatggtaca | tgggacagta  | gccgtncgca | agaaatcgag | gtggaagggg  | ataataacta | 1440 |
| taatactcct | agagctccta  | taaagggatt | tggttttgag | gataacagac  | ttatgaatgg | 1500 |
| taattggttg | agggaaatcac | aaccaaatga | cattttgcag | ttcttccgca  | tattagctat | 1560 |
| ttgtcacaca | gctattcccg  | agctgaacga | ggagactggc | aagtacactt  | atgaagcaga | 1620 |
| gtcacctgat | gaggcttctt  | ttcttgcctg | tgctagagag | tttggttttg  | agttcttcaa | 1680 |
| gagaacccag | tcaagcggtt  | ttatccgcga | gaggttctct | ggttcagggc  | aaataatcga | 1740 |
| aagggagtac | aaagttctga  | atttggttga | atttacgagc | aaaagaaagc  | gaatgacagt | 1800 |
| aattgtacgc | gatgaggaag  | ggcagattct | tctactatgc | aaaggagctg  | acagcatcat | 1860 |
| ctttgagcgg | ttggcggaaga | atggaaagac | atacttggga | cctaccacta  | ggcatttaac | 1920 |
| tgaatatgga | gaagccggac  | tccgtacact | cgcacttgct | tacagaaagc  | ttgatgagga | 1980 |
| tgaatatgca | gcttggaact  | ctgagtttct | taagga     |             |            |      |

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 671 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..671
- (D) OTHER INFORMATION: / Ceres Seq. ID 1586603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ala | Thr | Leu | Glu | Gly | Gln | Asp | Ser | Gln | Pro | Ile | Gln | Gly | Pro | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Phe | Ser | Arg | Thr | Val | Phe | Cys | Asn | Gln | Pro | His | Met | His | Lys | Lys | Lys |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Pro | Leu | Arg | Tyr | Arg | Ser | Asn | Tyr | Val | Ser | Thr | Thr | Arg | Tyr | Asn | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Thr | Phe | Phe | Pro | Lys | Ser | Leu | Tyr | Glu | Gln | Phe | His | Arg | Ala | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Leu | Tyr | Phe | Leu | Val | Ala | Ala | Ile | Leu | Ser | Val | Phe | Pro | Leu | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Phe | Asn | Lys | Trp | Ser | Met | Ile | Ala | Pro | Leu | Val | Phe | Val | Val | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Ser | Met | Leu | Lys | Glu | Ala | Leu | Glu | Asp | Trp | Arg | Arg | Phe | Met | Gln |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Val | Lys | Ile | Asn | Ala | Arg | Lys | Thr | Cys | Val | His | Lys | Ser | Asp | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Phe | Arg | Gln | Arg | Lys | Trp | Lys | Lys | Val | Ser | Val | Gly | Asp | Ile | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Val | Glu | Lys | Asp | Glu | Phe | Phe | Pro | Ala | Asp | Leu | Leu | Leu | Leu | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Ser | Tyr | Glu | Asp | Gly | Ile | Cys | Tyr | Val | Glu | Thr | Met | Asn | Leu | Asp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Gly | Glu | Thr | Asn | Leu | Lys | Val | Lys | Arg | Ser | Leu | Glu | Val | Ser | Leu | Pro |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Leu | Asp | Asp | Asp | Glu | Ser | Phe | Lys | Asn | Phe | Met | Ala | Thr | Ile | Arg | Cys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Asp | Pro | Asn | Pro | Asn | Leu | Tyr | Thr | Phe | Val | Gly | Asn | Leu | Glu | Phe |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Arg | Gln | Thr | Phe | Pro | Leu | Asp | Pro | Ser | Gln | Ile | Leu | Leu | Arg | Asp |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ser | Lys | Leu | Arg | Asn | Thr | Thr | Tyr | Val | Tyr | Gly | Val | Val | Val | Phe | Thr |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Gly | Phe | Asp | Thr | Lys | Val | Met | Gln | Asn | Ser | Thr | Lys | Ser | Pro | Ser | Lys |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Arg | Ser | Arg | Ile | Glu | Arg | Thr | Met | Asp | Tyr | Ile | Ile | Tyr | Thr | Leu | Leu |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Val | Leu | Leu | Ile | Leu | Ile | Ser | Cys | Ile | Ser | Ser | Ser | Gly | Phe | Ala | Trp |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Glu | Thr | Glu | Phe | His | Met | Pro | Lys | Met | Trp | Tyr | Leu | Arg | Pro | Gly | Glu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Pro | Ile | Asp | Phe | Thr | Asn | Pro | Ile | Asn | Pro | Ile | Tyr | Ala | Gly | Val | Val |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| His | Leu | Ile | Thr | Ala | Leu | Leu | Leu | Tyr | Gly | Tyr | Leu | Ile | Pro | Ile | Ser |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Leu | Tyr | Val | Ser | Ile | Glu | Val | Val | Lys | Val | Trp | Gln | Ala | Ser | Phe | Ile |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Asn | Gln | Asp | Leu | His | Met | Tyr | Asp | Asp | Glu | Ser | Gly | Val | Pro | Ala | Asn |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ala | Arg | Thr | Ser | Asn | Leu | Asn | Glu | Glu | Leu | Gly | Gln | Val | His | Thr | Ile |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Leu | Ser | Asp | Lys | Thr | Gly | Thr | Leu | Thr | Cys | Asn | Gln | Met | Asp | Phe | Leu |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |     |
| Lys | Cys | Ser | Ile | Ala | Gly | Thr | Ser | Tyr | Gly | Val | Arg | Ser | Ser | Glu | Val |
|     |     | 420 |     |     |     |     |     | 425 |     |     |     | 430 |     |     |     |
| Glu | Val | Ala | Ala | Ala | Lys | Gln | Met | Ala | Val | Asp | Leu | Glu | Glu | His | Gly |
|     |     | 435 |     |     |     | 440 |     |     |     |     | 445 |     |     |     |     |
| Glu | Ile | Ser | Ser | Thr | Pro | Gln | Ser | Gln | Thr | Lys | Val | Tyr | Gly | Thr | Trp |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Asp | Ser | Ser | Arg | Xaa | Gln | Glu | Ile | Glu | Val | Glu | Gly | Asp | Asn | Asn | Tyr |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Asn | Thr | Pro | Arg | Ala | Pro | Ile | Lys | Gly | Phe | Gly | Phe | Glu | Asp | Asn | Arg |
|     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |     |
| Leu | Met | Asn | Gly | Asn | Trp | Leu | Arg | Glu | Ser | Gln | Pro | Asn | Asp | Ile | Leu |
|     |     | 500 |     |     |     |     |     | 505 |     |     |     |     | 510 |     |     |

DOCKET "08668960"

(2) INFORMATION FOR SEQ ID NO:527:

(A) LENGTH: 644 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..644

(D) OTHER INFORMATION: / Ceres Seq. ID 1586604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

| Variable                   | Mean | SD   | Min     | Max         |
|----------------------------|------|------|---------|-------------|
| Age                        | 34.5 | 10.2 | 18      | 65          |
| Gender                     | 50%  | 50%  | Male    | Female      |
| Marital status             | 65%  | 35%  | Married | Single      |
| Education                  | 12.5 | 2.5  | 9       | 16          |
| Income                     | 3500 | 1500 | 1000    | 8000        |
| Occupation                 | 30%  | 70%  | Manager | Worker      |
| Health status              | 75%  | 25%  | Good    | Poor        |
| Smoking status             | 40%  | 60%  | Smoker  | Non-smoker  |
| Alcohol consumption        | 30%  | 70%  | Drinker | Non-drinker |
| Exercise frequency         | 2.5  | 1.5  | 0       | 5           |
| Dietary habits             | 60%  | 40%  | Healthy | Unhealthy   |
| Stress level               | 5.5  | 1.5  | 1       | 10          |
| Sleep quality              | 7.0  | 1.0  | 5       | 10          |
| Mental health              | 6.5  | 1.5  | 3       | 10          |
| Life satisfaction          | 7.5  | 1.5  | 5       | 10          |
| Work-life balance          | 6.0  | 1.5  | 3       | 10          |
| Family support             | 8.0  | 1.0  | 6       | 10          |
| Community involvement      | 4.0  | 1.5  | 1       | 10          |
| Personal growth            | 6.5  | 1.5  | 3       | 10          |
| Financial stability        | 7.0  | 1.5  | 4       | 10          |
| Healthcare access          | 8.5  | 1.0  | 7       | 10          |
| Environmental quality      | 6.0  | 1.5  | 3       | 10          |
| Transportation             | 7.5  | 1.5  | 4       | 10          |
| Public services            | 6.5  | 1.5  | 3       | 10          |
| Crime rate                 | 5.0  | 1.5  | 2       | 10          |
| Police presence            | 7.0  | 1.5  | 4       | 10          |
| Neighborhood safety        | 8.0  | 1.0  | 6       | 10          |
| Local economy              | 6.0  | 1.5  | 3       | 10          |
| Business growth            | 7.0  | 1.5  | 4       | 10          |
| Unemployment rate          | 5.0  | 1.5  | 2       | 10          |
| Wage growth                | 6.0  | 1.5  | 3       | 10          |
| Cost of living             | 7.0  | 1.5  | 4       | 10          |
| Real estate market         | 8.0  | 1.0  | 6       | 10          |
| Infrastructure development | 6.5  | 1.5  | 3       | 10          |
| Public transportation      | 7.5  | 1.5  | 4       | 10          |
| Green spaces               | 6.0  | 1.5  | 3       | 10          |
| Parks and recreation       | 7.0  | 1.5  | 4       | 10          |
| Cultural activities        | 6.5  | 1.5  | 3       | 10          |
| Arts and culture           | 7.0  | 1.5  | 4       | 10          |
| Historical landmarks       | 6.0  | 1.5  | 3       | 10          |
| Local festivals            | 7.5  | 1.5  | 4       | 10          |
| Community events           | 6.5  | 1.5  | 3       | 10          |
| Volunteer opportunities    | 7.0  | 1.5  | 4       | 10          |
| Charitable organizations   | 6.0  | 1.5  | 3       | 10          |
| Non-profit sector          | 7.5  | 1.5  | 4       | 10          |
| Government services        | 6.5  | 1.5  | 3       | 10          |
| Public housing             | 7.0  | 1.5  | 4       | 10          |
| Waste management           | 6.0  | 1.5  | 3       | 10          |
| Water supply               | 7.5  | 1.5  | 4       | 10          |
| Electricity supply         | 6.5  | 1.5  | 3       | 10          |
| Internet access            | 8.0  | 1.0  | 6       | 10          |
| Digital literacy           | 7.0  | 1.5  | 4       | 10          |
| Online services            | 6.0  | 1.5  | 3       | 10          |
| E-commerce                 | 7.5  | 1.5  | 4       | 10          |
| Mobile banking             | 6.5  | 1.5  | 3       | 10          |
| Digital marketing          | 7.0  | 1.5  | 4       | 10          |
| Online education           | 6.0  | 1.5  | 3       | 10          |
| Distance learning          | 7.5  | 1.5  | 4       | 10          |
| Online healthcare          | 6.5  | 1.5  | 3       | 10          |
| Telemedicine               | 7.0  | 1.5  | 4       | 10          |
| Online shopping            | 6.0  | 1.5  | 3       | 10          |
| Online travel              | 7.5  | 1.5  | 4       | 10          |
| Online entertainment       | 6.5  | 1.5  | 3       | 10          |
| Online news                | 7.0  | 1.5  | 4       | 10          |
| Online social media        | 6.0  | 1.5  | 3       | 10          |
| Online dating              | 7.5  | 1.5  | 4       | 10          |
| Online job searching       | 6.5  | 1.5  | 3       | 10          |
| Online business            | 7.0  | 1.5  | 4       | 10          |
| Online investment          | 6.0  | 1.5  | 3       | 10          |
| Online banking             | 7.5  | 1.5  | 4       | 10          |
| Online insurance           | 6.5  | 1.5  | 3       | 10          |
| Online legal services      | 7.0  | 1.5  | 4       | 10          |
| Online healthcare          | 6.0  | 1.5  | 3       | 10          |
| Online education           | 7.5  | 1.5  | 4       | 10          |
| Online entertainment       | 6.5  | 1.5  | 3       | 10          |
| Online news                | 7.0  | 1.5  | 4       | 10          |
| Online social media        | 6.0  | 1.5  | 3       | 10          |
| Online dating              | 7.5  | 1.5  | 4       | 10          |
| Online job searching       | 6.5  | 1.5  | 3       | 10          |
| Online business            | 7.0  | 1.5  | 4       | 10          |
| Online investment          | 6.0  | 1.5  | 3       | 10          |
| Online banking             | 7.5  | 1.5  | 4       | 10          |
| Online insurance           | 6.5  | 1.5  | 3       | 10          |
| Online legal services      | 7.0  | 1.5  | 4       |             |

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| 225 |     | 230 |     | 235 |     | 240 |
| Lys | Ser | Pro | Ser | Lys | Arg | Ser |
|     |     |     |     | 245 |     | 250 |
| Ile | Tyr | Thr | Leu | Val | Leu | Leu |
|     |     |     |     |     |     | 255 |
| Ser | Gly | Phe | Ala | Trp | Glu | Thr |
|     |     |     |     |     |     | 260 |
| Leu | Arg | Pro | Gly | Glu | Pro | Ile |
|     |     |     |     |     |     | 265 |
| Tyr | Ala | Gly | Val | Val | His | Leu |
|     |     |     |     |     |     | 270 |
| 305 |     |     |     |     |     | 310 |
| Leu | Ile | Pro | Ile | Ser | Leu | Tyr |
|     |     |     |     |     |     | 315 |
| Gln | Ala | Ser | Phe | Ile | Asn | Gln |
|     |     |     |     |     |     | 320 |
| Gly | Val | Pro | Ala | Asn | Ala | Arg |
|     |     |     |     |     |     | 325 |
| Gln | Val | His | Thr | Ile | Leu | Ser |
|     |     |     |     |     |     | 330 |
| 385 |     |     |     |     |     | 380 |
| Arg | Ser | Ser | Glu | Val | Glu | Val |
|     |     |     |     |     |     | 390 |
| Leu | Glu | Glu | His | Gly | Glu | Ile |
|     |     |     |     |     |     | 395 |
| Val | Tyr | Gly | Thr | Trp | Asp | Ser |
|     |     |     |     |     |     | 400 |
| Gly | Asp | Asn | Asn | Tyr | Asn | Thr |
|     |     |     |     |     |     | 405 |
| Phe | Glu | Asp | Asn | Arg | Leu | Met |
|     |     |     |     |     |     | 410 |
| Pro | Asn | Asp | Ile | Leu | Gln | Phe |
|     |     |     |     |     |     | 415 |
| Ala | Ile | Pro | Glu | Leu | Asn | Glu |
|     |     |     |     |     |     | 420 |
| Glu | Ser | Pro | Asp | Glu | Ala | Ser |
|     |     |     |     |     |     | 425 |
| Phe | Glu | Phe | Phe | Lys | Arg | Thr |
|     |     |     |     |     |     | 430 |
| 545 |     |     |     |     |     | 540 |
| Leu | Leu | Glu | Phe | Thr | Ser | Lys |
|     |     |     |     |     |     | 545 |
| Asp | Glu | Glu | Gly | Gln | Ile | Leu |
|     |     |     |     |     |     | 550 |
| Ile | Phe | Glu | Arg | Leu | Ala | Lys |
|     |     |     |     |     |     | 555 |
| Thr | Arg | His | Leu | Thr | Glu | Tyr |
|     |     |     |     |     |     | 560 |
| Leu | Ala | Tyr | Arg | Lys | Leu | Asp |
|     |     |     |     |     |     | 565 |
| 625 |     |     |     |     |     | 620 |
| Glu | Phe | Leu | Lys |     |     |     |

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 585 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..585

(D) OTHER INFORMATION: / Ceres Seq. ID 1586605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Ala | Pro | Leu | Val | Phe | Val | Val | Gly | Leu | Ser | Met | Leu | Lys | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Leu | Glu | Asp | Trp | Arg | Arg | Phe | Met | Gln | Asp | Val | Lys | Ile | Asn | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Lys | Thr | Cys | Val | His | Lys | Ser | Asp | Gly | Val | Phe | Arg | Gln | Arg | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Trp | Lys | Lys | Val | Ser | Val | Gly | Asp | Ile | Val | Lys | Val | Glu | Lys | Asp | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Phe | Pro | Ala | Asp | Leu | Leu | Leu | Ser | Ser | Ser | Tyr | Glu | Asp | Gly |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Cys | Tyr | Val | Glu | Thr | Met | Asn | Leu | Asp | Gly | Glu | Thr | Asn | Leu | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Lys | Arg | Ser | Leu | Glu | Val | Ser | Leu | Pro | Leu | Asp | Asp | Asp | Glu | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Lys | Asn | Phe | Met | Ala | Thr | Ile | Arg | Cys | Glu | Asp | Pro | Asn | Pro | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Leu | Tyr | Thr | Phe | Val | Gly | Asn | Leu | Glu | Phe | Glu | Arg | Gln | Thr | Phe | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Leu | Asp | Pro | Ser | Gln | Ile | Leu | Leu | Arg | Asp | Ser | Lys | Leu | Arg | Asn | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Tyr | Val | Tyr | Gly | Val | Val | Val | Phe | Thr | Gly | Phe | Asp | Thr | Lys | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Met | Gln | Asn | Ser | Thr | Lys | Ser | Pro | Ser | Lys | Arg | Ser | Arg | Ile | Glu | Arg |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Thr | Met | Asp | Tyr | Ile | Ile | Tyr | Thr | Leu | Leu | Val | Leu | Leu | Ile | Leu | Ile |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Cys | Ile | Ser | Ser | Ser | Gly | Phe | Ala | Trp | Glu | Thr | Glu | Phe | His | Met |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Pro | Lys | Met | Trp | Tyr | Leu | Arg | Pro | Gly | Glu | Pro | Ile | Asp | Phe | Thr | Asn |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Pro | Ile | Asn | Pro | Ile | Tyr | Ala | Gly | Val | Val | His | Leu | Ile | Thr | Ala | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Leu | Tyr | Gly | Tyr | Leu | Ile | Pro | Ile | Ser | Leu | Tyr | Val | Ser | Ile | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Val | Lys | Val | Trp | Gln | Ala | Ser | Phe | Ile | Asn | Gln | Asp | Leu | His | Met |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Tyr | Asp | Asp | Glu | Ser | Gly | Val | Pro | Ala | Asn | Ala | Arg | Thr | Ser | Asn | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asn | Glu | Glu | Leu | Gly | Gln | Val | His | Thr | Ile | Leu | Ser | Asp | Lys | Thr | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Thr | Leu | Thr | Cys | Asn | Gln | Met | Asp | Phe | Leu | Lys | Cys | Ser | Ile | Ala | Gly |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Thr | Ser | Tyr | Gly | Val | Arg | Ser | Ser | Glu | Val | Glu | Val | Ala | Ala | Ala | Lys |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gln | Met | Ala | Val | Asp | Leu | Glu | Glu | His | Gly | Glu | Ile | Ser | Ser | Thr | Pro |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Gln | Ser | Gln | Thr | Lys | Val | Tyr | Gly | Thr | Trp | Asp | Ser | Ser | Arg | Xaa | Gln |
|     |     |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |     |
| Glu | Ile | Glu | Val | Glu | Gly | Asp | Asn | Asn | Tyr | Asn | Thr | Pro | Arg | Ala | Pro |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Ile | Lys | Gly | Phe | Gly | Phe | Glu | Asp | Asn | Arg | Leu | Met | Asn | Gly | Asn | Trp |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Leu | Arg | Glu | Ser | Gln | Pro | Asn | Asp | Ile | Leu | Gln | Phe | Phe | Arg | Ile | Leu |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Ala | Ile | Cys | His | Thr | Ala | Ile | Pro | Glu | Leu | Asn | Glu | Glu | Thr | Gly | Lys |
|     |     |     | 435 |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Tyr | Thr | Tyr | Glu | Ala | Glu | Ser | Pro | Asp | Glu | Ala | Ser | Phe | Leu | Ala | Ala |

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| Fitted model |                | Fitted model |                |
|--------------|----------------|--------------|----------------|
| Model        | Log-likelihood | Model        | Log-likelihood |
| Model 1      | -100.00        | Model 1      | -100.00        |
| Model 2      | -95.00         | Model 2      | -95.00         |
| Model 3      | -90.00         | Model 3      | -90.00         |
| Model 4      | -85.00         | Model 4      | -85.00         |
| Model 5      | -80.00         | Model 5      | -80.00         |
| Model 6      | -75.00         | Model 6      | -75.00         |
| Model 7      | -70.00         | Model 7      | -70.00         |
| Model 8      | -65.00         | Model 8      | -65.00         |
| Model 9      | -60.00         | Model 9      | -60.00         |
| Model 10     | -55.00         | Model 10     | -55.00         |
| Model 11     | -50.00         | Model 11     | -50.00         |
| Model 12     | -45.00         | Model 12     | -45.00         |
| Model 13     | -40.00         | Model 13     | -40.00         |
| Model 14     | -35.00         | Model 14     | -35.00         |
| Model 15     | -30.00         | Model 15     | -30.00         |
| Model 16     | -25.00         | Model 16     | -25.00         |
| Model 17     | -20.00         | Model 17     | -20.00         |
| Model 18     | -15.00         | Model 18     | -15.00         |
| Model 19     | -10.00         | Model 19     | -10.00         |
| Model 20     | -5.00          | Model 20     | -5.00          |
| Model 21     | 0.00           | Model 21     | 0.00           |
| Model 22     | 5.00           | Model 22     | 5.00           |
| Model 23     | 10.00          | Model 23     | 10.00          |
| Model 24     | 15.00          | Model 24     | 15.00          |
| Model 25     | 20.00          | Model 25     | 20.00          |
| Model 26     | 25.00          | Model 26     | 25.00          |
| Model 27     | 30.00          | Model 27     | 30.00          |
| Model 28     | 35.00          | Model 28     | 35.00          |
| Model 29     | 40.00          | Model 29     | 40.00          |
| Model 30     | 45.00          | Model 30     | 45.00          |
| Model 31     | 50.00          | Model 31     | 50.00          |
| Model 32     | 55.00          | Model 32     | 55.00          |
| Model 33     | 60.00          | Model 33     | 60.00          |
| Model 34     | 65.00          | Model 34     | 65.00          |
| Model 35     | 70.00          | Model 35     | 70.00          |
| Model 36     | 75.00          | Model 36     | 75.00          |
| Model 37     | 80.00          | Model 37     | 80.00          |
| Model 38     | 85.00          | Model 38     | 85.00          |
| Model 39     | 90.00          | Model 39     | 90.00          |
| Model 40     | 95.00          | Model 40     | 95.00          |
| Model 41     | 100.00         | Model 41     | 100.00         |
| Model 42     | 105.00         | Model 42     | 105.00         |
| Model 43     | 110.00         | Model 43     | 110.00         |
| Model 44     | 115.00         | Model 44     | 115.00         |
| Model 45     | 120.00         | Model 45     | 120.00         |
| Model 46     | 125.00         | Model 46     | 125.00         |
| Model 47     | 130.00         | Model 47     | 130.00         |
| Model 48     | 135.00         | Model 48     | 135.00         |
| Model 49     | 140.00         | Model 49     | 140.00         |
| Model 50     | 145.00         | Model 50     | 145.00         |
| Model 51     | 150.00         | Model 51     | 150.00         |
| Model 52     | 155.00         | Model 52     | 155.00         |
| Model 53     | 160.00         | Model 53     | 160.00         |
| Model 54     | 165.00         | Model 54     | 165.00         |
| Model 55     | 170.00         | Model 55     | 170.00         |
| Model 56     | 175.00         | Model 56     | 175.00         |
| Model 57     | 180.00         | Model 57     | 180.00         |
| Model 58     | 185.00         | Model 58     | 185.00         |
| Model 59     | 190.00         | Model 59     | 190.00         |
| Model 60     | 195.00         | Model 60     | 195.00         |
| Model 61     | 200.00         | Model 61     | 200.00         |
| Model 62     | 205.00         | Model 62     | 205.00         |
| Model 63     | 210.00         | Model 63     | 210.00         |
| Model 64     | 215.00         | Model 64     | 215.00         |
| Model 65     | 220.00         | Model 65     | 220.00         |
| Model 66     | 225.00         | Model 66     | 225.00         |
| Model 67     | 230.00         | Model 67     | 230.00         |
| Model 68     | 235.00         | Model 68     | 235.00         |
| Model 69     | 240.00         | Model 69     | 240.00         |
| Model 70     | 245.00         | Model 70     | 245.00         |
| Model 71     | 250.00         | Model 71     | 250.00         |
| Model 72     | 255.00         | Model 72     | 255.00         |
| Model 73     | 260.00         | Model 73     | 260.00         |
| Model 74     | 265.00         | Model 74     | 265.00         |
| Model 75     | 270.00         | Model 75     | 270.00         |
| Model 76     | 275.00         | Model 76     | 275.00         |
| Model 77     | 280.00         | Model 77     | 280.00         |
| Model 78     | 285.00         | Model 78     | 285.00         |
| Model 79     | 290.00         | Model 79     | 290.00         |
| Model 80     | 295.00         | Model 80     | 295.00         |
| Model 81     | 300.00         | Model 81</   |                |

Glu Glu Glu Glu Glu Glu Glu Lys Glu Glu Glu Glu Glu Glu Glu  
1 5 10 15  
Glu Glu Asn Arg Phe Arg Val Lys Lys Lys Lys Lys Lys Lys Lys  
20 25 30  
Lys Lys Ile Glu Glu Asp  
35

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..705
- (D) OTHER INFORMATION: / Ceres Seq. ID 1586696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atgcgatggc atgctgagca ccaatcgaag gagggagaaa tgaatcatcc ttcaaatgcg  | 60  |
| gcagagtggg gatatttcca agagttacat ccccggtttg ctgaagaacc ccgtaacgtt  | 120 |
| tatctcgggt tgtgtactga tgggttcaat ccatttggca tgtctcgtaa tcattcgttg  | 180 |
| tggcctgtga tcctaactcc atataatatt gatgttatgc atatagagaa gaattttctt  | 240 |
| gacaacatca tgaacactct cttgggtggt aagggtaaat caaaagacaa tatcatgtca  | 300 |
| agattggata ttgagaaata ttgttctcgg ccaggcttac atattcatag tacggatggt  | 360 |
| tattcttcag atttggctag ttgtgtagat ttggagaatg gtaagttttc aggcataaag  | 420 |
| ggatcatgatt gtcattgttt tatggagcga ctacttccat ttatctttgc tgaacttctt | 480 |
| gaccgaaatg tccaccttgc attatcagga attggagcat ttttccggga cctatgttcg  | 540 |
| agaactttac agacaagtcg cgttcaaatt ctcaaacaga acatagtttt aatcatctgt  | 600 |
| aacttggaaa agatctttcc accatcattt ttcgatgtta tggaacattt acctatccat  | 660 |
| ctccatacg aagctgaatt ggtggccct gtccaatata ggtga                    |     |

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..234
- (D) OTHER INFORMATION: / Ceres Seq. ID 1586697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Arg Trp His Ala Glu His Gln Ser Lys Glu Gly Glu Met Asn His |  |
| 1 5 10 15                                                       |  |
| Pro Ser Asn Ala Ala Glu Trp Arg Tyr Phe Gln Glu Leu His Pro Arg |  |
| 20 25 30                                                        |  |
| Phe Ala Glu Glu Pro Arg Asn Val Tyr Leu Gly Leu Cys Thr Asp Gly |  |
| 35 40 45                                                        |  |
| Phe Asn Pro Phe Gly Met Ser Arg Asn His Ser Leu Trp Pro Val Ile |  |
| 50 55 60                                                        |  |
| Leu Thr Pro Tyr Asn Ile Asp Val Met His Ile Glu Lys Asn Phe Leu |  |
| 65 70 75 80                                                     |  |
| Asp Asn Ile Met Asn Thr Leu Leu Gly Val Lys Gly Lys Ser Lys Asp |  |
| 85 90 95                                                        |  |
| Asn Ile Met Ser Arg Leu Asp Ile Glu Lys Tyr Cys Ser Arg Pro Gly |  |
| 100 105 110                                                     |  |
| Leu His Ile His Ser Thr Asp Gly Tyr Ser Ser Asp Leu Ala Ser Cys |  |
| 115 120 125                                                     |  |
| Val Asp Leu Glu Asn Gly Lys Phe Ser Gly Met Lys Gly His Asp Cys |  |
| 130 135 140                                                     |  |
| His Val Phe Met Glu Arg Leu Leu Pro Phe Ile Phe Ala Glu Leu Leu |  |

DOCKET "08060800"







- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 688 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

    (A) NAME/KEY: -

    (B) LOCATION: 1..688

    (D) OTHER INFORMATION: / Ceres Seq. ID 1587308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

|             |            |            |             |            |             |     |
|-------------|------------|------------|-------------|------------|-------------|-----|
| atccacacaa  | catttacaca | atacccttat | tctccacgta  | gaatcaagag | tactttctttt | 60  |
| ccttaaattct | ctacaaaaaa | aaaatcgatc | tattttactaa | gagatcataa | atatagattc  | 120 |
| atagacctat  | ttaagaaacg | acttaagaag | ctgttgatc   | atataccata | taaaatagca  | 180 |
| atggatatga  | taacgaagat | ggtgatggag | agaccggtgg  | tgatttacag | caagagctct  | 240 |
| tgctgtatgt  | ctcacacgat | caagactttg | ctctgcgatt  | tccgagcaaa | tccagcggtt  | 300 |
| tacgagctgg  | atgagatatc | tagagggagg | gagatcgagc  | aggcgttggt | gcggctcggg  | 360 |
| tgtagccccg  | cagttccggg | cgttttcatt | ggtggagagt  | tggtcgggtg | agccaacgag  | 420 |
| gtcatgagtc  | tacatcttaa | cggatccttg | attcccatgc  | ttaagcgggc | tggtgcattg  | 480 |
| tgggtttgac  | ttatcatggt | tttaactagt | ttacttaaca  | ctaagttaag | tacgcagaat  | 540 |
| aattttaaca  | catctatgat | cttggcatgg | tgatatgatg  | agtcacgctc | ggatcaataa  | 600 |
| tcagtgtggt  | gtcttttttt | ttttggttgt | cttactttaa  | gatatgtatc | gactgatacg  | 660 |
| aacttctatg  | aaataaaaaa | atattgac   |             |            |             |     |

(2) INFORMATION FOR SEQ ID NO:539:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 102 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS:

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (ix) FEATURE:

        (A) NAME/KEY: peptide

        (B) LOCATION: 1..102

        (D) OTHER INFORMATION: / Ceres Seq. ID 1587309

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Met | Ile | Thr | Lys | Met | Val | Met | Glu | Arg | Pro | Val | Ile | Tyr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Ser | Lys | Ser | Ser | Cys | Cys | Met | Ser | His | Thr | Ile | Lys | Thr | Leu | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Asp | Phe | Gly | Ala | Asn | Pro | Ala | Val | Tyr | Glu | Leu | Asp | Glu | Ile | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Gly | Arg | Glu | Ile | Glu | Gln | Ala | Leu | Leu | Arg | Leu | Gly | Cys | Ser | Pro |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Val | Pro | Gly | Val | Phe | Ile | Gly | Gly | Glu | Leu | Val | Gly | Gly | Ala | Asn |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     | 80  |     |
| Val | Met | Ser | Leu | His | Leu | Asn | Gly | Ser | Leu | Ile | Pro | Met | Leu | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Gly | Ala | Leu | Trp | Val |     |     |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:540:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 100 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS:

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (ix) FEATURE:

        (A) NAME/KEY: peptide

        (B) LOCATION: 1..100

        (D) OTHER INFORMATION: / Ceres Seq. ID 1587310

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

DOCTOY 08668960

Met Ile Thr Lys Met Val Met Glu Arg Pro Val Val Ile Tyr Ser Lys  
1 5 10 15  
Ser Ser Cys Cys Met Ser His Thr Ile Lys Thr Leu Leu Cys Asp Phe  
20 25 30  
Gly Ala Asn Pro Ala Val Tyr Glu Leu Asp Glu Ile Ser Arg Gly Arg  
35 40 45  
Glu Ile Glu Gln Ala Leu Leu Arg Leu Gly Cys Ser Pro Ala Val Pro  
50 55 60  
Gly Val Phe Ile Gly Gly Glu Leu Val Gly Gly Ala Asn Glu Val Met  
65 70 75 80  
Ser Leu His Leu Asn Gly Ser Leu Ile Pro Met Leu Lys Arg Ala Gly  
85 90 95  
Ala Leu Trp Val  
100

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: / Ceres Seq. ID 1587311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

Met Val Met Glu Arg Pro Val Val Ile Tyr Ser Lys Ser Ser Cys Cys  
1 5 10 15  
Met Ser His Thr Ile Lys Thr Leu Leu Cys Asp Phe Gly Ala Asn Pro  
20 25 30  
Ala Val Tyr Glu Leu Asp Glu Ile Ser Arg Gly Arg Glu Ile Glu Gln  
35 40 45  
Ala Leu Leu Arg Leu Gly Cys Ser Pro Ala Val Pro Gly Val Phe Ile  
50 55 60  
Gly Gly Glu Leu Val Gly Gly Ala Asn Glu Val Met Ser Leu His Leu  
65 70 75 80  
Asn Gly Ser Leu Ile Pro Met Leu Lys Arg Ala Gly Ala Leu Trp Val  
85 90 95

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1587406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

atgttctcta tcagtggagg tgcaaatcg tcagctttca gattcttctc cggctcaaaa 60  
cgtgaagcaa tttgggctca agaactttat tcataccaaa gggaaaataa atgtgagcat 120  
caagaaaagc agctaaatta tgtaaattga

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear







```

attcgcaggt cttttgtccc gatggctgac gaagccggga catccaattg gcgaaatgtg 300
cccagaccct tcatgccgac ggttaagatt gaggattttc tttatttcgg cccaaacgag 360
acagaagata tcttgctct taatgagcag aaagctttcg aaaaggctga gaagaagaag 420
aggaagaaca aaaaggatgat aatgccagat cctcccggct caacattgtg caccgagcgg 480
tctctctcgg accttagggc tcgatttggg cttggcgctg taaccttgcg tgtgccgagc 540
cctgacgagc gagccgacaa tccccctgcg ggtttctata ccttgtatga gggtttcttt 600
tatggttgc tcttatggct accaatccc aggctggctt tggagtatgt gcaatcatat 660
cagattgccc tttcccagat cacgatgcga tctttgagac atttgctcgg gattttgatt 720
cggagttatg aatccgaaac tgaaattacg ctcgttcatc tgaggaattt tctcgagatc 780
cggcggttc caaaatccaa agtggatcgg tattatatat ctctgctaa ggtaagaaga 840
ttattgacgg gttcccgcgc aaggacgatt cgtataccga ccacttcttc tacgtggctc 900
tcggagatgc tgttcacgat gatcttccc ggacaacgca ctctcaagtt tctcgagccg 960
attcctgacg atttcctctc ggcttatcac gcgttatcag ctcggaagtg tgattggtcg 1020
aaacacttct ctcgggatcg agtcaaacga gcactccgct ttcttcacgg tgtttcctgt 1080
cctaccagtt cagaatcttc ggaccacaga actcaattct tcgtcgatat gcagtcaact 1140
aagctcactt tgagggaggt gtacgcgaag aaaaaagaag ataaagagag acgcttggcg 1200
gaagagaaac gcctcgcgga tgcaggattg atttcaccgc gggtagcctc tccagatgcg 1260
actcaaaacc gggatgttgc tcccgaagtt gcggccccgg ttgacccgac gccttctaaa 1320
gctcaagagg tcgatcctac tgctgctgcg cctttgccc aggcggttgt tgcgctgcct 1380
gcgagcgaca agacggcgga taagcgtggt cggacggatg attcatcgct taagaagaaa 1440
agcaagaaga agaaggcctc gagtgcgag gcgggaaaag agctcccat ctttgaggac 1500
cgggttgttg cctcgatgaa ccgaatggtg cactcgtacg attcggccgt tagaacaaca 1560
tgaggcgcg caacagggtg gctgaagcgg atgctcggat ccaatctgcc gagcgagaaa 1620
gagatgaggg gctttcccaa gctgccgcgg cgaaaaaata gcaaaggagg aagccgaaaa 1680
ggaggctttc gtgaacaagg cgaatgcatt aagatggccg agctgaacct gagggcgagc 1740
tccgaggttg ttgcctcaa acgcatgctg gccgaggcga gggaactacg tgatagcgaa 1800
gtggtcggg cttctcaaac ggcaaatgt gagacctcc aggttttcat cgccagactt 1860
aaggctgcg aacagaaagt ctgccttctc gacgggatca acgatcagtt tctgtactta 1920
tcccaggcgc gggctaattgc gcaactgatc aaggcacttg aggaaggttg agtggtggcg 1980
accgagaaag accaggtcgn agaattgctg naagacttcg ccaatgccga ggtcgatttc 2040
gccaattttg tcgctag

```

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..685
- (D) OTHER INFORMATION: / Ceres Seq. ID 1587541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

```

Met Ser Pro Arg Gln Ser Pro Ser Ile Pro Ser Ala Ser Leu Val Asp
1 5 10 15
Ser Ser Asp Ser Asn His Pro Asp Asp Leu Pro Pro Ile Tyr Lys Arg
20 25 30
Arg Ala Val Trp Thr Ser Ser Glu Glu Asp Ala Val Ser Ser Ser Gly
35 40 45
Ala Pro Glu Gln Thr Thr Pro Phe Thr Ala Arg Glu Asp Thr Asn Ala
50 55 60
Asp Ile Ala Pro Glu Leu Asp Leu Pro Asp Asp Pro Glu Pro Pro Leu
65 70 75 80
Ile Arg Arg Ser Phe Val Pro Met Ala Asp Glu Ala Gly Thr Ser Asn
85 90 95
Trp Arg Asn Val Pro Glu Pro Phe Met Pro Thr Val Lys Ile Glu Asp
100 105 110
Phe Leu Tyr Phe Gly Pro Asn Glu Thr Glu Asp Ile Leu Arg Leu Asn
115 120 125
Glu Gln Lys Ala Phe Glu Lys Ala Glu Lys Lys Lys Arg Lys Asn Lys
130 135 140

```

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(2) INFORMATION FOR SEQ ID NO:550:

(A) LENGTH: 598 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..598

(D) OTHER INFORMATION: / Ceres Seq. ID 1587543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

| Socio-demographic characteristics |      |
|-----------------------------------|------|
| Age (years)                       | 52.0 |
| Male (%)                          | 52.0 |
| Female (%)                        | 48.0 |
| Marital status (%)                |      |
| Married                           | 52.0 |
| Single                            | 48.0 |
| Widowed                           | 0.0  |
| Divorced                          | 0.0  |
| Education (%)                     |      |
| High school or less               | 52.0 |
| College or more                   | 48.0 |
| Income (USD/monthly)              |      |
| Less than 1000                    | 52.0 |
| 1000 or more                      | 48.0 |
| Health status (%)                 |      |
| Good                              | 52.0 |
| Bad                               | 48.0 |
| Smoking status (%)                |      |
| Smoker                            | 52.0 |
| Non-smoker                        | 48.0 |
| Alcohol consumption (%)           |      |
| Drinker                           | 52.0 |
| Non-drinker                       | 48.0 |
| Exercise (%)                      |      |
| Regular                           | 52.0 |
| Irregular                         | 48.0 |
| Stress (%)                        |      |
| High                              | 52.0 |
| Low                               | 48.0 |
| Depression (%)                    |      |
| Yes                               | 52.0 |
| No                                | 48.0 |
| Family size (%)                   |      |
| 1-2                               | 52.0 |
| 3-4                               | 48.0 |
| 5 or more                         | 0.0  |
| Health insurance (%)              |      |
| Yes                               | 52.0 |
| No                                | 48.0 |
| Health status (%)                 |      |
| Good                              | 52.0 |
| Bad                               | 48.0 |
| Smoking status (%)                |      |
| Smoker                            | 52.0 |
| Non-smoker                        | 48.0 |
| Alcohol consumption (%)           |      |
| Drinker                           | 52.0 |
| Non-drinker                       | 48.0 |
| Exercise (%)                      |      |
| Regular                           | 52.0 |
| Irregular                         | 48.0 |
| Stress (%)                        |      |
| High                              | 52.0 |
| Low                               | 48.0 |
| Depression (%)                    |      |
| Yes                               | 52.0 |
| No                                | 48.0 |
| Family size (%)                   |      |
| 1-2                               | 52.0 |
| 3-4                               | 48.0 |
| 5 or more                         | 0.0  |
| Health insurance (%)              |      |
| Yes                               | 52.0 |
| No                                | 48.0 |



(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1587564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

Ile Ile Met Ser Tyr Leu Val Lys Leu Asp Val Val Ala Leu Asn Val  
1 5 10 15  
Ser Gly Lys Asn Tyr Met Ser Trp Ala Ser Asp Ile Lys Met His Leu  
20 25 30  
Arg Ser Asn Gly Leu Leu Ser Thr Ile Asn Ala Ser Glu Thr Thr Ser  
35 40 45  
Asp Glu Ser Lys Ala Lys Ala Met Pro Asp Met Asn Gly Leu Ile Ser  
50 55 60  
Thr Arg Met Ile Leu Cys Gly Glu Lys Val Ser Asp Tyr Asp Met Ile  
65 70 75 80  
Glu Lys Thr Leu Ser Thr Phe His Pro Gly Asn Arg Gly Pro Gly Pro  
85 90 95  
Cys Arg Gly Cys Gly His Gly Arg Gly Arg Gly Arg Gly His Gly Arg  
100 105 110  
Gly Lys Glu Lys Val Ser Ile Pro Ile Ile Ser Thr Arg Lys Lys Pro  
115 120 125  
Thr Lys Ile Met Leu Ala Val Leu Arg Lys Gly Met Leu Lys Ala Leu  
130 135 140  
Ala Thr Asp Ala Ala  
145

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1587565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

Met Ser Tyr Leu Val Lys Leu Asp Val Ala Leu Asn Val Ser Gly  
1 5 10 15  
Lys Asn Tyr Met Ser Trp Ala Ser Asp Ile Lys Met His Leu Arg Ser  
20 25 30  
Asn Gly Leu Leu Ser Thr Ile Asn Ala Ser Glu Thr Thr Ser Asp Glu  
35 40 45  
Ser Lys Ala Lys Ala Met Pro Asp Met Asn Gly Leu Ile Ser Thr Arg  
50 55 60  
Met Ile Leu Cys Gly Glu Lys Val Ser Asp Tyr Asp Met Ile Glu Lys  
65 70 75 80  
Thr Leu Ser Thr Phe His Pro Gly Asn Arg Gly Pro Gly Pro Cys Arg  
85 90 95  
Gly Cys Gly His Gly Arg Gly Arg Gly Arg Gly His Gly Arg Gly Lys  
100 105 110  
Glu Lys Val Ser Ile Pro Ile Ile Ser Thr Arg Lys Lys Pro Thr Lys  
115 120 125  
Ile Met Leu Ala Val Leu Arg Lys Gly Met Leu Lys Ala Leu Ala Thr  
130 135 140  
Asp Ala Ala  
145

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

09669980-10300









| Generalized Fuzzy |       |
|-------------------|-------|
| Model             | Value |
| Model 1           | 0.000 |
| Model 2           | 0.000 |
| Model 3           | 0.000 |
| Model 4           | 0.000 |
| Model 5           | 0.000 |
| Model 6           | 0.000 |
| Model 7           | 0.000 |
| Model 8           | 0.000 |
| Model 9           | 0.000 |
| Model 10          | 0.000 |
| Model 11          | 0.000 |
| Model 12          | 0.000 |
| Model 13          | 0.000 |
| Model 14          | 0.000 |
| Model 15          | 0.000 |
| Model 16          | 0.000 |
| Model 17          | 0.000 |
| Model 18          | 0.000 |
| Model 19          | 0.000 |
| Model 20          | 0.000 |
| Model 21          | 0.000 |
| Model 22          | 0.000 |
| Model 23          | 0.000 |
| Model 24          | 0.000 |
| Model 25          | 0.000 |
| Model 26          | 0.000 |
| Model 27          | 0.000 |
| Model 28          | 0.000 |
| Model 29          | 0.000 |
| Model 30          | 0.000 |
| Model 31          | 0.000 |
| Model 32          | 0.000 |
| Model 33          | 0.000 |
| Model 34          | 0.000 |
| Model 35          | 0.000 |
| Model 36          | 0.000 |
| Model 37          | 0.000 |
| Model 38          | 0.000 |
| Model 39          | 0.000 |
| Model 40          | 0.000 |
| Model 41          | 0.000 |
| Model 42          | 0.000 |
| Model 43          | 0.000 |
| Model 44          | 0.000 |
| Model 45          | 0.000 |
| Model 46          | 0.000 |
| Model 47          | 0.000 |
| Model 48          | 0.000 |
| Model 49          | 0.000 |
| Model 50          | 0.000 |
| Model 51          | 0.000 |
| Model 52          | 0.000 |
| Model 53          | 0.000 |
| Model 54          | 0.000 |
| Model 55          | 0.000 |
| Model 56          | 0.000 |
| Model 57          | 0.000 |
| Model 58          | 0.000 |
| Model 59          | 0.000 |
| Model 60          | 0.000 |
| Model 61          | 0.000 |
| Model 62          | 0.000 |
| Model 63          | 0.000 |
| Model 64          | 0.000 |
| Model 65          | 0.000 |
| Model 66          | 0.000 |
| Model 67          | 0.000 |
| Model 68          | 0.000 |
| Model 69          | 0.000 |
| Model 70          | 0.000 |
| Model 71          | 0.000 |
| Model 72          | 0.000 |
| Model 73          | 0.000 |
| Model 74          | 0.000 |
| Model 75          | 0.000 |
| Model 76          | 0.000 |
| Model 77          | 0.000 |
| Model 78          | 0.000 |
| Model 79          | 0.000 |
| Model 80          | 0.000 |
| Model 81          | 0.000 |
| Model 82          | 0.000 |
| Model 83          | 0.000 |
| Model 84          | 0.000 |
| Model 85          | 0.000 |
| Model 86          | 0.000 |
| Model 87          | 0.000 |
| Model 88          | 0.000 |
| Model 89          | 0.000 |
| Model 90          | 0.000 |
| Model 91          | 0.000 |
| Model 92          | 0.000 |
| Model 93          | 0.000 |
| Model 94          | 0.000 |
| Model 95          | 0.000 |
| Model 96          | 0.000 |
| Model 97          | 0.000 |
| Model 98          | 0.000 |
| Model 99          | 0.000 |
| Model 100         | 0.000 |

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..452

- (D) OTHER INFORMATION: / Ceres Seq. ID 1587597

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

(X1) SEQUENCE DESCRIPTION

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Asn | Glu | Lys | Glu | Val | Tyr | Gln | Gln | Ser | Ile | Gly | Ala | Val | Cys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Met | Leu | Asp | Trp | Pro | Arg | Glu | Arg | Met | Leu | Val | Gln | Val | Leu | Asp | Asp |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |

Ser Ser Glu Leu Asp Val Gln Gln Leu Ile Lys Ala Glu Val Gln Lys  
35 40 45  
Trp Gln Gln Arg Gly Val Arg Ile Val Tyr Arg His Arg Leu Ile Arg  
50 55 60  
Thr Gly Tyr Lys Ala Gly Asn Leu Lys Ala Ala Met Asn Cys Glu Tyr  
65 70 75 80  
Val Lys Asp Tyr Glu Phe Val Ala Ile Phe Asp Ala Asp Phe Gln Pro  
85 90 95  
Pro Ala Asp Phe Leu Lys Lys Thr Val Pro His Phe Lys Gly Asn Glu  
100 105 110  
Glu Leu Ala Leu Val Gln Thr Arg Trp Ala Phe Val Asn Lys Asp Glu  
115 120 125  
Asn Leu Leu Thr Arg Leu Gln Asn Ile Asn Leu Ser Phe His Phe Glu  
130 135 140  
Val Glu Gln Gln Val Asn Gly Val Phe Ile Asn Phe Phe Gly Phe Asn  
145 150 155 160  
Gly Thr Ala Gly Val Trp Arg Ile Lys Ala Leu Glu Asp Cys Gly Gly  
165 170 175  
Trp Leu Glu Arg Thr Thr Val Glu Asp Met Asp Ile Ala Val Arg Ala  
180 185 190  
His Leu Cys Gly Trp Lys Phe Ile Tyr Leu Asn Asp Val Lys Cys Leu  
195 200 205  
Cys Glu Leu Pro Glu Ser Tyr Glu Ala Tyr Lys Lys Gln Gln Tyr Arg  
210 215 220  
Trp His Ser Gly Pro Met Gln Leu Phe Arg Leu Cys Phe Phe Asp Ile  
225 230 235 240  
Leu Arg Ser Lys Val Ser Ala Ala Lys Lys Ala Asn Met Ile Phe Leu  
245 250 255  
Phe Phe Leu Leu Arg Lys Leu Ile Leu Pro Phe Tyr Ser Phe Thr Leu  
260 265 270  
Phe Cys Val Ile Leu Pro Leu Thr Met Phe Phe Pro Glu Ala Asn Leu  
275 280 285  
Pro Ser Trp Val Val Cys Tyr Ile Pro Gly Ile Met Ser Ile Leu Asn  
290 295 300  
Ile Ile Pro Ala Pro Arg Ser Phe Pro Phe Ile Val Pro Tyr Leu Leu  
305 310 315 320  
Phe Glu Asn Thr Met Ser Val Thr Lys Phe Gly Ala Met Ile Ser Gly  
325 330 335  
Leu Phe Lys Phe Asp Ser Ser Tyr Glu Trp Val Val Thr Lys Lys Leu  
340 345 350  
Gly Arg Ser Ser Glu Ala Asp Leu Val Ala Tyr Ala Glu Ser Gly Ser  
355 360 365  
Leu Val Glu Ser Thr Thr Ile Gln Arg Ser Ser Ser Asp Ser Gly Leu  
370 375 380  
Thr Glu Leu Ser Lys Leu Gly Ala Ala Lys Lys Ala Gly Lys Thr Lys  
385 390 395 400  
Arg Asn Arg Leu Tyr Arg Thr Glu Ile Ala Leu Ala Phe Ile Leu Leu  
405 410 415  
Ala Ala Ser Val Arg Ser Leu Leu Ser Ala Gln Gly Ile His Phe Tyr  
420 425 430  
Phe Leu Leu Phe Gln Gly Ile Thr Phe Val Ile Val Gly Leu Asp Leu  
435 440 445  
Ile Gly Glu Gln  
450

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

00000000 00000000

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2049

(D) OTHER INFORMATION: / Ceres Seq. ID 1587598

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

atgtctcgct cccagaacga ggagtttcaa caatgggtgga acaagcaacg agataggaac 60  
aatcacgacg ttctttacgc cggcgacgat gaagcattcc tcacogttga aatccgtact 120  
ccggccaccg ttgaccctga taaggatcgg atccggactc gtaccgttcg tcagctctct 180  
cgtctctacc tcctcaagtt caagcaactc gcatcttctt tcctctggat cggtaactct 240  
ttcctttacc ttgttcgcac cgccaatcgc cgcattgcc aagataatcc tccatccgtg 300  
tcttctctcg ctgattgtga ccgtttaatc aagggaattc tcgttggtgt tgtgcttctt 360  
ctctgtttcg agcttgccgc ttatttcaag ggatggcaact tcacacctcc ctctgttgcc 420  
tccgccgagg tcgctgtgga ggtggtttac gcttggtggt tggagatcag ggcattctac 480  
cttgccccac cgcttcagag cttgaccaat gtatgtatag ttctcttctt gattcaatcg 540  
gttgaccgtc tgggtcttgt gcttggtatc ttctggatca agctccgccg tattaagcct 600  
gttgcatcta tggagtacc gactaaattg gttggagagg gagttagatt ggaagattat 660  
ccaatggtga ttgttcagat tccaatgtgc aatgaaaagg aggtttacca acaatctatt 720  
ggagctgtgt gtatgcttga ctggccaagg gaaagaatgc tagttcaggt tcttgatgac 780  
tccagtgaat tggatgttca gcagcttata aaagcggaag tacaaaaatg gcaacaaagg 840  
ggtgtccgga tagtgtatag acatcgtctc atacgtactg gttacaaggc tggaaacctt 900  
aaagctgcaa tgaactgtga atatgtcaaa gactacgagt ttgtcgccat atttgatgca 960  
gatttccagc cacctgcgga tttcttgaag aaaactgtgc ctcatthtaa gggtaatgaa 1020  
gaattagcct tgggtccaaac acgggtgggt tttgtgaaca aagacgaaa cttgcttaca 1080  
agactccaga acataaattt gtctttccac tttgaagttg aacagcaggt caatgggtgt 1140  
tttattaact tctttggctt taatggaact gctggtgttt ggagaatcaa agccctcgag 1200  
gattgcgggg gatggttga gcgaacaact gttgaggaca tggatattgc cgttcgtgag 1260  
catctttgtg gatggaagtt catttatctg aatgatgtta agtgtctctg tgaacttccg 1320  
gagtcctatg aggcatacaa aaaacagcaa taccgctggc attcgggtcc aatgcaattg 1380  
ttccgtttgt gcttctttga cattcttcgg tcaaagggtg gtgctgccaa gaaagcaaat 1440  
atgatatttc tcttcttctt gctacggaag cttatcttgc cattctactc attcacgctc 1500  
ttctggtca ttcttccatt aacgatgttc ttcccagaag ctaacttacc atcttggtgt 1560  
gtttgtatata tccctgggat catgtccatc ttaaaccatc tcccagcccc aagatccttc 1620  
cctttcatag ttccgtatct ccttttcgaa aacaccatgt cagttaccaa atttgagacc 1680  
atgatctctg gtttgttcaa gtttgatagt tcttacgagt gggtagtcac caaaaagcta 1740  
gggagatcct ctgaggcgga tctggttgca tacgcagagt ccggtctttt ggttgagtc 1800  
acaaccatcc aacgatcatc ctctgattca ggtctgaccg agcttagcaa actaggagca 1860  
gcaaagaaag ctggcaaaac caaaagaaac cgtctgtaca gaacggaaat cgcactcgcg 1920  
tttatcctct tggcagcctc ggtgagaagc ttgttgcctg cgcaagggat ccatttctat 1980  
ttctcttgt tccaaggaat cacgttcgtt attgtcggtc tagatttgat cggggaacag 2040  
gtcagttag

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 682 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..682

(D) OTHER INFORMATION: / Ceres Seq. ID 1587599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

Met Ser Arg Ser Gln Asn Glu Glu Phe Gln Gln Trp Trp Asn Lys Gln  
1 5 10 15  
Arg Asp Arg Asn Asn His Asp Val Leu Tyr Ala Gly Asp Asp Glu Ala  
20 25 30  
Phe Leu Thr Val Glu Ile Arg Thr Pro Ala Thr Val Asp Pro Asp Lys  
35 40 45  
Asp Arg Ile Arg Thr Arg Thr Val Arg Gln Leu Ser Arg Leu Tyr Leu  
50 55 60  
Leu Lys Phe Lys Gln Leu Ala Ser Ser Phe Leu Trp Ile Gly Asn Ser

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Phe | Leu | Tyr | Leu | Val | Arg | Thr | Ala | Asn | Arg | Arg | Ile | Ala | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |
| Pro | Pro | Ser | Val | Ser | Ser | Ser | Ala | Arg | Leu | Tyr | Arg | Leu | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |
| Phe | Leu | Val | Gly | Val | Val | Leu | Leu | Leu | Cys | Phe | Glu | Leu | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |
| Phe | Lys | Gly | Trp | His | Phe | Thr | Pro | Pro | Ser | Val | Ala | Ser | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |
| Ala | Val | Glu | Val | Val | Tyr | Ala | Trp | Trp | Leu | Glu | Ile | Arg | Ala |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |
| Leu | Ala | Pro | Pro | Leu | Gln | Ser | Leu | Thr | Asn | Val | Cys | Ile | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |
| Leu | Ile | Gln | Ser | Val | Asp | Arg | Leu | Val | Leu | Val | Leu | Gly | Cys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |
| Ile | Lys | Leu | Arg | Arg | Ile | Lys | Pro | Val | Ala | Ser | Met | Glu | Tyr |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |
| Lys | Leu | Val | Gly | Glu | Gly | Val | Arg | Leu | Glu | Asp | Tyr | Pro | Met |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |
| Val | Gln | Ile | Pro | Met | Cys | Asn | Glu | Lys | Glu | Val | Tyr | Gln | Gln |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     |
| Gly | Ala | Val | Cys | Met | Leu | Asp | Trp | Pro | Arg | Glu | Arg | Met | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     | 255 |
| Val | Leu | Asp | Asp | Ser | Ser | Glu | Leu | Asp | Val | Gln | Gln | Leu | Ile |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |
| Glu | Val | Gln | Lys | Trp | Gln | Gln | Arg | Gly | Val | Arg | Ile | Val | Tyr |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |
| Arg | Leu | Ile | Arg | Thr | Gly | Tyr | Lys | Ala | Gly | Asn | Leu | Lys | Ala |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |
| Asn | Cys | Glu | Tyr | Val | Lys | Asp | Tyr | Glu | Phe | Val | Ala | Ile | Phe |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     |
| Asp | Phe | Gln | Pro | Pro | Ala | Asp | Phe | Leu | Lys | Lys | Thr | Val | Pro |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     | 335 |
| Lys | Gly | Asn | Glu | Glu | Leu | Ala | Leu | Val | Gln | Thr | Arg | Trp | Ala |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |
| Asn | Lys | Asp | Glu | Asn | Leu | Leu | Thr | Arg | Leu | Gln | Asn | Ile | Asn |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     |     |     |
| Phe | His | Phe | Glu | Val | Glu | Gln | Gln | Val | Asn | Gly | Val | Phe | Ile |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |
| Phe | Gly | Phe | Asn | Gly | Thr | Ala | Gly | Val | Trp | Arg | Ile | Lys | Ala |
| 385 |     |     |     |     | 390 |     |     |     | 395 |     |     |     |     |
| Asp | Cys | Gly | Gly | Trp | Leu | Glu | Arg | Thr | Thr | Val | Glu | Asp | Met |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     | 415 |
| Ala | Val | Arg | Ala | His | Leu | Cys | Gly | Trp | Lys | Phe | Ile | Tyr | Leu |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |
| Val | Lys | Cys | Leu | Cys | Glu | Leu | Pro | Glu | Ser | Tyr | Glu | Ala | Tyr |
|     | 435 |     |     |     |     |     | 440 |     |     |     |     | 445 |     |
| Gln | Gln | Tyr | Arg | Trp | His | Ser | Gly | Pro | Met | Gln | Leu | Phe | Arg |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |
| Phe | Phe | Asp | Ile | Leu | Arg | Ser | Lys | Val | Ser | Ala | Ala | Lys | Lys |
| 465 |     |     |     |     | 470 |     |     |     | 475 |     |     |     |     |
| Met | Ile | Phe | Leu | Phe | Phe | Leu | Leu | Arg | Lys | Leu | Ile | Leu | Pro |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     | 495 |
| Ser | Phe | Thr | Leu | Phe | Cys | Val | Ile | Leu | Pro | Leu | Thr | Met | Phe |
|     | 500 |     |     |     |     |     |     | 505 |     |     |     | 510 |     |
| Glu | Ala | Asn | Leu | Pro | Ser | Trp | Val | Val | Cys | Tyr | Ile | Pro | Gly |
|     | 515 |     |     |     |     |     | 520 |     |     |     |     | 525 |     |
| Ser | Ile | Leu | Asn | Ile | Ile | Pro | Ala | Pro | Arg | Ser | Phe | Pro | Phe |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |
| Pro | Tyr | Leu | Leu | Phe | Glu | Asn | Thr | Met | Ser | Val | Thr | Lys | Phe |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     | 560 |

DOCKET "08668860"









|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ser | Lys | Ile | Leu | Asp | Ser | Phe | Glu | Glu | Glu | Ile | Glu | Ala | Thr | Ile | 340 | 345 | 350 |
| Met | Lys | Lys | Ile | Glu | Asp | Glu | Ile | Arg | Asn | Ala | Ile | Glu | Glu | Glu | Glu | 355 | 360 | 365 |
| Lys | Leu | Ala | Glu | Met | Glu | Glu | Leu | Ala | Val | Val | Ala | Val | Ala | Glu | Thr | 370 | 375 | 380 |
| Glu | Glu | Val | Glu | Glu | Ser | Lys | Glu | Val | Val | Pro | Asp | Cys | Ile | Pro | Gln | 385 | 390 | 400 |
| Asn | Glu | Glu | Arg | Ser | Glu | Gln | Gly | Asn | Arg | Glu | Pro | Asp | Pro | Ser | Pro | 405 | 410 | 415 |
| Glu | Val | Val | Met | Arg | Arg | Ser | Leu | Gln | Glu | Glu | Thr | Thr | Glu | Lys | Glu | 420 | 425 | 430 |
| Lys | Thr | Thr | Ala | Thr | Gln | Ile | Arg | Phe | Arg | Gln | Met | Phe | Thr | Arg | Lys | 435 | 440 | 445 |
| Thr | Ser | Gly | Glu | Glu | Asp | Thr | Thr | Arg | Ser | Arg | Arg | Arg | Asn | His | His | 450 | 455 | 460 |
| His | His | Gln | Pro | Lys | Lys | Arg | Ile | Val | Thr | Ala | Val | Asp | Ser | Asn | Ala | 465 | 470 | 475 |
| Ser | Ser | Arg | Arg | Arg | Ser | Ile | Asp | Arg | Pro | Pro | Leu | His | Leu | Gln | Pro | 485 | 490 | 495 |
| Pro | Arg | Ser | Ser | Cys | Ser | Tyr | Pro | Ala | Ala | Pro | Pro | Ile | Ile | Thr | Ala | 500 | 505 | 510 |
| Ala | Ala | Ala | Val | Gly | Glu | Gln | Arg | Val | Ala | Gly | Ala | Asn | Lys | Val | Gln | 515 | 520 | 525 |
| Pro | Pro | Val | Leu | Pro | Arg | Cys | Lys | Ser | Glu | Pro | Arg | Lys | Ser | Ala | Ser | 530 | 535 | 540 |
| Lys | Leu | Ala | Pro | Glu | Ala | Cys | Phe | Trp | Lys | Asn | Arg | Lys | Leu | Val | Ala | 545 | 550 | 555 |
| Thr | Pro | Ser | Gly | Asn | Arg | Arg | Cys | Arg | Arg | Gly | Val | Gly | Phe |     |     | 565 | 570 | 575 |

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..535
- (D) OTHER INFORMATION: / Ceres Seq. ID 1587620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Arg | Leu | Ser | Ser | Lys | Ser | Ile | His | Ser | Pro | Ala | Arg | Ser | Ala | Cys | 1   | 5   | 10  | 15 |
| Leu | Thr | Thr | Ser | Leu | Ser | Arg | Arg | Leu | Arg | Thr | Ser | Gly | Arg | Lys | Arg | 20  | 25  | 30  |    |
| Ser | Gly | Ser | Gly | Tyr | Glu | Asn | Ser | Asn | Asn | Asn | Asn | Asn | Asn | Asn | Ile | 35  | 40  | 45  |    |
| Glu | Pro | Ser | Ser | Pro | Lys | Lys | His | Val | Lys | Lys | Lys | Met | Arg | Ala | Arg | 50  | 55  | 60  |    |
| Ser | Arg | Arg | Lys | Gly | Gly | Glu | Asn | Ser | Phe | Arg | Arg | Ser | Val | Asp | Gln | 65  | 70  | 75  | 80 |
| Asn | Asp | Gly | Gly | Gly | Gly | Cys | Arg | Phe | Lys | Ala | Ser | Glu | Asn | Arg | Leu | 85  | 90  | 95  |    |
| Val | His | Leu | Pro | Val | Thr | Ile | Cys | Glu | Ser | Leu | Arg | Ser | Phe | Gly | Ser | 100 | 105 | 110 |    |
| Glu | Leu | Asn | Cys | Phe | Phe | Pro | Cys | Arg | Ser | Ser | Cys | Thr | Glu | Asn | Ser | 115 | 120 | 125 |    |
| His | Gly | Asp | Gly | Arg | Arg | Ala | Glu | Ser | Asn | Asn | Asp | Gly | Cys | Gly | Gly | 130 | 135 | 140 |    |
| Gly | Gly | Gly | Gly | Ser | Asn | Ser | Cys | Gly | Ala | Val | Phe | Thr | Arg | Trp | Phe |     |     |     |    |

09689980 101300



(2) INFORMATION FOR SEQ ID NO:568:

(A) LENGTH: 344 amino acids

(C) STRANDEDNESS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1587655

| Met | Ser | Ser | Ala | Thr | Ala | Thr | Tyr | Asn | Tyr | Asp | Val | Phe | Leu | Ser | Phe |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Gly | Pro | Asp | Thr | Arg | Arg | Lys | Phe | Ile | Ser | Phe | Leu | Tyr | Lys | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Val | Gly | Arg | Asp | Ile | Arg | Thr | Phe | Lys | Asp | Asp | Lys | Glu | Leu | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Gly | Gln | Met | Ile | Ser | Pro | Glu | Leu | Lys | Arg | Ala | Ile | Glu | Glu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Phe | Ala | Val | Val | Val | Val | Ser | Glu | Asn | Tyr | Ala | Ala | Ser | Ser | Trp |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Cys | Leu | Asn | Glu | Leu | Val | Glu | Ile | Met | Lys | Val | Gln | Lys | Asn | Lys | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Ile | Thr | Val | Met | Pro | Ile | Phe | Tyr | Gly | Val | Asp | Pro | Cys | Asp | Leu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Arg | Gln | Ile | Gly | Asp | Val | Ala | Glu | Gln | Phe | Lys | Lys | His | Glu | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Glu | Glu | Asp | Leu | Glu | Lys | Val | Ala | Ser | Trp | Arg | Arg | Ala | Leu | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Leu | Ala | Ser | Ile | Ser | Gly | Asp | Cys | Ser | Ser | Lys | Cys | Glu | Asp | Asp |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Glu | Leu | Val | Asp | Val | Ile | Ala | Asp | Lys | Ile | Ser | Lys | Glu | Leu | Met |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Val | Thr | Thr | Ile | Ser | Asn | Gly | Arg | Asn | Leu | Val | Gly | Ile | Asp | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| His | Met | Lys | Glu | Leu | Asn | Leu | Leu | Met | Asp | Leu | Asn | Ser | Asn | Lys | Gly |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Arg | Met | Val | Gly | Ile | Trp | Val | Arg | Gly | Gly | Ser | Cys | Arg | Ser | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Ala | Lys | Tyr | Val | Tyr | Gln | Thr | Ser | Cys | Gln | His | Phe | Asp | Ser | His |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Cys | Phe | Leu | Gly | Asn | Val | Lys | Arg | Ile | Cys | His | Gly | Asn | Tyr | Phe | Glu |

245 250 255  
Ser His Leu His Lys Glu Leu Leu Ala Asn Ile Lys Gly Glu Asn Ser  
260 265 270  
Ser Lys Gln Ser Leu Lys Lys Gln Lys Val Leu Leu Val Ala Asp Asp  
275 280 285  
Val Asp Lys Leu Glu Gln Leu Asp Ala Leu Ala Gly Asp Phe Asn Gly  
290 295 300  
Phe Gly Pro Gly Ser Val Val Ile Ile Thr Thr Lys Asp Lys Gln Leu  
305 310 315 320  
Leu Ile Ser Tyr Gly Ile Gln Leu Val Tyr Glu Ala Glu Phe Leu Thr  
325 330 335  
Phe Gln Lys Phe Cys Arg Ser Phe  
340

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..293
- (D) OTHER INFORMATION: / Ceres Seq. ID 1587657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

Met Ile Ser Pro Glu Leu Lys Arg Ala Ile Glu Glu Ser Lys Phe Ala  
1 5 10 15  
Val Val Val Val Ser Glu Asn Tyr Ala Ala Ser Ser Trp Cys Leu Asn  
20 25 30  
Glu Leu Val Glu Ile Met Lys Val Gln Lys Asn Lys Gly Ser Ile Thr  
35 40 45  
Val Met Pro Ile Phe Tyr Gly Val Asp Pro Cys Asp Leu Arg Arg Gln  
50 55 60  
Ile Gly Asp Val Ala Glu Gln Phe Lys Lys His Glu Ala Arg Glu Glu  
65 70 75 80  
Asp Leu Glu Lys Val Ala Ser Trp Arg Arg Ala Leu Thr Ser Leu Ala  
85 90 95  
Ser Ile Ser Gly Asp Cys Ser Ser Lys Cys Glu Asp Asp Ser Glu Leu  
100 105 110  
Val Asp Val Ile Ala Asp Lys Ile Ser Lys Glu Leu Met Leu Val Thr  
115 120 125  
Thr Ile Ser Asn Gly Arg Asn Leu Val Gly Ile Asp Lys His Met Lys  
130 135 140  
Glu Leu Asn Leu Leu Met Asp Leu Asn Ser Asn Lys Gly Lys Arg Met  
145 150 155 160  
Val Gly Ile Trp Val Arg Gly Gly Ser Cys Arg Ser Ala Leu Ala Lys  
165 170 175  
Tyr Val Tyr Gln Thr Ser Cys Gln His Phe Asp Ser His Cys Phe Leu  
180 185 190  
Gly Asn Val Lys Arg Ile Cys His Gly Asn Tyr Phe Glu Ser His Leu  
195 200 205  
His Lys Glu Leu Leu Ala Asn Ile Lys Gly Glu Asn Ser Ser Lys Gln  
210 215 220  
Ser Leu Lys Lys Gln Lys Val Leu Leu Val Ala Asp Asp Val Asp Lys  
225 230 235 240  
Leu Glu Gln Leu Asp Ala Leu Ala Gly Asp Phe Asn Gly Phe Gly Pro  
245 250 255  
Gly Ser Val Val Ile Ile Thr Thr Lys Asp Lys Gln Leu Leu Ile Ser  
260 265 270  
Tyr Gly Ile Gln Leu Val Tyr Glu Ala Glu Phe Leu Thr Phe Gln Lys  
275 280 285

DOCKET# 08668960

(xi) SEQUENCE DESCRIPTION: SEQ ID: 1

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ser | Ile | Thr | Gly | Cys | Ala | Ala | Arg | Thr | His | Tyr | Ser | Ser | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |

Val Asp Ala Ala Ser Val Pro Phe Pro Arg Ser Arg Ser Thr Ser Ser  
20 25 30  
Ala Phe Ser Ser Ser Ala Ser Ser Arg Arg Arg Ser Ser Asp Phe Thr  
35 40 45  
Phe Asp Asp Asp Tyr Ser Glu Leu Leu Arg Ala Ala Ser Val Arg Val  
50 55 60

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1587781

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

Met Ile Ile Gln Gln Gln Gln Gln Gln Gln Gln Arg Gln Glu Asn  
1 5 10 15  
Arg Val Ala Met Gly Ala Val Thr Val Lys Gly Gly Leu Pro Lys Ser  
20 25 30  
Ser Ser Val Gly Met Thr Met Ala Arg Ile Asp Glu Glu Asp Glu Glu  
35 40 45  
Glu Gly Ser Val Lys Asn Gln Lys Lys Gly Ser Asp Phe Leu Tyr Pro  
50 55 60  
Arg Ser Arg Ser His Ala Val Thr Ile Arg Gly Ser Lys Phe  
65 70 75

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 495 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..495

(D) OTHER INFORMATION: / Ceres Seq. ID 1587821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

tctttgtgca tgcaaaactcg atccaaaggt tctgcacacc aattaccatt cagagacaga 60  
attgacagaa taactcgtga gttacaagaa accaaagcaa aggcagcctg tgatcagcca 120  
agaccaattt ctatggatca acagaacaaa ccagttgatg ttcaaggccc acctaattgtt 180  
gatcaaccaa gaaacattgg tgctgggtgat gccccaagga atcatcacca aagacaaggg 240  
atagtgccac aaccagttca aaacaacaac tttgagatca agagtgggtct catctccatg 300  
atccaaggaa acaagtttta tgggtctacct atggaagatc ccttggaacca tcttgacagc 360  
tttaataggc tctgtggccg tacaaagatc aatgggtgtca ctaaagatat gtttaagctc 420  
agattatttc ccttctcttt gggagacaag gcacaacact gggagaagac tctgccccca 480  
gactccatca actaa

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

0969960 10100



- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..120
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1587824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

Met Asp Gln Gln Asn Lys Pro Val Asp Val Gln Gly Pro Pro Asn Val  
1 5 10 15  
Asp Gln Pro Arg Asn Ile Gly Ala Gly Asp Ala Pro Arg Asn His His  
20 25 30  
Gln Arg Gln Gly Ile Val Pro Gln Pro Val Gln Asn Asn Asn Phe Glu  
35 40 45  
Ile Lys Ser Gly Leu Ile Ser Met Ile Gln Gly Asn Lys Phe Tyr Gly  
50 55 60  
Leu Pro Met Glu Asp Pro Leu Asp His Leu Asp Ser Phe Asn Arg Leu  
65 70 75 80  
Cys Gly Arg Thr Lys Ile Asn Gly Val Thr Lys Asp Met Phe Lys Leu  
85 90 95  
Arg Leu Phe Pro Phe Ser Leu Gly Asp Lys Ala Gln His Trp Glu Lys  
100 105 110  
Thr Leu Pro Pro Asp Ser Ile Asn  
115 120

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..376
- (D) OTHER INFORMATION: / Ceres Seq. ID 1587825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

atgcttctcg acactgcctc caatgaaaac ttcctgaaaa aggatgtagc agaaggatgg 60  
gagtttgtca aaaatctagc acaatctgat ggggtgtaca atgaagacta tgatcgctca 120  
gtgagaggag ctggaggcca tgaggataaa cagagcaagg atatcaaggc tctgaatgaa 180  
aagtttagaca agctgttgct ggctcagcag aagcagatac actacatcac tgatgaagag 240  
cacttcccaa tgcaagaaag ggggaatgat caaactgaag agctgtgcta catccagaac 300  
caaggagggt tcaacaaggg ctacaacaac tacaagccca acccaaacct ttcttacaca 360  
agcactaatg tagcta

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1587826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

Met Leu Leu Asp Thr Ala Ser Asn Glu Asn Phe Leu Lys Lys Asp Val  
1 5 10 15  
Ala Glu Gly Trp Glu Leu Val Lys Asn Leu Ala Gln Ser Asp Gly Cys  
20 25 30  
Tyr Asn Glu Asp Tyr Asp Arg Ser Val Arg Gly Ala Gly Gly His Glu

00589900-0360











100 105 110  
Lys Ala

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: / Ceres Seq. ID 1592524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gln | Phe | Lys | Val | Tyr | Glu | Ile | Asp | Phe | Gln | Phe | Ile | Pro | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Glu | Glu | Asp | Cys | Val | Cys | Lys | Ile | Thr | Met | Ile | Trp | Glu | Lys | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Asp | Asp | Phe | Pro | Glu | Pro | Ser | Tyr | Met | Gln | Leu | Leu | Lys | Ser |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Met | Val | Ile | Asp | Met | Glu | Asp | His | Val | Leu | Lys | Ala |     |     |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..473
- (D) OTHER INFORMATION: / Ceres Seq. ID 1592525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| atcaacacaaa | acaaaacata | aaaaacaagt | ggaagcttta | aaacgagagg | gagagagcaa | 60  |
| aaatggcgac  | gtcgggaacg | tacgtgacgg | aagttccgct | aaaaggatcg | gccgagaaat | 120 |
| actacaagag  | gtggaagaac | gagaaccatg | tcttccctga | tgctatcggc | caccacatcc | 180 |
| aaaatgttac  | cgttcacgaa | ggcgaacatg | actctcacgg | gtctatcagg | agttggaact | 240 |
| acacatggga  | tggaaaggag | gaggtgttca | aggagagaag | agagatagac | gatgagacca | 300 |
| aaacgttgac  | gttaagagga | cttgagggtc | acgtgatgga | gcagctcaaa | gtgtacgacg | 360 |
| tcgtctacca  | attcattccc | aaatctgagg | atacctgcat | cggcaaaatc | actttaatat | 420 |
| gggagaagcg  | caacgatgat | tcccatatt  | gaacttgatt | tgaaatccta | ata        |     |

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1592526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Thr | Ser | Gly | Thr | Tyr | Val | Thr | Glu | Val | Pro | Leu | Lys | Gly | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Glu | Lys | Tyr | Tyr | Lys | Arg | Trp | Lys | Asn | Glu | Asn | His | Val | Phe | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Ala | Ile | Gly | His | His | Ile | Gln | Asn | Val | Thr | Val | His | Glu | Gly | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |



| Table 1. Demographic characteristics of the study population |             |
|--------------------------------------------------------------|-------------|
| Age (years)                                                  | 65.5 ± 1.2  |
| Gender (male/female)                                         | 100/100     |
| Education (years)                                            | 12.5 ± 0.5  |
| Marital status (married/divorced/widowed)                    | 150/50/50   |
| Occupation (retired/working)                                 | 150/50      |
| Income (USD/month)                                           | 1,200 ± 200 |
| Comorbidities (hypertension/diabetes/cholesterol)            | 120/80/60   |
| Medication (antidepressants/antipsychotics)                  | 100/50      |
| Alcohol consumption (yes/no)                                 | 50/150      |
| Smoking status (smoker/non-smoker)                           | 30/170      |
| Family history (depression/schizophrenia)                    | 20/10       |
| Stress levels (high/low)                                     | 80/70       |
| Life events (recent/none)                                    | 60/40       |
| Support system (strong/weak)                                 | 70/30       |
| Health status (good/poor)                                    | 130/20      |
| Quality of life (high/low)                                   | 110/40      |
| Social functioning (good/poor)                               | 120/30      |
| Work status (employed/unemployed)                            | 40/60       |
| Living arrangement (alone/together)                          | 30/70       |
| Religious beliefs (strong/weak)                              | 60/40       |
| Cultural values (traditional/modern)                         | 50/50       |
| Healthcare access (easy/difficult)                           | 70/30       |
| Health insurance (yes/no)                                    | 140/10      |
| Healthcare utilization (frequent/infrequent)                 | 80/20       |
| Healthcare satisfaction (high/low)                           | 90/10       |
| Healthcare accessibility (good/poor)                         | 100/0       |
| Healthcare quality (high/low)                                | 110/0       |
| Healthcare safety (high/low)                                 | 120/0       |
| Healthcare effectiveness (high/low)                          | 130/0       |
| Healthcare equity (high/low)                                 | 140/0       |
| Healthcare transparency (high/low)                           | 150/0       |
| Healthcare accountability (high/low)                         | 160/0       |
| Healthcare responsiveness (high/low)                         | 170/0       |
| Healthcare patient-centeredness (high/low)                   | 180/0       |
| Healthcare collaboration (high/low)                          | 190/0       |
| Healthcare communication (high/low)                          | 200/0       |
| Healthcare partnership (high/low)                            | 210/0       |
| Healthcare shared decision-making (high/low)                 | 220/0       |
| Healthcare patient engagement (high/low)                     | 230/0       |
| Healthcare patient empowerment (high/low)                    | 240/0       |
| Healthcare patient autonomy (high/low)                       | 250/0       |
| Healthcare patient responsibility (high/low)                 | 260/0       |
| Healthcare patient accountability (high/low)                 | 270/0       |
| Healthcare patient transparency (high/low)                   | 280/0       |
| Healthcare patient accountability (high/low)                 | 290/0       |
| Healthcare patient transparency (high/low)                   | 300/0       |
| Healthcare patient accountability (high/low)                 | 310/0       |
| Healthcare patient transparency (high/low)                   | 320/0       |
| Healthcare patient accountability (high/low)                 | 330/0       |
| Healthcare patient transparency (high/low)                   | 340/0       |
| Healthcare patient accountability (high/low)                 | 350/0       |
| Healthcare patient transparency (high/low)                   | 360/0       |
| Healthcare patient accountability (high/low)                 | 370/0       |
| Healthcare patient transparency (high/low)                   | 380/0       |
| Healthcare patient accountability (high/low)                 | 390/0       |
| Healthcare patient transparency (high/low)                   | 400/0       |
| Healthcare patient accountability (high/low)                 | 410/0       |
| Healthcare patient transparency (high/low)                   | 420/0       |
| Healthcare patient accountability (high/low)                 | 430/0       |
| Healthcare patient transparency (high/low)                   | 440/0       |
| Healthcare patient accountability (high/low)                 | 450/0       |
| Healthcare patient transparency (high/low)                   | 460/0       |
| Healthcare patient accountability (high/low)                 | 470/0       |
| Healthcare patient transparency (high/low)                   | 480/0       |
| Healthcare patient accountability (high/low)                 | 490/0       |
| Healthcare patient transparency (high/low)                   | 500/0       |







(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 280 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..280  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1592546  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:  
agctagacat tttcgttttc atctcccccac gaatcaaaga tggctttttgc cattgcttct 60  
gctctcactt ccacactcac attatccacg agcagagtc aaatcctac ccagagaaga 120  
ccacatgtag cgtccacatc atccaccggt ggaagattaa tgagagagcg cttggtggtg 180  
gttcgtgccg gcaaagaagt ttctagcgtc tgtgaaaatg agatattata tgtgcaactt 240  
ttttcttttt ttttttgtgt cttttsttca astttgaaat  
(2) INFORMATION FOR SEQ ID NO:603:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 42 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..42  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1592547  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:  
Ala Arg His Phe Arg Phe His Leu Pro Thr Asn Gln Arg Trp Leu Leu  
1                    5                    10                    15  
Pro Leu Leu Leu Leu Ser Leu Pro His Ser His Tyr Pro Arg Ala Glu  
                    20                    25                    30  
Ser Lys Ile Leu Pro Arg Glu Asp His Met  
                    35                    40  
(2) INFORMATION FOR SEQ ID NO:604:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 67 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..67  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1592548  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:  
Leu Asp Ile Phe Val Phe Ile Ser Pro Arg Ile Lys Asp Gly Phe Cys  
1                    5                    10                    15  
His Cys Phe Cys Ser His Phe His Thr His Ile Ile His Glu Gln Ser  
                    20                    25                    30  
Pro Lys Ser Tyr Pro Glu Lys Thr Thr Cys Ser Val His Ile Ile His  
                    35                    40                    45  
Arg Trp Lys Ile Asn Glu Arg Ala Leu Gly Gly Gly Ser Cys Arg Gln  
                    50                    55                    60  
Arg Ser Phe  
65  
(2) INFORMATION FOR SEQ ID NO:605:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 80 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:

0968990, 10130



(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..92  
(D) OTHER INFORMATION: / Ceres Seq. ID 1592569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Ser | Gly | Phe | Ser | Gly | Asp | Glu | Thr | Ala | Pro | Phe | Phe | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Leu | Gly | Ala | Xaa | Ala | Ala | Leu | Val | Phe | Ser | Cys | Met | Gly | Ala | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Gly | Thr | Ala | Lys | Ser | Gly | Val | Gly | Val | Ala | Ser | Met | Gly | Val | Met |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Pro | Glu | Leu | Val | Met | Lys | Ser | Ile | Val | Pro | Val | Val | Met | Ala | Gly |
|     |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Leu | Asp | Ile | Tyr | Gly | Leu | Ile | Ile | Ala | Val | Ile | Ile | Ser | Thr | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Asn | Pro | Lys | Ala | Lys | Phe | Phe | Phe | Phe | Phe | Phe |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..64  
(D) OTHER INFORMATION: / Ceres Seq. ID 1592570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ala | Ala | Tyr | Gly | Thr | Ala | Lys | Ser | Gly | Val | Gly | Val | Ala | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Gly | Val | Met | Arg | Pro | Glu | Leu | Val | Met | Lys | Ser | Ile | Val | Pro | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Met | Ala | Gly | Val | Leu | Asp | Ile | Tyr | Gly | Leu | Ile | Ile | Ala | Val | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ser | Thr | Gly | Ile | Asn | Pro | Lys | Ala | Lys | Phe | Phe | Phe | Phe | Phe | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..494  
(D) OTHER INFORMATION: / Ceres Seq. ID 1592602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

attcgtcaat ccagagacta gggttttctt cccgccgaaa cctcaccgga aattctctcc

| Table 1. Demographic characteristics of the study population |             |
|--------------------------------------------------------------|-------------|
| Age (years)                                                  | 65.0 ± 10.0 |
| Gender                                                       |             |
| Male                                                         | 50.0%       |
| Female                                                       | 50.0%       |
| Education (years)                                            | 12.0 ± 2.0  |
| Marital status                                               |             |
| Married                                                      | 60.0%       |
| Single                                                       | 40.0%       |
| Occupation                                                   |             |
| Retired                                                      | 70.0%       |
| Unemployed                                                   | 30.0%       |
| Income (USD/month)                                           | 1,200 ± 300 |
| Health status                                                |             |
| Good                                                         | 60.0%       |
| Fair                                                         | 40.0%       |
| Poor                                                         | 0.0%        |
| Comorbidities                                                |             |
| Hypertension                                                 | 30.0%       |
| Diabetes                                                     | 20.0%       |
| Cholesterol                                                  | 10.0%       |
| Smoking status                                               |             |
| Smoker                                                       | 10.0%       |
| Non-smoker                                                   | 90.0%       |
| Alcohol consumption                                          |             |
| Regular                                                      | 5.0%        |
| Occasional                                                   | 15.0%       |
| Never                                                        | 80.0%       |



- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..511  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1592627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| acttttcagc | gtttctgacc | aaattctctc  | cggttttctt | tctgcttcag | gtgatatttt | 60  |
| aacaaagttc | ttagtacaat | gggatctgtt  | gatgctgcta | atggaagtgg | gaagaaacct | 120 |
| acagttatat | ttgttcttgg | tgggtccagga | agtggaaaag | gtacccagtg | tgcttatatt | 180 |
| gttgaacatt | atggttacac | acatctgagt  | gctggagatc | ttcttagagc | tgagattaaa | 240 |
| tcaggttctg | aaaatggaac | tatgatccag  | aatatgatta | aagaggggaa | gattgtacct | 300 |
| tctgaggtta | ctatcaagct | tctacagaaa  | gctattcagg | aaaacgggaa | tgacaagttc | 360 |
| ctcattgatg | gtttccctcg | taatgaggaa  | aaccgagcag | catttgaaaa | agttactgag | 420 |
| attgaaccaa | agtttgtctt | attcttcgat  | tgctctgagg | aagagatgga | gaagcgctg  | 480 |
| ttgggccgaa | accaggggga | gagaggatga  | c          |            |            |     |

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1592628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Ser | Val | Asp | Ala | Ala | Asn | Gly | Ser | Gly | Lys | Lys | Pro | Thr | Val |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Ile | Phe | Val | Leu | Gly | Gly | Pro | Gly | Ser | Gly | Lys | Gly | Thr | Gln | Cys | Ala |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Tyr | Ile | Val | Glu | His | Tyr | Gly | Tyr | Thr | His | Leu | Ser | Ala | Gly | Asp | Leu |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Leu | Arg | Ala | Glu | Ile | Lys | Ser | Gly | Ser | Glu | Asn | Gly | Thr | Met | Ile | Gln |  |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |  |
| Asn | Met | Ile | Lys | Glu | Gly | Lys | Ile | Val | Pro | Ser | Glu | Val | Thr | Ile | Lys |  |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     | 80  |  |
| Leu | Leu | Gln | Lys | Ala | Ile | Gln | Glu | Asn | Gly | Asn | Asp | Lys | Phe | Leu | Ile |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Asp | Gly | Phe | Pro | Arg | Asn | Glu | Glu | Asn | Arg | Ala | Ala | Phe | Glu | Lys | Val |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Thr | Glu | Ile | Glu | Pro | Lys | Phe | Val | Leu | Phe | Phe | Asp | Cys | Pro | Glu | Glu |  |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |  |
| Glu | Met | Glu | Lys | Arg | Leu | Leu | Gly | Arg | Asn | Gln | Gly | Glu | Arg | Gly |     |  |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |  |

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1592629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ile | Gln | Asn | Met | Ile | Lys | Glu | Gly | Lys | Ile | Val | Pro | Ser | Glu | Val |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Thr | Ile | Lys | Leu | Leu | Gln | Lys | Ala | Ile | Gln | Glu | Asn | Gly | Asn | Asp | Lys |  |







Ala Leu Ala Lys Gln Asn Lys Leu Gln Gly Asn Ala Ala Val Pro Leu  
65 70 75 80  
Ile Pro Lys Thr Ala Asn Ala  
85

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..493
- (D) OTHER INFORMATION: / Ceres Seq. ID 1592649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| attattgaac ggtgtttgtt attcggagaa gaagaagaag aagaactgaa gaagcatatt   | 60  |
| cgacgggtcac caccaaacct ctccgtcgcg atttttcactc tccgtttatc gaacatctga | 120 |
| gatctctctc cacttccgtc accgaagatg cattccagtc atcttcttct cgaggagccg   | 180 |
| atcaggatgg cttcaatcct cgagccttcc aaatctagtt tcttcccggc attgactaag   | 240 |
| atcgtcggaa ctctagggtcc taaatcccga tccgtcgagg ctctctccgg ctgtctcaaa  | 300 |
| gccggcatgt ctgtggctcg atttgatttc tcgtggggag atgttgatta tcaccaggag   | 360 |
| acacttgata atttgaaagt tgctgtgagg agcactaaga agctttgtgc tgttatgctt   | 420 |
| gatactgttg gacctgagct acaagttatt aacaaatctg agaaagctat tactttgaag   | 480 |
| ctgatggcct tgt                                                      |     |

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1592650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met His Ser Ser His Leu Leu Leu Glu Pro Ile Arg Met Ala Ser     |  |
| 1 5 10 15                                                       |  |
| Ile Leu Glu Pro Ser Lys Ser Ser Phe Phe Pro Ala Leu Thr Lys Ile |  |
| 20 25 30                                                        |  |
| Val Gly Thr Leu Gly Pro Lys Ser Arg Ser Val Glu Ala Leu Ser Gly |  |
| 35 40 45                                                        |  |
| Cys Leu Lys Ala Gly Met Ser Val Ala Arg Phe Asp Phe Ser Trp Gly |  |
| 50 55 60                                                        |  |
| Asp Ala Asp Tyr His Gln Glu Thr Leu Asp Asn Leu Lys Val Ala Val |  |
| 65 70 75 80                                                     |  |
| Arg Ser Thr Lys Lys Leu Cys Ala Val Met Leu Asp Thr Val Gly Pro |  |
| 85 90 95                                                        |  |
| Glu Leu Gln Val Ile Asn Lys Ser Glu Lys Ala Ile Thr Leu Lys Leu |  |
| 100 105 110                                                     |  |
| Met Ala Leu                                                     |  |
| 115                                                             |  |

(2) INFORMATION FOR SEQ ID NO:623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..102  
(D) OTHER INFORMATION: / Ceres Seq. ID 1592651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

Met Ala Ser Ile Leu Glu Pro Ser Lys Ser Ser Phe Phe Pro Ala Leu  
1 5 10 15  
Thr Lys Ile Val Gly Thr Leu Gly Pro Lys Ser Arg Ser Val Glu Ala  
20 25 30  
Leu Ser Gly Cys Leu Lys Ala Gly Met Ser Val Ala Arg Phe Asp Phe  
35 40 45  
Ser Trp Gly Asp Ala Asp Tyr His Gln Glu Thr Leu Asp Asn Leu Lys  
50 55 60  
Val Ala Val Arg Ser Thr Lys Lys Leu Cys Ala Val Met Leu Asp Thr  
65 70 75 80  
Val Gly Pro Glu Leu Gln Val Ile Asn Lys Ser Glu Lys Ala Ile Thr  
85 90 95  
Leu Lys Leu Met Ala Leu  
100

(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..62  
(D) OTHER INFORMATION: / Ceres Seq. ID 1592652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

Met Ser Val Ala Arg Phe Asp Phe Ser Trp Gly Asp Ala Asp Tyr His  
1 5 10 15  
Gln Glu Thr Leu Asp Asn Leu Lys Val Ala Val Arg Ser Thr Lys Lys  
20 25 30  
Leu Cys Ala Val Met Leu Asp Thr Val Gly Pro Glu Leu Gln Val Ile  
35 40 45  
Asn Lys Ser Glu Lys Ala Ile Thr Leu Lys Leu Met Ala Leu  
50 55 60

(2) INFORMATION FOR SEQ ID NO:625:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 450 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..450  
(D) OTHER INFORMATION: / Ceres Seq. ID 1592659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| tcaaaattaa tacacacatt cattaaagaa aaacaccagg acgagattac ttttggcgaa | 60  |
| aagtccaaat taggacgagg gggatgact gcaaaagtta aagctgctgt taatgcagct  | 120 |
| tatggtggcg ttctgttat cataaccagt ggatatgcag ctgagaatat aagtaaagtc  | 180 |
| cttagaggac tgcgtgttgg taccctgttc catcaagatg ctcatattat ggctccggtc | 240 |
| gtagatacta cttctcgtga catggcagtt gctgcaagg aaagctcaag aaagcttcag  | 300 |
| gccttatctt cagaagatag gaaacaaatt ctacacgaca ttgccaatgc ccttgaagta | 360 |
| aatgagsaaa caattaaaag ctgagaatga tttagaatgt tgctgcagca caagaagctg | 420 |
| gatatgaaga gtctttggta gctcgcttag                                  |     |

(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids





(2) INFORMATION FOR SEQ ID NO:631:

(A) LENGTH: 494 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..494

(D) OTHER INFORMATION: / Ceres Seq. ID 1592718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

| (X1) SEQUENCE DESCRIPTION: Sequence 1 |            |            |            |            |            |  |     |  |
|---------------------------------------|------------|------------|------------|------------|------------|--|-----|--|
| atcaacacaaa                           | acaaaacata | aaaaacaagt | ggaagcttta | aaacgagagg | gagagagcaa |  | 60  |  |
| aaatggcgac                            | gtcggaacg  | tacgtgacgg | aagttccgct | aaaaggatcg | gccgagaaat |  | 120 |  |
| actacaagag                            | gtggaagaac | gagaaccatg | tcttcctga  | tgctatcggc | caccacatcc |  | 180 |  |
| aaaaatgttac                           | cgttcacgaa | ggcgaacatg | actctcacgg | gtctatcagg | agttggaact |  | 240 |  |
| acacatggga                            | tggaaaggag | gaggtgttca | aggagagaag | agagatagac | gatgagacca |  | 300 |  |
| aaacgttgac                            | gttaagagga | cttgagggtc | acgtgatgga | gcagctcaaa | gtgtacgacg |  | 360 |  |
| tcgctctacca                           | attcattccc | aaatctgagg | atacctgcat | cggcanaatc | actttaatat |  | 420 |  |
| gggagawgaa                            | tgatggaatg | gagcactgtg | tgtttgtgac | tcaggggctg | tttttgttgt |  | 480 |  |
| tgttttatgac                           | tggg       |            |            |            |            |  |     |  |

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1592719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Thr | Ser | Gly | Thr | Tyr | Val | Thr | Glu | Val | Pro | Leu | Lys | Gly | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Glu | Lys | Tyr | Tyr | Lys | Arg | Trp | Lys | Asn | Glu | Asn | His | Val | Phe | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Ala | Ile | Gly | His | His | Ile | Gln | Asn | Val | Thr | Val | His | Glu | Gly | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Asp | Ser | His | Gly | Ser | Ile | Arg | Ser | Trp | Asn | Tyr | Thr | Trp | Asp | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Glu | Glu | Val | Phe | Lys | Glu | Arg | Arg | Glu | Ile | Asp | Asp | Glu | Thr | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Leu | Thr | Leu | Arg | Gly | Leu | Glu | Gly | His | Val | Met | Glu | Gln | Leu | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Tyr | Asp | Val | Val | Tyr | Gln | Phe | Ile | Pro | Lys | Ser | Glu | Asp | Thr | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Gly | Xaa | Ile | Thr | Leu | Ile | Trp | Glu | Xaa | Asn | Asp | Gly | Met | Glu | His |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Cys | Val | Phe | Val | Thr | Gln | Gly | Leu | Phe | Leu | Leu | Leu | Phe | Val | Thr | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 base pairs

(B) TYPE: nucleic acid

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Leu | Gly | Lys | Val | Ser | Val | Ser | Phe | Thr | His | Thr | Ile | Lys | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Glu | Pro | Phe | Phe | Ser | Val | Leu | Leu | Ser | Ala | Met | Phe | Leu | Gly | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Pro | Thr | Pro | Trp | Val | Leu | Gly | Ala | Ile | Val | Pro | Ile | Val | Gly | Gly |



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

Leu Leu His Arg Arg Leu His Lys Thr Leu Ile Ser Gln Ser Pro Thr  
1 5 10 15  
Arg Ser Ile Ser Leu His Glu Asn Glu Gly Cys Cys Arg Ile Leu Leu  
20 25 30  
Ala Val Leu Ser Gly Lys Ala Ser Pro Thr Ser Ala Asp Ile Lys Thr  
35 40 45  
Ile Leu Gly Ser Val Gly Ala Glu Thr Glu Asp Ser Gln Ile Glu Leu  
50 55 60  
Leu Leu Lys Glu Val Lys Gly Lys Asp Leu Ala Glu Leu Ile Ala Ala  
65 70 75 80  
Gly Arg Glu Lys Leu Ala Ser Val Pro Ser Gly Gly Gly Gly Gly Val  
85 90 95  
Ala Val Ala Ser Ala Thr Ser Gly Gly Gly Gly Gly Gly Ala Pro  
100 105 110  
Ala Ala Glu Ser Lys Lys Glu Glu Lys Lys Glu Glu Lys Glu Glu Ser  
115 120 125  
Asp Asp Asp Met Gly Phe Ser Leu Phe Glu  
130 135

(2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..495
- (D) OTHER INFORMATION: / Ceres Seq. ID 1592789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

gtgccgcgctc gaaatatgag aaacgaatga tttgatcatc aatcaacgag aaacacacac 60  
ggagaaagag aatctcaaata tagctccagc tcctgatcga ttccgatttt cacaattcct 120  
tccttgatc tgctcttacc ttgtcacgat ttcacttccc tgtgtttttt atttatactt 180  
ggatcatccaa taacgaaact ttgatcaaac tggaaactaca gtttatttga actccctgaa 240  
gcatttagat ggcagaaaaa gcttgataa agcgtcttca aaaagaatac agagcgcttt 300  
gcaaggaacc agtctcgcat gttgttgctc gtccttcccc aaatgacatt cttgaatggc 360  
attatgtgtt ggaaggcagt gagggaaacgc cttttgcagg tggattttac tatggaaaga 420  
tcaagttccc tccagaatat cttacaagc cacctggaat cacaatgacc acaccaaattg 480  
gtcgatttgt gacgc

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1592790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

Met Ala Glu Lys Ala Cys Ile Lys Arg Leu Gln Lys Glu Tyr Arg Ala  
1 5 10 15  
Leu Cys Lys Glu Pro Val Ser His Val Val Ala Arg Pro Ser Pro Asn  
20 25 30  
Asp Ile Leu Glu Trp His Tyr Val Leu Glu Gly Ser Glu Gly Thr Pro  
35 40 45  
Phe Ala Gly Gly Phe Tyr Tyr Gly Lys Ile Lys Phe Pro Pro Glu Tyr  
50 55 60  
Pro Tyr Lys Pro Pro Gly Ile Thr Met Thr Thr Pro Asn Gly Arg Phe

00000000 00000000



80

[illegible]

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Phe | Leu | Asn | Gly | Ile | Met | Cys | Trp | Lys | Ala | Val | Arg | Glu | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Leu | Gln | Val | Asp | Phe | Thr | Met | Glu | Arg | Ser | Ser | Ser | Leu | Gln | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Leu | Thr | Ser | His | Leu | Glu | Ser | Gln |     |     |     |     |     |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     |     |     |     |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

| (A1) SEQUENCE SUBSTITUTIONS |            |            |            |            |            |     |
|-----------------------------|------------|------------|------------|------------|------------|-----|
| aggcatcttt                  | taggtcatat | caatacaaaa | tacacatata | dvatatTTTT | caacacctga | 60  |
| ggtgcgcgaa                  | gacagacabt | tksttcatcc | tdctccgtaa | ttctcaaaat | tagggTTTTd | 120 |
| vtccgcgcag                  | ytctctcagt | tgtactgcaa | gcattctttt | stagatattt | aagatgtcaa | 180 |
| ggacgaggac                  | tgctgcttct | gaggctcatg | actccatgga | atctgaggaa | agggtagacc | 240 |
| ttgatggtga                  | caatgatcct | gaggagattc | tggaggagga | agttgaatac | gaagaagttg | 300 |
| aagaggagga                  | ggagattgaa | gagatagaag | aggagatgga | ggaggaggtt | gaagtggaag | 360 |
| aagaggagga                  | ggagagggat | gctgttgcaa | cggaaagaga | agaagaaaag | aaaggcatg  | 420 |
| ttgaacttct                  | tgcacttctc | ccacatggtt | cagaggttta | nttgagggga | ttcctactga | 480 |





(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1592825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Ser | Glu | Lys | Glu | Ala | Ala | Leu | Ala | Ala | Thr | Pro | Ser | Asp | Ser |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Pro | Thr | Ile | Phe | Asp | Lys | Ile | Ile | Ser | Lys | Glu | Ile | Pro | Ser | Thr | Val |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Val | Phe | Glu | Asp | Asp | Lys | Val | Leu | Ala | Phe | Arg | Asp | Ile | Thr | Pro | Gln |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |  |
| Gly | Pro | Val | His | Ile | Leu | Leu | Ile | Pro | Lys | Val | Arg | Asp | Gly |     |     |  |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |  |

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 485 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..485

(D) OTHER INFORMATION: / Ceres Seq. ID 1592832

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

|             |            |            |            |             |             |  |     |
|-------------|------------|------------|------------|-------------|-------------|--|-----|
| aaaaccatca  | ctccttttgc | attgtgtgaa | accttcgagt | tttctcttca  | tcttctcaaa  |  | 60  |
| gtaacaaaact | ttctccaaac | agattattat | taaaacaatc | tcatacaagaa | ctacgatgaa  |  | 120 |
| attcccgggt  | gtaaaagttc | ttattatctc | tcttctcatc | acatcttctt  | tggtcatact  |  | 180 |
| ctcaaccgcg  | gattcgtcac | catgcggagg | aaaatgcaac | gtgagatggt  | caaaggcagg  |  | 240 |
| aagacaagat  | aggtgtctca | agtattgtaa | tatatgttgc | gagaagtgtg  | actatttgtg  |  | 300 |
| tccttcaggc  | acttatggaa | acaaagatga | atgcccttgt | taccgcgata  | tgaagaactc  |  | 360 |
| caaaggcacg  | tccaaatgtc | cttgatcatg | ttcttaagat | tatccttata  | gacacaatat  |  | 420 |
| cttgaaatgt  | taagattgtg | cttgatgcc  | gagtgaagga | aggattggga  | actaggcggtg |  | 480 |
| attgg       |            |            |            |             |             |  |     |

(2) INFORMATION FOR SEQ ID NO:651:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1592833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Lys | Phe | Pro | Ala | Val | Lys | Val | Leu | Ile | Ile | Ser | Leu | Leu | Ile | Thr |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Ser | Ser | Leu | Phe | Ile | Leu | Ser | Thr | Ala | Asp | Ser | Ser | Pro | Cys | Gly | Gly |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Lys | Cys | Asn | Val | Arg | Cys | Ser | Lys | Ala | Gly | Arg | Gln | Asp | Arg | Cys | Leu |  |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |  |
| Lys | Tyr | Cys | Asn | Ile | Cys | Cys | Glu | Lys | Cys | Asn | Tyr | Cys | Val | Pro | Ser |  |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |  |
| Gly | Thr | Tyr | Gly | Asn | Lys | Asp | Glu | Cys | Pro | Cys | Tyr | Arg | Asp | Met | Lys |  |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |  |
| Asn | Ser | Lys | Gly | Thr | Ser | Lys | Cys | Pro |     |     |     |     |     |     |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:





(2) INFORMATION FOR SEO ID NO:657:

(A) LENGTH: 437 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

(2) INFORMATION FOR SEQ ID NO:658:

(A) LENGTH: 111 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

(2) INFORMATION FOR SEQ ID NO:659:

(A) LENGTH: 84 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Asn | Ser | Glu | Lys | Asn | Pro | Leu | Leu | Ser | Asp | Glu | Lys | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Ser | Thr | Glu | Glu | Asn | Lys | Ser | Ser | Lys | Pro | Glu | Ser | Ala | Ser | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ser | Thr | Ser | Ser | Ala | Met | Pro | Gly | Leu | Asn | Phe | Asn | Ala | Phe | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Ser | Asn | Met | Ala | Ser | Ile | Leu | Asn | Asp | Pro | Ser | Ile | Arg | Glu | Met |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Glu | Gln | Ile | Ala | Lys | Asp | Pro | Ala | Phe | Asn | Gln | Leu | Ala | Glu | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |



Leu Gln Arg Ser Ile Pro Asn Ala Gly Gln Glu Gly Gly Phe Pro Asn  
85 90 95  
Phe Asp Pro Gln Tyr Val Asn Thr Met Gln Gln Val Met His Asn  
100 105 110  
Pro Glu Phe Lys Thr Met Ala Glu Lys Leu Gly Thr Ala Leu Val Gln  
115 120 125  
Asp Pro Gln Met Ser Pro Phe Leu Asp  
130 135

(2) INFORMATION FOR SEQ ID NO:662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1592864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

Met Pro Gly Leu Asn Phe Asn Ala Phe Asp Phe Ser Asn Met Ala Ser  
1 5 10 15  
Ile Leu Asn Asp Pro Ser Ile Arg Glu Met Ser Glu Gln Ile Ala Lys  
20 25 30  
Asp Pro Ala Phe Asn Gln Leu Ala Glu Gln Leu Gln Arg Ser Ile Pro  
35 40 45  
Asn Ala Gly Gln Glu Gly Gly Phe Pro Asn Phe Asp Pro Gln Gln Tyr  
50 55 60  
Val Asn Thr Met Gln Gln Val Met His Asn Pro Glu Phe Lys Thr Met  
65 70 75 80  
Ala Glu Lys Leu Gly Thr Ala Leu Val Gln Asp Pro Gln Met Ser Pro  
85 90 95  
Phe Leu Asp

(2) INFORMATION FOR SEQ ID NO:663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1592865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

Met Ala Ser Ile Leu Asn Asp Pro Ser Ile Arg Glu Met Ser Glu Gln  
1 5 10 15  
Ile Ala Lys Asp Pro Ala Phe Asn Gln Leu Ala Glu Gln Leu Gln Arg  
20 25 30  
Ser Ile Pro Asn Ala Gly Gln Glu Gly Gly Phe Pro Asn Phe Asp Pro  
35 40 45  
Gln Gln Tyr Val Asn Thr Met Gln Gln Val Met His Asn Pro Glu Phe  
50 55 60  
Lys Thr Met Ala Glu Lys Leu Gly Thr Ala Leu Val Gln Asp Pro Gln  
65 70 75 80  
Met Ser Pro Phe Leu Asp  
85

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs

09669901030

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..414
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1592866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| accaacacca | catctctctc | tatctatgga | agcattagga  | aactttgatt | acgaaagcta | 60  |
| caccaatttt | acaaaattgc | catctcccca | atgggggtgat | cagttcctca | agttttccat | 120 |
| tgctgattcg | gattttgatg | tccttgaaag | agagattgaa  | gtactaaagc | ctaaagtaag | 180 |
| agagaacata | ttcgtgtcgt | cttccacaga | caaagacgcg  | atgaaaaaga | caattctttc | 240 |
| tattcatttt | ctggacagtc | ttggtctctc | ttatcatttt  | gagaaggaaa | tcgaagagag | 300 |
| cctaaaacat | gstttcgaga | agatagaaga | tttgatcgct  | gatgaaaata | aaattgcaca | 360 |
| caatstscas | satcttccga | gttttcagga | catacggkta  | ctacatgtct | tcgg       |     |

(2) INFORMATION FOR SEQ ID NO:665:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 137 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..137
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1592867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Thr | Pro | His | Leu | Ser | Leu | Ser | Met | Glu | Ala | Leu | Gly | Asn | Phe | Asp |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Tyr | Glu | Ser | Tyr | Thr | Asn | Phe | Thr | Lys | Leu | Pro | Ser | Ser | Gln | Trp | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Gln | Phe | Leu | Lys | Phe | Ser | Ile | Ala | Asp | Ser | Asp | Phe | Asp | Val | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Arg | Glu | Ile | Glu | Val | Leu | Lys | Pro | Lys | Val | Arg | Glu | Asn | Ile | Phe |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Val | Ser | Ser | Ser | Thr | Asp | Lys | Asp | Ala | Met | Lys | Lys | Thr | Ile | Leu | Ser |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | His | Phe | Leu | Asp | Ser | Leu | Gly | Leu | Ser | Tyr | His | Phe | Glu | Lys | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ile | Glu | Glu | Ser | Leu | Lys | His | Xaa | Phe | Glu | Lys | Ile | Glu | Asp | Leu | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Asp | Glu | Asn | Lys | Ile | Ala | His | Asn | Xaa | Xaa | Xaa | Leu | Pro | Ser | Phe |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Asp | Ile | Arg | Xaa | Leu | His | Val | Phe |     |     |     |     |     |     |     |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:666:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 129 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..129
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1592868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ala | Leu | Gly | Asn | Phe | Asp | Tyr | Glu | Ser | Tyr | Thr | Asn | Phe | Thr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Lys | Leu | Pro | Ser | Ser | Gln | Trp | Gly | Asp | Gln | Phe | Leu | Lys | Phe | Ser | Ile |

09609980 101300

20 25 30  
Ala Asp Ser Asp Phe Asp Val Leu Glu Arg Glu Ile Glu Val Leu Lys  
35 40 45  
Pro Lys Val Arg Glu Asn Ile Phe Val Ser Ser Ser Thr Asp Lys Asp  
50 55 60  
Ala Met Lys Lys Thr Ile Leu Ser Ile His Phe Leu Asp Ser Leu Gly  
65 70 75 80  
Leu Ser Tyr His Phe Glu Lys Glu Ile Glu Glu Ser Leu Lys His Xaa  
85 90 95  
Phe Glu Lys Ile Glu Asp Leu Ile Ala Asp Glu Asn Lys Ile Ala His  
100 105 110  
Asn Xaa Xaa Xaa Leu Pro Ser Phe Gln Asp Ile Arg Xaa Leu His Val  
115 120 125  
Phe

(2) INFORMATION FOR SEQ ID NO:667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..383
- (D) OTHER INFORMATION: / Ceres Seq. ID 1592877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

aaaaaagtcc attgtttcaa gcaatactct caagtctaaa gaagaataaa aaaaatggat 60  
gaagaagttg agaacaaagt rttactccat ggatcattcg cgagtcctta cagcaaaagg 120  
attgagttag ccctaaggct taaatccata ccttacmaat tcgtgcaaga rgatctccag 180  
aacaagagcc aaaccctgct ccggtataac ccggttcaca agaagatccc ggttcttgct 240  
cacaacggta aacccatctc tgaatcactg tttatcattg aatasatcga cgaaacgtgg 300  
agacacgggtc cacatatattt gccacaagac ccttatagaa gatctaaagt ccggttttrk 360  
gctaactaca tccaattaca tct

(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1592878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

Met Asp Glu Glu Val Glu Asn Lys Xaa Leu Leu His Gly Ser Phe Ala  
1 5 10 15  
Ser Pro Tyr Ser Lys Arg Ile Glu Leu Ala Leu Arg Leu Lys Ser Ile  
20 25 30  
Pro Tyr Xaa Phe Val Gln Xaa Asp Leu Gln Asn Lys Ser Gln Thr Leu  
35 40 45  
Leu Arg Tyr Asn Pro Val His Lys Lys Ile Pro Val Leu Val His Asn  
50 55 60  
Gly Lys Pro Ile Ser Glu Ser Leu Phe Ile Ile Glu Xaa Ile Asp Glu  
65 70 75 80  
Thr Trp Arg His Gly Pro His Ile Leu Pro Gln Asp Pro Tyr Arg Arg  
85 90 95  
Ser Lys Val Arg Phe Xaa Ala Asn Tyr Ile Gln Leu His  
100 105

(2) INFORMATION FOR SEQ ID NO:669:

09569501

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO.66: |             |            |            |            |            |     |
|------------------------------------------|-------------|------------|------------|------------|------------|-----|
| atcaacagtt                               | ttaaaaaaag  | acataactca | accaatctca | ctttgaaaaa | gacatgaaca | 60  |
| aaacccgcct                               | togtgetctc  | tccccacctt | ccggtatgca | acaccgtaag | agatgtcgat | 120 |
| tgagaggctg                               | aaactacgta  | aggccagaag | ttaaacaacg | caacttctca | aaagatgaag | 180 |
| acgatctcat                               | cctcaagctt  | catgcacttc | ttggcaatag | atggtcattg | atagcgggaa | 240 |
| gnttgccagg                               | acgaaccgac  | aacgaavwta | ggatccattg | ggaaacttac | ctaaaaagga | 300 |
| agctcgtaaa                               | aatggggaatc | gaccaacca  | atcatcgtct | ccaccatcac | accaactaca | 360 |
| tttctagacg                               | tcacctccat  | tcttcacata | aggaacatga | aaccaagatt | attagtgatc | 420 |
| aatctttctc                               | ggtatccgaa  | tcatgtggtg | taacaatttc | gttggtctgg | tattggagaa | 480 |
| ttgcgaactc                               | ccgtttccga  | accacgggca | cgtt       |            |            |     |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

(2) INFORMATION FOR SEQ ID NO:671:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 139 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide







(D) OTHER INFORMATION: / Ceres Seq. ID 1592926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

Met Leu Thr Trp Thr Val Phe Tyr Val Thr Asn Arg Gly Lys Lys Ala  
1 5 10 15  
Thr Gln Leu Ala Asp Ala Val Val Glu Glu Arg Glu Asp Gly Ala Thr  
20 25 30  
Asp Val Ile Ile Val Gly Ala Gly Val Gly Gly Ser Ala Leu Ala Tyr  
35 40 45  
Ala Leu Ala Lys Asp Gly Arg Arg Val His Val Ile Glu Arg Asp Leu  
50 55 60  
Arg Glu Pro Glu Arg Ile Met Gly Glu Phe Met Gln Pro Gly Gly Arg  
65 70 75 80  
Leu Met Leu Ser Lys Leu Gly Leu Glu Asp Cys Leu Glu Gly Ile Asp  
85 90 95  
Ala Gln Lys Ala Thr Gly Met Thr Val Tyr Lys Asp Gly Lys Glu Ala  
100 105 110  
Val Ala Ser Phe Pro Val Asp Asn Asn Asn Phe Pro Tyr Asp Pro Ser  
115 120 125  
Ala Arg Ser Phe His Asn  
130

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..499

(D) OTHER INFORMATION: / Ceres Seq. ID 1592932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

attaaattat gtgcatatgt aaaatgattg ttggttataa tactaaataa taaagtttat 60  
aacaatattt tacaaatttg gaagttgcaa ctataaatgg taaattcgggt ccttaagatt 120  
agaagacaaa gaagagtcgt gttggtgagc taactaccca acctgtgaag ctacccccat 180  
tctctctcaa cgtttttcgtt ttgaaatggc gaggaagaag atcagagagt atgactcaaa 240  
gaggttgggtg aaggaacatt tcaaaaggct ttctggcaaa gagcttccta tcagatccgt 300  
tcagattaat gaaacaactg atctaaatga gctagttgaa aaggaacctt ggctctcgtc 360  
tgagaagctg gtggtgaaac ctgacatggt gtttggaag cgtggcaaga gtgggttggt 420  
tgccttgaaa ttagattttg ctgatgttgc cacttttggt aaagaacggt tgggaaaaga 480  
ggtagagatg agtggatgc

(2) INFORMATION FOR SEQ ID NO:680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1592933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

Met Ala Arg Lys Lys Ile Arg Glu Tyr Asp Ser Lys Arg Leu Val Lys  
1 5 10 15  
Glu His Phe Lys Arg Leu Ser Gly Lys Glu Leu Pro Ile Arg Ser Val  
20 25 30  
Gln Ile Asn Glu Thr Thr Asp Leu Asn Glu Leu Val Glu Lys Glu Pro  
35 40 45  
Trp Leu Ser Ser Glu Lys Leu Val Val Lys Pro Asp Met Leu Phe Gly  
50 55 60

FILE # 00000000



Lys Arg Gly Lys Ser Gly Leu Val Ala Leu Lys Leu Asp Phe Ala Asp  
65 70 75 80  
Val Ala Thr Phe Val Lys Glu Arg Leu Gly Lys Glu Val Glu Met Ser  
85 90 95  
Gly Cys

(2) INFORMATION FOR SEQ ID NO:681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..467
- (D) OTHER INFORMATION: / Ceres Seq. ID 1592963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| aaaattgaaa | ttcgaaaaca  | gaacaaaaaa  | aaaaatctct | ctcaatctct | ctcagatctg | 60  |
| aatccatcca | tcaccgatct  | ctaattggcgg | caccaccagc | atcatcctcg | gcgagggaag | 120 |
| agttcgtgta | cctcgcaaag  | ctcgcagasa  | agcggaaagt | tacgaagaaa | tggttgaatt | 180 |
| catggaaaaa | gtcgtctgaag | ccgttgacaa  | agacgaactc | accgtcgaag | aacgtaattc | 240 |
| cctctccgtc | gcttacaaaa  | acgtaatcgg  | tgctcgtcgt | gcttcctgga | gaatcatctc | 300 |
| ttccattgaa | caaaaagaag  | agagtcgtgg  | taacgatgac | catgtgacca | cgatccgtga | 360 |
| ttacagaagc | aagatcgaat  | ctgagttatc  | gaaaatctgt | gacggtattc | ttaagcttct | 420 |
| tgatactaga | cttgttcctg  | cttctgctaa  | tgagattctt | aaggttt    |            |     |

(2) INFORMATION FOR SEQ ID NO:682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: / Ceres Seq. ID 1592964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Pro | Pro | Ala | Ser | Ser | Ser | Ala | Arg | Glu | Glu | Phe | Val | Tyr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Ala | Lys | Leu | Ala | Xaa | Lys | Arg | Asn | Val | Thr | Lys | Lys | Trp | Leu | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Trp | Lys | Lys | Ser | Leu | Lys | Pro | Leu | Thr | Lys | Thr | Asn | Ser | Pro | Ser |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Lys | Asn | Val | Ile | Ser | Ser | Pro | Ser | Leu | Thr | Lys | Thr |     |     |     |     |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |

(2) INFORMATION FOR SEQ ID NO:683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1592965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Glu | Phe | Met | Glu | Lys | Val | Ala | Glu | Ala | Val | Asp | Lys | Asp | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Thr | Val | Glu | Glu | Arg | Asn | Leu | Leu | Ser | Val | Ala | Tyr | Lys | Asn | Val |

20 25 30  
Ile Gly Ala Arg Arg Ala Ser Trp Arg Ile Ile Ser Ser Ile Glu Gln  
35 40 45  
Lys Glu Glu Ser Arg Gly Asn Asp Asp His Val Thr Thr Ile Arg Asp  
50 55 60  
Tyr Arg Ser Lys Ile Glu Ser Glu Leu Ser Lys Ile Cys Asp Gly Ile  
65 70 75 80  
Leu Lys Leu Leu Asp Thr Arg Leu Val Pro Ala Ser Ala Asn Gly Asp  
85 90 95  
Ser Lys Val

(2) INFORMATION FOR SEQ ID NO:684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1592966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

Met Glu Lys Val Ala Glu Ala Val Asp Lys Asp Glu Leu Thr Val Glu  
1 5 10 15  
Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly Ala Arg  
20 25 30  
Arg Ala Ser Trp Arg Ile Ile Ser Ile Glu Gln Lys Glu Glu Ser  
35 40 45  
Arg Gly Asn Asp Asp His Val Thr Thr Ile Arg Asp Tyr Arg Ser Lys  
50 55 60  
Ile Glu Ser Glu Leu Ser Lys Ile Cys Asp Gly Ile Leu Lys Leu Leu  
65 70 75 80  
Asp Thr Arg Leu Val Pro Ala Ser Ala Asn Gly Asp Ser Lys Val  
85 90 95

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..496

(D) OTHER INFORMATION: / Ceres Seq. ID 1592975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

actttcaact taatcacaca caaggagaga agagagaaaag agagaaagag agacagagat 60  
aatggcggtac agtgcgtggtt tcttacacca gagcgcatg gcttcatcag ccgcacgac 120  
atcatcttcc tctcatccc agcgtcacgt gtcgctctcc aaacctgttc agatcatctg 180  
taaagctcaa cagtctcatg aagacgataa ctccgccgtc tcccgccgtc ttgctctcac 240  
tctctcgtc ggcgcgctg ctgttggttc caaagtatct cctgctgatg ccgcctacgg 300  
tgaagctgca aacgtgtttg ggaagccaaa gacgaacaca gacttcttgc catacaatgg 360  
agatgggttc aaagtgcagg ttccagcaaa atggaacca agcaaagaga ttgagtatcc 420  
aggacaagtc cttaggttcg aagacaactt cgatgctact agcaatctca atgtcatggt 480  
cactcctacc gacaag

(2) INFORMATION FOR SEQ ID NO:686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:



- (A) NAME/KEY: -  
(B) LOCATION: 1..373  
(D) OTHER INFORMATION: / Ceres Seq. ID 1593000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

|            |            |            |             |              |             |     |
|------------|------------|------------|-------------|--------------|-------------|-----|
| attcactcac | caaagcatca | cataacactc | acacasacac  | tttbnocttct  | cttatttttct | 60  |
| cagttctttt | aactcttttc | tctacctata | ttcaaattggc | caccgtcgcgag | gttgaacaag  | 120 |
| tgactccagt | agcagctgag | aacatcgagg | tgccaccacc  | aaaggctgtg   | gagtcggagg  | 180 |
| aagtcaccac | cgtctccgag | tctcttccag | ctccggtaac  | agaatctcaa   | gcgcctgtcg  | 240 |
| aagtaacaac | taaagatttg | gtcgtggaag | agacagagaa  | accaatcgaa   | gaaacagagg  | 300 |
| aagctcaagt | tgaaactccg | gagttgtgga | gatcaagaaa  | gatgaagaag   | ctccggagtt  | 360 |
| tcaacttgag | ctt        |            |             |              |             |     |

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1593001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Thr | Lys | Ala | Ser | His | Asn | Thr | His | Thr | Xaa | Thr | Xaa | Xaa | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Ile | Phe | Ser | Val | Leu | Leu | Thr | Leu | Phe | Ser | Thr | Tyr | Ile | Gln | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Thr | Val | Glu | Val | Glu | Gln | Val | Thr | Pro | Val | Ala | Ala | Glu | Asn | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Val | Pro | Pro | Pro | Lys | Ala | Val | Glu | Ser | Glu | Glu | Val | Thr | Thr | Val |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ser | Glu | Ser | Leu | Pro | Ala | Pro | Val | Thr | Glu | Ser | Gln | Ala | Pro | Val | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Thr | Thr | Lys | Asp | Leu | Val | Val | Glu | Glu | Thr | Glu | Lys | Pro | Ile | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Glu | Thr | Glu | Glu | Ala | Gln | Val | Glu | Thr | Pro | Glu | Leu | Trp | Arg | Ser | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Met | Lys | Lys | Leu | Arg | Ser | Phe | Asn | Leu | Ser |     |     |     |     |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1593002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Thr | Val | Glu | Val | Glu | Gln | Val | Thr | Pro | Val | Ala | Ala | Glu | Asn |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Glu | Val | Pro | Pro | Pro | Lys | Ala | Val | Glu | Ser | Glu | Glu | Val | Thr | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Ser | Glu | Ser | Leu | Pro | Ala | Pro | Val | Thr | Glu | Ser | Gln | Ala | Pro | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Val | Thr | Thr | Lys | Asp | Leu | Val | Val | Glu | Glu | Thr | Glu | Lys | Pro | Ile |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Glu | Thr | Glu | Glu | Ala | Gln | Val | Glu | Thr | Pro | Glu | Leu | Trp | Arg | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |

(2) INFORMATION FOR SEQ ID NO:691:

(A) LENGTH: 443 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..443

(D) OTHER INFORMATION: / Ceres Seq. ID 1593014

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| accaataagc | aatttgctca  | ttagagaaca | gagaaaaaaa | aaaacaatgg | caactcaagc  | 60  |
| cgccgggata | ttcaactcgc  | ccataacaac | cgccgcaagc | ctccggsgtc | aagaaactcc  | 120 |
| actttttctc | aacaaccac   | cgtcccaat  | cmctctcct  | caccaaacc  | gcgatccgcg  | 180 |
| ccgagaaaac | agattcctcc  | gccgccgctg | ctgcagcccc | cgcacgaaa  | gaagctcccg  | 240 |
| tgggattcac | gccaccgcag  | ctagacccaa | acacaccgtc | tccgatcttc | gctggaagca  | 300 |
| ccggtggtct | tctacgtaaa  | gcgcaagtgg | aagagttcta | cgttatcacg | tggaaactcac | 360 |
| cgaaagaaca | gactctttgag | atgccgacag | gaggagcagc | gatcatgaga | gaagatgtct  | 420 |
| gctttatctt | ctagtatca   | gct        |            |            |             |     |

(A) LENGTH: 105 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1593015

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ile | Ser | Asn | Leu | Leu | Ile | Arg | Glu | Gln | Arg | Lys | Lys | Lys | Thr | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Thr | Gln | Ala | Ala | Gly | Ile | Phe | Asn | Ser | Ala | Ile | Thr | Thr | Ala | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Leu | Arg | Xaa | Gln | Glu | Thr | Pro | Leu | Phe | Leu | Asn | Asn | Pro | Pro | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Ile | Xaa | Leu | Leu | His | Gln | Asn | Arg | Asp | Pro | Arg | Arg | Glu | Asn | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Leu | Arg | Arg | Arg | Cys | Cys | Ser | Pro | Arg | His | Glu | Arg | Ser | Ser | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Ile | His | Ala | Thr | Ala | Ala | Arg | Pro | Lys | His | Thr | Val | Ser | Asp | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Trp | Lys | His | Arg | Trp | Ser | Ser | Thr |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(A) LENGTH: 90 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..90

(D) OTHER INFORMATION: / Ceres Seq. ID 1593016

Met Ala Thr Gln Ala Ala Gly Ile Phe Asn Ser Ala Ile Thr Thr Ala



(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..96  
(D) OTHER INFORMATION: / Ceres Seq. ID 1593019  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:  
Met Lys Gln Tyr Ser Asn Val Leu Asp Lys Pro Leu Ser Lys Gly Lys  
1 5 10 15  
Gln Glu Val Ser Leu Thr Ala Phe Ala Phe Leu Phe Ser Glu Leu Val  
20 25 30  
Gln Tyr Asn Gln Thr Gln Val Asp Asn Ile Ala Glu Leu Glu Arg Arg  
35 40 45  
Leu Glu Asp Ala Gly Tyr Ala Val Gly Ser Ser Ser Arg Ala Ser Leu  
50 55 60  
Gln Pro Gly Lys Gly Lys Gln Lys Arg Asp Thr Val Thr Gly Asn Ser  
65 70 75 80  
Val Phe Arg Ser Gln Tyr Cys Val Glu Ser Val Val Trp Lys Gly Cys  
85 90 95

(2) INFORMATION FOR SEQ ID NO:697:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..59  
(D) OTHER INFORMATION: / Ceres Seq. ID 1593020  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:  
Met Leu Gly Met Gln Leu Asp Leu Val Leu Glu Leu Leu Cys Asn Arg  
1 5 10 15  
Glu Lys Gly Asn Arg Arg Glu Thr Arg Leu Leu Gly Ile Leu Ser Phe  
20 25 30  
Val His Ser Thr Val Trp Lys Val Leu Phe Gly Lys Val Ala Asp Ser  
35 40 45  
Leu Glu Lys Gly Thr Glu His Glu Asp Ala Cys  
50 55

(2) INFORMATION FOR SEQ ID NO:698:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 457 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..457  
(D) OTHER INFORMATION: / Ceres Seq. ID 1593051  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:  
ccgacgaccg tgaatcacca gcaaaggatt cgtgtcaatg ttcttgtgag atcgaaacttt 60  
ctctggggttc gtgcagaagc tttgcttttt tgagtatcgc gtttaaggca catcgaagaa 120  
gagagaccct aatttgatat tttgagttct atcgatggct tcgctactag ctgcgaggtc 180  
gttcagtgtc ctccgagctc gacatctcgc tttttcaggg caagggtttac agggatctca 240  
tctctgtggg ctacagtccc gtgctatatc ttatggaagc aacaaagatg atgaagaagc 300  
tgagcagctt gctaaagaga tctccaagga ctggagtact gtctttgaac ggagcatgaa 360  
caccctatct ctcactgaaa tggtcagggg tttgtcactg accctcaagt acttctttga 420

09689980 104390





20 25 30  
Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Ile Ile Phe  
35 40 45  
Ser Asn Arg Gly Lys Leu Tyr Glu Phe Cys Ser Ser Ser Met Leu  
50 55 60  
Arg Thr Leu Glu Arg Tyr Gln Lys Cys Asn Tyr Gly Ala Pro Glu Pro  
65 70 75 80  
Asn Val Pro Ser Arg Glu Ala Leu Ala Val Glu Leu Ser Ser Gln Gln  
85 90 95  
Glu Tyr Leu Lys Leu Lys Glu Arg Tyr Asp Ala Leu Gln Arg Thr His  
100 105 110  
Phe Phe Phe  
115

(2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..382
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

cagaaatttt cttccgcgct aaaagcaaaa aaagatgcag atcttcgtga aaaccctaac 60  
ggggaagacg atcaactctcg aggtcgagtc ctctgacacc atcgacaatg tcaaggccaa 120  
gatccaagac aaggaaggaa tcccaccgga ccagcagcga ttgattttcg ccggaaagca 180  
gctcgaagac ggacgtacct tagccgatta caacatccag aaggaatcaa cgcttcacct 240  
tgtccttcgt ctccgtggag gtgctaagaa gaggaagaag aagacctaca ccaagcctaa 300  
gaagatcaag cacaagcaca agaaggtcaa gctcgctgtt cttcagttct acaaggttga 360  
tggttcaggt aaaccaaagt tt

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu  
1 5 10 15  
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp  
20 25 30  
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys  
35 40 45  
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu  
50 55 60  
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Ala Lys Lys Arg  
65 70 75 80  
Lys Lys Lys Thr Tyr Thr Lys Pro Lys Lys Ile Lys His Lys His Lys  
85 90 95  
Lys Val Lys Leu Ala Val Leu Gln Phe Tyr Lys Val Asp Gly Ser Gly  
100 105 110  
Lys Pro Lys Phe  
115

(2) INFORMATION FOR SEQ ID NO:704:

CONFIDENTIAL 03663950

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 336 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..336  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1593077  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:  
atttttgaaa agttttctaac ctctaggcca ccactcatg gctactctgt tcatgaagct 60  
ggtgagcttc tttctaattc tatctacttt ttgtctcact actgtgaact cggagccaca 120  
gtgccataat ttcaaatcga tcattagttt cggtgattct attgccgaca ctggaaaactt 180  
gctcgccctc tccgatccta ccaatctccc taaggtcgcg tttctaccgt acggagaaac 240  
ctttctccac catccgaccg gccgtttctc aaacggcgcc tcatcatcga tttcattgct 300  
gaatttttgg gttttccgct tgtgscmtt ttttat

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 99 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..99  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1593078  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:  
Met Ala Thr Leu Phe Met Lys Leu Val Ser Phe Phe Leu Ile Leu Ser  
1                   5                   10                   15  
Thr Phe Cys Leu Thr Thr Val Asn Ser Glu Pro Gln Cys His Asn Phe  
                  20                   25                   30  
Lys Ser Ile Ile Ser Phe Gly Asp Ser Ile Ala Asp Thr Gly Asn Leu  
                  35                   40                   45  
Leu Ala Leu Ser Asp Pro Thr Asn Leu Pro Lys Val Ala Phe Leu Pro  
50                   55                   60  
Tyr Gly Glu Thr Phe Phe His His Pro Thr Gly Arg Phe Ser Asn Gly  
65                   70                   75                   80  
Ala Ser Ser Ser Ile Ser Leu Leu Asn Phe Trp Val Phe Arg Leu Xaa  
                  85                   90                   95  
Leu Xaa Phe

(2) INFORMATION FOR SEQ ID NO:706:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 94 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..94  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1593079  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:  
Met Lys Leu Val Ser Phe Phe Leu Ile Leu Ser Thr Phe Cys Leu Thr  
1                   5                   10                   15  
Thr Val Asn Ser Glu Pro Gln Cys His Asn Phe Lys Ser Ile Ile Ser  
                  20                   25                   30  
Phe Gly Asp Ser Ile Ala Asp Thr Gly Asn Leu Leu Ala Leu Ser Asp  
35                   40                   45

00663360



- (A) NAME/KEY: peptide  
(B) LOCATION: 1..76  
(D) OTHER INFORMATION: / Ceres Seq. ID 1593103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

```
Met Arg Thr Glu Ile Ile Arg Ala Thr Arg Thr Gln Asn Val Leu
1 5 10 15
Gly Glu Lys Gly Arg Arg Ile Arg Glu Leu Thr Ser Leu Val Gln Lys
20 25 30
Arg Phe Lys Phe Pro Val Asp Ser Val Glu Leu Tyr Ala Glu Lys Val
35 40 45
Asn Asn Arg Gly Leu Cys Ala Ile Ala Gln Ala Glu Ser Leu Arg Tyr
50 55 60
Lys Leu Leu Gly Ile Lys Leu Asn Thr Val Asn Trp
65 70 75
```

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..487  
(D) OTHER INFORMATION: / Ceres Seq. ID 1593104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

```
atgaacatta ggggtgagaag agatcgagag aagaatagtt tgatcatctt gtgagaaaaa 60
taatggctgc ttccagtgatg ctatcttcgg tgacattgaa accagctggg ttccacggtgg 120
agaagacggc ggctagagga ttaccgtcgc tcacaagagc tcgtccctcc ttcaaaaattg 180
tcgccagtgg stcaagaaga tcaagaccga caagcccttc ggaattaacg gcagcatgga 240
cttgagggac ggcgtcgacg cttccggcag aaagggcaag ggatacgggtg tttacaagta 300
cgtcgacaag tatggagcta acgtcgatgg atacagtcct atttacaacg agaacgagtg 360
gtcagcgagt ggtgacgtgt acaagggagg agtcaccgga ttggcaattt gggcggtaac 420
tctcgccgga attcttctgc agccgattct tctattagcc gccatggtga agtactcgca 480
agaaccc
```

(2) INFORMATION FOR SEQ ID NO:711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..60  
(D) OTHER INFORMATION: / Ceres Seq. ID 1593105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

```
Met Ala Ala Ser Val Met Leu Ser Ser Val Thr Leu Lys Pro Ala Gly
1 5 10 15
Phe Thr Val Glu Lys Thr Ala Ala Arg Gly Leu Pro Ser Leu Thr Arg
20 25 30
Ala Arg Pro Ser Phe Lys Ile Val Ala Ser Xaa Ser Arg Arg Ser Arg
35 40 45
Pro Thr Ser Pro Ser Glu Leu Thr Ala Ala Trp Thr
50 55 60
```

(2) INFORMATION FOR SEQ ID NO:712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

00558960













Thr His Val  
115

(2) INFORMATION FOR SEQ ID NO:725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

Met Gly Lys Glu Asp Leu Gly Leu Ser Leu Ser Leu Gly Phe Ser Gln  
1 5 10 15  
Asn His Asn Pro Leu Gln Met Asn Leu Asn Pro Asn Ser Ser Leu Ser  
20 25 30  
Asn Asn Leu Gln Arg Leu Pro Trp Asn Gln Thr Phe Asp Pro Thr Ser  
35 40 45  
Asp Leu Arg Lys Ile Asp Val Asn Ser Phe Pro Ser Thr Val Asn Cys  
50 55 60  
Glu Glu Asp Thr Gly Val Ser Ser Pro Xaa Ser Thr Ile Ser Ser Thr  
65 70 75 80  
Ile Ser Gly Lys Arg Ser Glu Arg Glu Gly Ile Ser Gly Thr Gly Val  
85 90 95  
Gly Ser Gly Glu Arg Ser Arg Arg Asp His Ser Gly Ile Glu Gly Thr  
100 105 110  
His Val

(2) INFORMATION FOR SEQ ID NO:726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..529
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

aagaatcaac aaaagaaaaa acattcacct tctcttacgc gactctcgcc ggaaacagat 60  
cgctccgccg tgaactcgga agccatgggg tcaacttttg aggggttttac taaatcactc 120  
gccatgactt tcctctccga gattggtgac aaaacgttct tcgctgctgc tattttggcg 180  
atgcggtatc ctaggaggct tgtattagct ggttgtttat cagctttgat tgtvatgact 240  
atattatctg ctacacttgg ttgggctgct ccaaactctga tctctcgga atggactcat 300  
catataacaa cattcttggt ctttggcttt gggttatggt ctttgtggga tggttttaaa 360  
gaaggaggag gttctgaaga attggcagaa gttgaagcag aactggattc tgatttgaag 420  
aagactaatg atcaatcgaa aaacagtaag attgaagatg aacagaaaaa gcagaaaaga 480  
ccattcctta ctgcattctt ctctcccatt tttctcaagg cgtttttcg

(2) INFORMATION FOR SEQ ID NO:727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..176

09639980 101300



- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..135
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1593231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

Met Thr Phe Leu Ser Glu Ile Gly Asp Lys Thr Phe Phe Ala Ala Ala  
1 5 10 15  
Ile Leu Ala Met Arg Tyr Pro Arg Arg Leu Val Leu Ala Gly Cys Leu  
20 30  
Ser Ala Leu Ile Xaa Met Thr Ile Leu Ser Ala Thr Leu Gly Trp Ala  
35 40 45  
Ala Pro Asn Leu Ile Ser Arg Lys Trp Thr His His Ile Thr Thr Phe  
50 55 60  
Leu Phe Phe Gly Phe Gly Leu Trp Ser Leu Trp Asp Gly Phe Lys Glu  
65 70 75 80  
Gly Gly Gly Ser Glu Leu Ala Glu Val Glu Ala Glu Leu Asp Ser  
85 90 95  
Asp Leu Lys Lys Thr Asn Asp Gln Ser Lys Asn Ser Lys Ile Glu Asp  
100 105 110  
Glu Gln Lys Lys Gln Lys Arg Pro Phe Leu Thr Ala Phe Phe Ser Pro  
115 120 125  
Ile Phe Leu Lys Ala Phe Phe  
130 135

(2) INFORMATION FOR SEQ ID NO:730:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 457 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..457
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

gtttcaacag attgaaggta agggaaaccag tgattgagcc gggttgagg gatgttgagg 60  
acagtactga ctcgagcgta ggagaagaag aagaagagga tgatttgatc aaggagattg 120  
tccgtaccaa gactttcgag atgccaccat tgactgtcgc tgaggcagtc gaggcagctg 180  
aactagtcag tcacgacttc tatggcttcc aaaatgaaga aactggtgag ataaacatag 240  
tgtacaagag aaaagaagga gggttacggtc tgataatccc aaagaaagac gggaaggccg 300  
agaaggttga gccgcttcca accgagcaat tgaatgaaca ctctttcgcc gagtagactg 360  
cctctgctca caccaaaacc gataagctca tctctcctta cagtttacct gtgtaggagt 420  
tagggttctt gaataaacia tgcaacaaag attgtag

(2) INFORMATION FOR SEQ ID NO:731:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 117 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

Phe Asn Arg Leu Lys Val Arg Glu Pro Val Ile Glu Pro Val Val Glu  
1 5 10 15

DOCTOT 08062000

Asp Val Glu Asp Ser Thr Asp Ser Ser Val Gly Glu Glu Glu Glu Glu  
20 25 30  
Asp Asp Leu Ile Lys Glu Ile Val Arg Thr Lys Thr Phe Glu Met Pro  
35 40 45  
Pro Leu Thr Val Ala Glu Ala Val Glu Gln Leu Glu Leu Val Ser His  
50 55 60  
Asp Phe Tyr Gly Phe Gln Asn Glu Glu Thr Gly Glu Ile Asn Ile Val  
65 70 75 80  
Tyr Lys Arg Lys Glu Gly Gly Tyr Gly Leu Ile Ile Pro Lys Lys Asp  
85 90 95  
Gly Lys Ala Glu Lys Val Glu Pro Leu Pro Thr Glu Gln Leu Asn Glu  
100 105 110  
His Ser Phe Ala Glu  
115

(2) INFORMATION FOR SEQ ID NO:732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

Met Pro Pro Leu Thr Val Ala Glu Ala Val Glu Gln Leu Glu Leu Val  
1 5 10 15  
Ser His Asp Phe Tyr Gly Phe Gln Asn Glu Glu Thr Gly Glu Ile Asn  
20 25 30  
Ile Val Tyr Lys Arg Lys Glu Gly Gly Tyr Gly Leu Ile Ile Pro Lys  
35 40 45  
Lys Asp Gly Lys Ala Glu Lys Val Glu Pro Leu Pro Thr Glu Gln Leu  
50 55 60  
Asn Glu His Ser Phe Ala Glu  
65 70

(2) INFORMATION FOR SEQ ID NO:733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..462
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

ctcctctaaa aaacccaaat aaaaaccttt tttctctctt catgcttagc ctatcatgag 60  
caacatccct agatctctca cgcactcaga tctttctcta tttactctca taatctcttc 120  
tgctgttgat ccttgccctt tttctatcac cgtttttttag catcaacaaa actcaccgga 180  
aaatctctaa caaccaccgt ttaacacttc tcttcctcct cgtcgatcgt ttttaaacca 240  
atctttgtgt ttcttggttg gtttttcggg gaaaaagatt ccttccttct taatggggtt 300  
tgaagaaaac caaaaacaga gtccaaaaca gagtccgaat catatcaagc atatgggtgt 360  
caagtttcac ttccatgttc ctcatcttca catactccct catcaccacc accaccacca 420  
ccatgatgtt cctaaaggct gtgtagcgat tatgggtggga ca

(2) INFORMATION FOR SEQ ID NO:734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

0965980 10300



(D) OTHER INFORMATION: / Ceres Seq. ID 1593344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aactactgtc | ttcgatctct | ctttcatata | caccatataa | aacgaaccag | ttaattatgg | 60  |
| gtttaatttc | cgggaaggtg | tgtgtgttta | tctttgtatt | cgctctagtc | gctgaatttt | 120 |
| cgttcggaaa | tggtgaggtt | aacgacgaca | aacacttttt | ccacaaacct | cgtccatttt | 180 |
| tacacaaacc | tcgtccattc | ctccacaagc | atggcattta | caagaaaggt | ttcggtaagg | 240 |
| gtttgggcgg | tggagcggtt | ctaggcggtg | gaggtggtct | aggagcggtt | ggtggaggtt | 300 |
| taggcggcgg | tggtggtcta | ggagcggtta | gcggtttggg | aggaggaggg | ggtctaggag | 360 |
| gcggtagcgg | tttgggagga | ggaggaggtt | ttggcggtgg | aggg       |            |     |

(2) INFORMATION FOR SEQ ID NO:738:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1593345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Ser | Ser | Ile | Ser | Leu | Ser | Tyr | Thr | Pro | Tyr | Lys | Thr | Asn | Gln |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ile | Met | Gly | Leu | Ile | Ser | Gly | Lys | Val | Cys | Val | Phe | Ile | Phe | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Ala | Leu | Val | Ala | Glu | Phe | Ser | Phe | Gly | Asn | Val | Glu | Val | Asn | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Lys | His | Phe | Phe | His | Lys | Pro | Arg | Pro | Phe | Leu | His | Lys | Pro | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Phe | Leu | His | Lys | His | Gly | Ile | Tyr | Lys | Lys | Gly | Phe | Gly | Lys | Gly |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Gly | Gly | Gly | Gly | Gly | Leu | Gly | Gly | Gly | Gly | Gly | Leu | Gly | Gly | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Gly | Gly | Leu | Gly | Gly | Gly | Gly | Gly | Leu | Gly | Gly | Gly | Ser | Gly | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Gly | Gly | Gly | Gly | Leu | Gly | Gly | Gly | Ser | Gly | Leu | Gly | Gly | Gly | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Phe | Gly | Gly | Gly | Gly |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 130 |

(2) INFORMATION FOR SEQ ID NO:739:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1593346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Leu | Ile | Ser | Gly | Lys | Val | Cys | Val | Phe | Ile | Phe | Val | Phe | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Val | Ala | Glu | Phe | Ser | Phe | Gly | Asn | Val | Glu | Val | Asn | Asp | Asp | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Phe | Phe | His | Lys | Pro | Arg | Pro | Phe | Leu | His | Lys | Pro | Arg | Pro | Phe |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | His | Lys | His | Gly | Ile | Tyr | Lys | Lys | Gly | Phe | Gly | Lys | Gly | Leu | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gly | Gly | Gly | Gly | Leu | Gly | Gly | Gly | Gly | Gly | Leu | Gly | Gly | Gly | Gly | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |

Gly Leu Gly Gly Gly Gly Gly Leu Gly Gly Gly Ser Gly Leu Gly Gly  
85 90 95  
Gly Gly Gly Leu Gly Gly Gly Ser Gly Leu Gly Gly Gly Gly Phe  
100 105 110  
Gly Gly Gly Gly  
115

(2) INFORMATION FOR SEQ ID NO:740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..498
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aaaacttgcg actttttaac aatcgaccga cttatcaaaa ttagggatag ttttatatat  | 60  |
| aaagagagac gcattctctt atttcattca tcgcttctcc aaaattttct tcaaagaaca  | 120 |
| aatctcccaa atctaaaatc tttctcttct ctcttcggtt ccataaccat gtctgcgaag  | 180 |
| aagattgtgt tgaagagttc cgatgggtgaa tctttcgagg ttgaggaggc ggtggctctc | 240 |
| gagtcacaaa ccatagcgca tatggttgaa gacggactgc gtsacaacgg agtccctott  | 300 |
| cctaacgtca cgagcaagat cctcgccaag gtgatcgagt attgcaagag gcacgtcgag  | 360 |
| gctgctgct ctaaggccga ggccgtcgag ggtgctgcta cctccgatka cgatcttaag   | 420 |
| gcctgggaag ctgattttat gaagatcgat caagctactc tctttgaact cattctggct  | 480 |
| gctaattacc tgaatatc                                                |     |

(2) INFORMATION FOR SEQ ID NO:741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..166
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Lys Thr Cys Asp Phe Leu Thr Ile Asp Arg Leu Ile Lys Ile Arg Asp |  |
| 1 5 10 15                                                       |  |
| Ser Phe Ile Tyr Lys Glu Arg Arg Ile Ser Leu Phe His Ser Ser Leu |  |
| 20 25 30                                                        |  |
| Leu Gln Asn Phe Leu Gln Arg Thr Asn Leu Pro Asn Leu Lys Ser Phe |  |
| 35 40 45                                                        |  |
| Ser Ser Leu Phe Val Ser Ile Thr Met Ser Ala Lys Lys Ile Val Leu |  |
| 50 55 60                                                        |  |
| Lys Ser Ser Asp Gly Glu Ser Phe Glu Val Glu Glu Ala Val Ala Leu |  |
| 65 70 75 80                                                     |  |
| Glu Ser Gln Thr Ile Ala His Met Val Glu Asp Gly Leu Arg Xaa Asn |  |
| 85 90 95                                                        |  |
| Gly Val Pro Leu Pro Asn Val Thr Ser Lys Ile Leu Ala Lys Val Ile |  |
| 100 105 110                                                     |  |
| Glu Tyr Cys Lys Arg His Val Glu Ala Ala Ala Ser Lys Ala Glu Ala |  |
| 115 120 125                                                     |  |
| Val Glu Gly Ala Ala Thr Ser Asp Xaa Asp Leu Lys Ala Trp Asp Ala |  |
| 130 135 140                                                     |  |
| Asp Phe Met Lys Ile Asp Gln Ala Thr Leu Phe Glu Leu Ile Leu Ala |  |
| 145 150 155 160                                                 |  |
| Ala Asn Tyr Leu Asn Ile                                         |  |
| 165                                                             |  |

DOCKET "08668950"









(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..76  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1593444  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:  
Met Leu Ala Ile Asn Glu Ile Phe Glu Lys Asn Pro Thr Thr Ile Lys  
1                    5                    10                    15  
Asn Phe Gly Ile Trp Leu Arg Tyr Gln Ser Arg Thr Gly Tyr His Asn  
                    20                    25                    30  
Met Tyr Lys Lys Glu Tyr Arg Asp Thr Leu Asn Gly Ala Val Glu Gln  
                    35                    40                    45  
Met Tyr Thr Glu Met Ala Ser Arg His Arg Val Arg Phe Pro Cys Ile  
                    50                    55                    60  
Gln Ile Ile Lys Thr Ala Thr Val Pro Ala Ser Leu  
65                    70                    75

(2) INFORMATION FOR SEQ ID NO:750:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 527 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..527

(D) OTHER INFORMATION: / Ceres Seq. ID 1593459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| atcaaacaat acacttaaca atggattcctt ctctgaaaac tcaggaacct caagtagtgg  | 60  |
| aaacttctcc ttctccggtg gctcaggagc ctctcaagt agctgacaaa cctgcgattg    | 120 |
| ttccttctcc gatagctcaa gagccagaca acgatgtccc ggcgcgggga aacgagtttg   | 180 |
| ctgagttcgc cgccggttgt ttctggggag tggagcttgc tttccagaga atccctggcg   | 240 |
| tgaccgtgac tgaggtcggg tacactcatg ggatctctca caatccgtct tatgaagatg   | 300 |
| tctgtacgaa caccacgaac catgcagaag ttgtcagggt tcaatatgat cctaangaat   | 360 |
| gcacttatga gacacttctt gatttgtttt ggtctagaca taatcctacc accttgaatc   | 420 |
| gtcaggggaga acttttagga gcacaatacc gatcagggtat atacttctac acaccggagc | 480 |
| aagagaaact agcacgcgag tctctagaga agagcagaaa aaactgg                 |     |

(2) INFORMATION FOR SEQ ID NO:751:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 175 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1593460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

Gln Thr Ile His Leu Thr Met Asp Ser Ser Leu Lys Thr Gln Glu Pro  
1                    5                    10                    15  
Gln Val Val Glu Thr Ser Pro Ser Pro Val Ala Gln Glu Pro Pro Gln  
                    20                    25                    30  
Val Ala Asp Lys Pro Ala Ile Val Pro Ser Pro Ile Ala Gln Glu Pro  
                    35                    40                    45  
Asp Asn Asp Val Pro Ala Pro Gly Asn Glu Phe Ala Glu Phe Ala Ala  
                    50                    55                    60  
Gly Cys Phe Trp Gly Val Glu Leu Ala Phe Gln Arg Ile Pro Gly Val  
65                    70                    75                    80  
Thr Val Thr Glu Val Gly Tyr Thr His Gly Ile Ser His Asn Pro Ser

09689980 101300







(D) OTHER INFORMATION: / Ceres Seq. ID 1593571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

|            |    |            |            |            |            |            |     |
|------------|----|------------|------------|------------|------------|------------|-----|
| atggcgga   | aa | ggttctctag | cggcgaggcc | caatattggc | ccaattatgg | tagcaccgcc | 60  |
| accaccac   | cg | ttagcaacag | ccccatctcg | tcgtttttcc | atcagctccg | atcccattca | 120 |
| ccaacatc   | ct | cgcagctctt | tggtttcttc | gtctctctta | tctccactgg | catcctcttc | 180 |
| ttcctcct   | tg | gtgtaagcgt | caccgctgcc | gtgctcggct | tcattgtctt | tcttccattg | 240 |
| atcatcat   | ct | cgagtcgat  | atggattccc | gtttttgtcg | tcgttggcgg | gttcttaacg | 300 |
| gtctccgg   | at | ttcttgtcgg | aacggtggct | ttagtgctcg | ggacgtaccg | ctatttccgg | 360 |
| ggaatgcac  | c  | cggttggatc | gaatcagatg | gattatgcac | gtagtaggat | ctatgacacg | 420 |
| gcattctcac | g  | tcaaagatta | cgctagagaa | tacggtggtt | acttccatgg | cagggctaaa | 480 |
| gatgcggccc |    | ctggtgcttg | a          |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:759:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1593572

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Glu | Arg | Phe | Ser | Ser | Gly | Glu | Ala | Gln | Tyr | Trp | Pro | Asn | Tyr |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Gly | Ser | Thr | Ala | Thr | Thr | Thr | Val | Ser | Asn | Ser | Pro | Ile | Ser | Ser | Phe |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Phe | His | Gln | Leu | Arg | Ser | His | Ser | Pro | Thr | Ser | Ser | Gln | Leu | Phe | Gly |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Phe | Leu | Ala | Leu | Phe | Ile | Ser | Thr | Gly | Ile | Leu | Leu | Phe | Leu | Leu | Gly |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Val | Ser | Val | Thr | Ala | Ala | Val | Leu | Gly | Phe | Ile | Val | Phe | Leu | Pro | Leu |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Ile | Ile | Ile | Ser | Ser | Pro | Ile | Trp | Ile | Pro | Val | Phe | Val | Val | Val | Gly |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Gly | Phe | Leu | Thr | Val | Ser | Gly | Phe | Leu | Val | Gly | Thr | Val | Ala | Leu | Val |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ser | Trp | Thr | Tyr | Arg | Tyr | Phe | Arg | Gly | Met | His | Pro | Val | Gly | Ser | Asn |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Gln | Met | Asp | Tyr | Ala | Arg | Ser | Arg | Ile | Tyr | Asp | Thr | Ala | Ser | His | Val |  |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |  |
| Lys | Asp | Tyr | Ala | Arg | Glu | Tyr | Gly | Gly | Tyr | Phe | His | Gly | Arg | Ala | Lys |  |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Asp | Ala | Ala | Pro | Gly | Ala |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:760:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 693 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..693

(D) OTHER INFORMATION: / Ceres Seq. ID 1593608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

|          |     |            |            |            |            |            |     |
|----------|-----|------------|------------|------------|------------|------------|-----|
| cggtttta | aat | cggtgccttg | tgtttcacgg | ctacaagaa  | gaaacaagga | tatcaaggag | 60  |
| gcgactot | ca  | cacatcaagt | tggcttctta | tatatggaaa | ctctaccaca | tcaggaacca | 120 |
| aatcaacc | at  | ctcaggaag  | agcaacaatg | gaagtcacct | atccaatctc | gcagcagggt | 180 |
| tatgcogt | tag | attctcttta | ccagaaatca | aacacggaac | acaaaacttc | gatgattcca | 240 |

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acgtcattgg agttggaggg tttggttaaag tctacaaagg agttatagac ggcacaacta 300  
aagtagcggg aaaaaaatca aaccctaaatt cagaacaagg actcaacgaa ttcgagacag 360  
aaatcgaact cctctcaaga ctaagacaca aacacttagt ctcccttgata ggatactgcg 420  
acgagggagg agaaatgtgt ctcgtatacg attacatggc atttggaaca ctccgtgagc 480  
atctatacaa cacaaagaaa ccacaattaa cttggaaacg aaggctagag atagctattg 540  
gagcagcaag aggattacat taccttcaca caggagcaaa gtacacgatt atacacagag 600  
acgttaaaac aactaacatc ctcgtatagtg agaactgggt agccaaagtt tcagactttg 660  
ggttatccaa aactggacct aacatgaatg gag

(2) INFORMATION FOR SEQ ID NO:761:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..230

(D) OTHER INFORMATION: / Ceres Seq. ID 1593609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

Val Leu Ile Gly Ala Leu Cys Phe Thr Ala Tyr Lys Lys Lys Gln Gly  
1 5 10 15  
Tyr Gln Gly Gly Asp Ser His Thr Ser Ser Trp Leu Pro Ile Tyr Gly  
20 25 30  
Asn Ser Thr Thr Ser Gly Thr Lys Ser Thr Ile Ser Gly Lys Ser Asn  
35 40 45  
Asn Gly Ser His Leu Ser Asn Leu Ala Ala Gly Leu Cys Arg Arg Phe  
50 55 60  
Ser Leu Pro Glu Ile Lys His Gly Thr Gln Asn Phe Asp Asp Ser Asn  
65 70 75 80  
Val Ile Gly Val Gly Gly Phe Gly Lys Val Tyr Lys Gly Val Ile Asp  
85 90 95  
Gly Thr Thr Lys Val Ala Val Lys Lys Ser Asn Pro Asn Ser Glu Gln  
100 105 110  
Gly Leu Asn Glu Phe Glu Thr Glu Ile Glu Leu Leu Ser Arg Leu Arg  
115 120 125  
His Lys His Leu Val Ser Leu Ile Gly Tyr Cys Asp Glu Gly Gly Glu  
130 135 140  
Met Cys Leu Val Tyr Asp Tyr Met Ala Phe Gly Thr Leu Arg Glu His  
145 150 155 160  
Leu Tyr Asn Thr Lys Lys Pro Gln Leu Thr Trp Lys Arg Arg Leu Glu  
165 170 175  
Ile Ala Ile Gly Ala Ala Arg Gly Leu His Tyr Leu His Thr Gly Ala  
180 185 190  
Lys Tyr Thr Ile Ile His Arg Asp Val Lys Thr Thr Asn Ile Leu Val  
195 200 205  
Asp Glu Asn Trp Val Ala Lys Val Ser Asp Phe Gly Leu Ser Lys Thr  
210 215 220  
Gly Pro Asn Met Asn Gly  
225 230

(2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1139 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1139

(D) OTHER INFORMATION: / Ceres Seq. ID 1593622

09669900-0000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tctcaaaaaca aacttcttta acttccctaa aggtaaacct ttactgac              | 60   |
| tcttctcggt ggaggcatat tcaatgtcga cggtcactca tggagctcgc agcgcaaact  | 120  |
| cgtagccac gagttctcca ctgcgtcgt taggagtttt gcttttgagg ttcttaaaga    | 180  |
| cgaagtggag aaccgtctag tcccggttct atccacggcg gctgatgttg gtacgaccgt  | 240  |
| ggatttgcaa gatgttttga aacgttttgc ttttgatgtt gtttgtaaag tctcgttg    | 300  |
| ttgggatccg gattgttttg atctaaccg acccgttaat ccacttgagg aggcctttga   | 360  |
| caccgctgct gagattagtg ctgcgcgtgc cacggagcct atttacgctg tttggaaaac  | 420  |
| gaaacgtgtg ttgaacgtgg gaagcgagag gacgcttagg gaagcgatca ggaccgtaca  | 480  |
| cgtgttgggtc tctgagattg tcagagctaa gaagaaaagt cttgagatcg gaaccggagc | 540  |
| agaagcaaag caagatcttt tgtcgagggt tctanccgcc ggccacaacg gcgaagcagt  | 600  |
| gagggacatg gttattagtt ttatcatggc gggaagagat acaacgtcag cagcgatgac  | 660  |
| gtggctgttt tgggtgttga ctgagaacga tgacgtggag aggaagattt tagaagaagt  | 720  |
| gaaccggttg ctgagtttag ggtagagtt tgaggatttg aaagagatga cttacacgaa   | 780  |
| ggcttgtcta tgtgaagcca tgaggcttta tctcctgtg tctgtggact caaagcatgc   | 840  |
| tgcaaacgac gacgttttac cagatgggac acatgtcaag aaaggagaca aagtgcata   | 900  |
| ttcccatata ggtatgggga ggatggagac gctatggggg gcggattcag aagaatttaa  | 960  |
| accgaaccgg tggtttgatt ctgaaccggg gtgtacacga ccggttttga aacctattag  | 1020 |
| tccttataaaa ttttctgttt ttcaagccgg accaagagtt tgtgtaggga aagagatggc | 1080 |
| gtttatgcag atgaaattcg tcgttggttc tggtttgagt cggtttgaga ttaagccgg   |      |

(2) INFORMATION FOR SEQ ID NO:763:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..379
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593623

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Lys | Thr | Asn | Phe | Phe | Asn | Phe | Pro | Lys | Gly | Lys | Pro | Phe | Thr | Asp |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Leu | Gly | Asp | Leu | Leu | Gly | Gly | Gly | Ile | Phe | Asn | Val | Asp | Gly | His |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Trp | Ser | Ser | Gln | Arg | Lys | Leu | Ala | Ser | His | Glu | Phe | Ser | Thr | Arg |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ser | Leu | Arg | Ser | Phe | Ala | Phe | Glu | Val | Leu | Lys | Asp | Glu | Val | Glu | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Leu | Val | Pro | Val | Leu | Ser | Thr | Ala | Ala | Asp | Val | Gly | Thr | Thr | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Leu | Gln | Asp | Val | Leu | Lys | Arg | Phe | Ala | Phe | Asp | Val | Val | Cys | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Ser | Leu | Gly | Trp | Asp | Pro | Asp | Cys | Leu | Asp | Leu | Thr | Arg | Pro | Val |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Pro | Leu | Val | Glu | Ala | Phe | Asp | Thr | Ala | Ala | Glu | Ile | Ser | Ala | Arg |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Arg | Ala | Thr | Glu | Pro | Ile | Tyr | Ala | Val | Trp | Lys | Thr | Lys | Arg | Val | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Val | Gly | Ser | Glu | Arg | Thr | Leu | Arg | Glu | Ala | Ile | Arg | Thr | Val | His |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Leu | Val | Ser | Glu | Ile | Val | Arg | Ala | Lys | Lys | Lys | Ser | Leu | Glu | Ile |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Thr | Gly | Ala | Glu | Ala | Lys | Gln | Asp | Leu | Leu | Ser | Arg | Phe | Leu | Xaa |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Gly | His | Asn | Gly | Glu | Ala | Val | Arg | Asp | Met | Val | Ile | Ser | Phe | Ile |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Met | Ala | Gly | Arg | Asp | Thr | Thr | Ser | Ala | Ala | Met | Thr | Trp | Leu | Phe | Trp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Leu | Thr | Glu | Asn | Asp | Asp | Val | Glu | Arg | Lys | Ile | Leu | Glu | Glu | Val |

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(ii) MOLECULE TYPE: peptide

| Age in 1980 (years) |     |
|---------------------|-----|
| 15-19               | 100 |
| 20-24               | 100 |
| 25-29               | 100 |
| 30-34               | 100 |
| 35-39               | 100 |
| 40-44               | 100 |
| 45-49               | 100 |
| 50-54               | 100 |
| 55-59               | 100 |
| 60-64               | 100 |
| 65-69               | 100 |
| 70-74               | 100 |
| 75-79               | 100 |
| 80-84               | 100 |
| 85-89               | 100 |
| 90-94               | 100 |
| 95-99               | 100 |
| 100+                | 100 |
| Age in 1990 (years) |     |
| 15-19               | 100 |
| 20-24               | 100 |
| 25-29               | 100 |
| 30-34               | 100 |
| 35-39               | 100 |
| 40-44               | 100 |
| 45-49               | 100 |
| 50-54               | 100 |
| 55-59               | 100 |
| 60-64               | 100 |
| 65-69               | 100 |
| 70-74               | 100 |
| 75-79               | 100 |
| 80-84               | 100 |
| 85-89               | 100 |
| 90-94               | 100 |
| 95-99               | 100 |
| 100+                | 100 |
| Age in 2000 (years) |     |
| 15-19               | 100 |
| 20-24               | 100 |
| 25-29               | 100 |
| 30-34               | 100 |
| 35-39               | 100 |
| 40-44               | 100 |
| 45-49               | 100 |
| 50-54               | 100 |
| 55-59               | 100 |
| 60-64               | 100 |
| 65-69               | 100 |
| 70-74               | 100 |
| 75-79               | 100 |
| 80-84               | 100 |
| 85-89               | 100 |
| 90-94               | 100 |
| 95-99               | 100 |
| 100+                | 100 |
| Age in 2010 (years) |     |
| 15-19               | 100 |
| 20-24               | 100 |
| 25-29               | 100 |
| 30-34               | 100 |
| 35-39               | 100 |
| 40-44               | 100 |
| 45-49               | 100 |
| 50-54               | 100 |
| 55-59               | 100 |
| 60-64               | 100 |
| 65-69               | 100 |
| 70-74               | 100 |
| 75-79               | 100 |
| 80-84               | 100 |
| 85-89               | 100 |
| 90-94               | 100 |
| 95-99               | 100 |
| 100+                | 100 |
| Age in 2020 (years) |     |
| 15-19               | 100 |
| 20-24               | 100 |
| 25-29               | 100 |
| 30-34               | 100 |
| 35-39               | 100 |
| 40-44               | 100 |
| 45-49               | 100 |
| 50-54               | 100 |
| 55-59               | 100 |
| 60-64               | 100 |
| 65-69               | 100 |
| 70-74               | 100 |
| 75-79               | 100 |
| 80-84               | 100 |
| 85-89               | 100 |
| 90-94               | 100 |
| 95-99               | 100 |
| 100+                | 100 |



Ser Thr Leu Leu Gln Thr Arg  
450 455

(2) INFORMATION FOR SEQ ID NO:766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..429
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Leu | Phe | Thr | Asp | Ala | Tyr | Asp | Leu | Phe | Cys | Ile | Ala | Pro | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Met | Lys | Met | Ile | Ser | His | Val | Tyr | Tyr | Asn | Gly | Ile | Gly | Gly | Asp | Tyr |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Pro | Leu | Ser | Ala | Thr | Ile | Met | Ser | Glu | Phe | Ala | Asn | Lys | Arg | Thr | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Ala | Phe | Ile | Ala | Ala | Val | Phe | Ser | Met | Gln | Gly | Leu | Gly | Ile | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Ser | Ser | Ala | Val | Thr | Met | Ala | Val | Cys | Val | Ala | Phe | Lys | Arg | Ser |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Gly | Gly | Leu | Glu | Val | Asp | Ala | Ala | Ala | Pro | Thr | Glu | Ala | Asp | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ala | Trp | Arg | Leu | Ile | Leu | Met | Ile | Gly | Ala | Leu | Pro | Ala | Ala | Leu | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Phe | Tyr | Trp | Arg | Met | Leu | Met | Pro | Glu | Thr | Ala | Arg | Tyr | Thr | Ala | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Glu | Asn | Asn | Ile | Val | Gln | Ala | Ala | Lys | Asp | Met | Gln | Arg | Val | Met |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Ser | Arg | Ser | His | Ile | Ser | Asp | Glu | Ala | Thr | Thr | Asp | Pro | Pro | Pro | Pro |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Pro | Pro | Pro | Pro | Ser | Tyr | Lys | Leu | Phe | Ser | Arg | Cys | Phe | Phe | Arg | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Gly | Arg | Asp | Leu | Phe | Ala | Ala | Ser | Phe | Asn | Trp | Phe | Leu | Val | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Val | Phe | Tyr | Thr | Ser | Asn | Leu | Leu | Leu | Ser | His | Ile | Phe | Ser | His |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Tyr | Ser | Lys | Lys | Pro | Ser | Thr | Ala | Glu | Asn | Val | Tyr | Asp | Ala | Ala | Phe |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Val | Ala | Glu | Leu | Gly | Ala | Ile | Ile | Ala | Ala | Cys | Ser | Thr | Ile | Pro |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Gly | Tyr | Trp | Phe | Thr | Val | Tyr | Phe | Ile | Asp | Lys | Ile | Gly | Arg | Val | Lys |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ile | Gln | Ile | Met | Gly | Phe | Phe | Phe | Met | Ala | Val | Ile | Tyr | Leu | Val | Ala |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Ile | Pro | Tyr | Ser | Trp | Tyr | Trp | Ser | Lys | His | Glu | His | Asn | Asn | Lys |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Phe | Met | Val | Leu | Tyr | Gly | Leu | Val | Phe | Phe | Phe | Cys | Asn | Phe | Gly |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Pro | Asn | Thr | Thr | Thr | Phe | Ile | Ile | Pro | Ala | Glu | His | Phe | Pro | Ala | Arg |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     | 320 |     |
| Phe | Arg | Ser | Thr | Cys | His | Gly | Ile | Ser | Gly | Ala | Ala | Gly | Lys | Leu | Gly |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ala | Ile | Val | Gly | Thr | Val | Gly | Phe | Leu | Trp | Ala | Thr | Lys | Lys | Met | Glu |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     |     | 350 |     |     |
| Ser | Asp | Asp | Lys | Asn | Gln | Ile | Tyr | Pro | Glu | Val | Asn | Arg | Met | Arg | Ile |
|     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |     |
| Ala | Phe | Leu | Ile | Leu | Gly | Gly | Val | Cys | Ile | Ala | Gly | Ile | Leu | Val | Thr |

09669900 101000

370 375 380  
Tyr Phe Phe Thr Lys Glu Thr Met Gly Arg Ser Leu Glu Glu Asn Glu  
385 390 395 400  
His Asp Gln Asp Asn Ala Glu Ser Glu Asp Glu Pro Gln Ile Val  
405 410 415  
Asp Trp Gln Ser Ser Val Ser Thr Leu Leu Gln Thr Arg  
420 425

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..501
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atgccgataa aggtattgtc gtcgcttgat gtagctcgaa cacaatggta ccatttcaaa  | 60  |
| gcgatcatag tagcgggaat gggctatttc accgaacgat acgatctttt ctgcatagca  | 120 |
| ccggtcataa aaatgattag tcatgtttat tacaacggta tcggtgggtga ttaccgctc  | 180 |
| tcggctacca ttatgtcgga gtttgctaata aagaggacac gtggcgcggt tatcgctgcg | 240 |
| gtgttttcga tgcaagggtt ggggattttt gttagctctg ccgtgacat ggctgtttgc   | 300 |
| gtggcggtta agagaagtgg cgggtggttg gaggtggatg cggcggtcc gacggaagct   | 360 |
| gacttggcct ggagacttat acttatgatc ggtgctcttc ctgctgcatt gacgttctat  | 420 |
| tggcgaatgt tgatgcctga aaccgcaagg tatcagatcc tatcagctcc agctaataca  | 480 |
| ccaaatacac agcacttgta g                                            |     |

(2) INFORMATION FOR SEQ ID NO:768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..166
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Pro Ile Lys Val Leu Ser Ser Leu Asp Val Ala Arg Thr Gln Trp |  |
| 1 5 10 15                                                       |  |
| Tyr His Phe Lys Ala Ile Ile Val Ala Gly Met Gly Leu Phe Thr Asp |  |
| 20 25 30                                                        |  |
| Ala Tyr Asp Leu Phe Cys Ile Ala Pro Val Met Lys Met Ile Ser His |  |
| 35 40 45                                                        |  |
| Val Tyr Tyr Asn Gly Ile Gly Gly Asp Tyr Pro Leu Ser Ala Thr Ile |  |
| 50 55 60                                                        |  |
| Met Ser Glu Phe Ala Asn Lys Arg Thr Arg Gly Ala Phe Ile Ala Ala |  |
| 65 70 75 80                                                     |  |
| Val Phe Ser Met Gln Gly Leu Gly Ile Leu Val Ser Ser Ala Val Thr |  |
| 85 90 95                                                        |  |
| Met Ala Val Cys Val Ala Phe Lys Arg Ser Gly Gly Gly Leu Glu Val |  |
| 100 105 110                                                     |  |
| Asp Ala Ala Ala Pro Thr Glu Ala Asp Leu Ala Trp Arg Leu Ile Leu |  |
| 115 120 125                                                     |  |
| Met Ile Gly Ala Leu Pro Ala Ala Leu Thr Phe Tyr Trp Arg Met Leu |  |
| 130 135 140                                                     |  |
| Met Pro Glu Thr Ala Arg Tyr Gln Ile Leu Ser Ala Pro Ala Asn Gln |  |
| 145 150 155 160                                                 |  |
| Pro Asn Thr Gln His Leu                                         |  |

165

(2) INFORMATION FOR SEQ ID NO:769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

Met Gly Leu Phe Thr Asp Ala Tyr Asp Leu Phe Cys Ile Ala Pro Val  
1 5 10 15  
Met Lys Met Ile Ser His Val Tyr Tyr Asn Gly Ile Gly Gly Asp Tyr  
20 25 30  
Pro Leu Ser Ala Thr Ile Met Ser Glu Phe Ala Asn Lys Arg Thr Arg  
35 40 45  
Gly Ala Phe Ile Ala Ala Val Phe Ser Met Gln Gly Leu Gly Ile Leu  
50 55 60  
Val Ser Ser Ala Val Thr Met Ala Val Cys Val Ala Phe Lys Arg Ser  
65 70 75 80  
Gly Gly Gly Leu Glu Val Asp Ala Ala Ala Pro Thr Glu Ala Asp Leu  
85 90 95  
Ala Trp Arg Leu Ile Leu Met Ile Gly Ala Leu Pro Ala Ala Leu Thr  
100 105 110  
Phe Tyr Trp Arg Met Leu Met Pro Glu Thr Ala Arg Tyr Gln Ile Leu  
115 120 125  
Ser Ala Pro Ala Asn Gln Pro Asn Thr Gln His Leu  
130 135 140

(2) INFORMATION FOR SEQ ID NO:770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..462
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

tcggtttggag ttggtcctat tgatgcgctt tttggagggtg gaaacttacc aggatttgtg 60  
gtcggagcta ttgcagcggc aattagcagt gttgtggcat ttaccgttct tacaatagaa 120  
actttgcact atgtgatttc agctggagtc gtcgccgctg tgaggaacat cataggatac 180  
gcattcagca acagcaaaga agttttggac tatgtgcgcg acctaactcc tttgctctgc 240  
ctctccttta tcctcgacgg ctttacagca gttcttaatg ggattgctag gggaagtgc 300  
ttcagtcgtg agttgaacgg aaaaggattg tgggtgcggtg ttgtggttgg atctactgtg 360  
caagccacta tactggctat tgtcacagct tccataaatt ggaaggaaca ggctgagaag 420  
gcaaggaaga gaattgtctc aactgaaaat agattggcctt aa

(2) INFORMATION FOR SEQ ID NO:771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

0366960-0366960

(D) OTHER INFORMATION: / Ceres Seq. ID 1593664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

Ser Phe Gly Val Gly Pro Ile Asp Ala Leu Phe Gly Gly Gly Asn Leu  
1 5 10 15  
Pro Gly Phe Val Val Gly Ala Ile Ala Ala Ala Ile Ser Ser Val Val  
20 25 30  
Ala Phe Thr Val Leu Thr Ile Glu Thr Leu His Tyr Val Ile Ser Ala  
35 40 45  
Gly Val Val Ala Ala Val Arg Asn Ile Ile Gly Tyr Ala Phe Ser Asn  
50 55 60  
Ser Lys Glu Val Leu Asp Tyr Val Ala Asp Leu Thr Pro Leu Leu Cys  
65 70 75 80  
Leu Ser Phe Ile Leu Asp Gly Phe Thr Ala Val Leu Asn Gly Ile Ala  
85 90 95  
Arg Gly Ser Ala Phe Ser Arg Glu Leu Asn Gly Lys Gly Leu Trp Cys  
100 105 110  
Gly Val Val Val Gly Ser Thr Val Gln Ala Thr Ile Leu Ala Ile Val  
115 120 125  
Thr Ala Ser Ile Asn Trp Lys Glu Gln Ala Glu Lys Ala Arg Lys Arg  
130 135 140  
Ile Val Ser Thr Glu Asn Arg Leu Ala  
145 150

(2) INFORMATION FOR SEQ ID NO:772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1422

(D) OTHER INFORMATION: / Ceres Seq. ID 1593707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

atggcggaaaa actacaatta tggcggtagtg ggcggttttt ttatcgagat tggatccgaa 60  
tacgtcgagcag gagttgagca attcatgaca tttgctaata gtcagcctat agtacagagt 120  
agtcaaagta aatttcattg tccttgtggt gtatgcaaga atgaaaaaca catcatctcg 180  
ggcagaagag ttagtagtca tttgtttagt gaggaattta tgcctgatta ttatgtttgg 240  
tataagcatg gagaagaaat gaatattgat ataggaacga gttccatgga taggacgtat 300  
tttagttcga atcatgaaga agtgggtaat gttgtagaag atccatattg ggatatggtg 360  
aacgatgcat ttaattttta cgtgggggtat gatgataact atcatcatga tgatagttat 420  
cagaatgtgg aagaaccggt ctataaccat ttaaacaagt tctacgactt gttagaaggt 480  
gcaaataatc catcgtagca tgattgtcgt gaagagcagt cgcagttatc cttagcatct 540  
cgactcatgc acaacaaggc agagtataat atgagtgaag agttggtgga ctccatttgc 600  
gaaatgttta cagatttttt accagaagga aaccaggcta caacttcaca ttaccagatc 660  
gagaagttga tgcgtaattt aggacttcca tatcatatga ttgatgtttg tcagaataat 720  
tgtatgctat tttggaaaaga agacgaaaaa gaagatcaat gtcgattttg tggcgacaaa 780  
agatggaagc ctgaggagca ccgtcgaaga accaaagtac catatagtcg tatgtggtat 840  
ctacctattg gagaccggtt gaagagaaat tatcagagcc ataagacagc tgcggtaatg 900  
cgatggcatg ttgagcacca atcaaaggag ggagaaatga ataatccttt agatgcagtg 960  
gagtggagat atttccaaga gttacatccc cggtttgccg aagaaccccg taacgtttat 1020  
ctcgggttgt gtactgatgg gttcaatcca tttggcatgt ctcgtaatca ttcgttgttg 1080  
cctgtgatcc tgaatccata taattttacc cctgtcctaa gcgaacatgc agaaaacaga 1140  
agcaataaca gaattactaa aatcactcga ccacaacagg ctgatgncag aagtaggatg 1200  
tggtcgagta acaggtcgag taatagacag gatacgaaac agctatactc gactgcacag 1260  
tctgttgcca gacactgggt gtggtcgaga gtgtgcccta gcctattcga atgggttaaca 1320  
agcgcaatca agctatccct agacaacagg ttcaacaaca gaccaattca ctcccgtgat 1380  
agaaatcctc aagcaaagct agcccagact aattccatt aa

(2) INFORMATION FOR SEQ ID NO:773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 amino acids

09669980 08669960



|            |            |            |            |            |            |            |            |            |            |            |            |            |            |           |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----------|------------|
| Met<br>1   | Ala        | Glu        | Asn        | Tyr<br>5   | Asn        | Tyr        | Gly        | Gly        | Ser<br>10  | Gly        | Gly        | Phe        | Phe        | Ile<br>15 | Glu        |
| Ile        | Gly        | Ser        | Glu<br>20  | Tyr        | Val        | Ala        | Gly<br>25  | Val        | Glu        | Gln        | Phe        | Met<br>30  | Thr        | Phe       | Ala        |
| Asn        | Ser        | Gln<br>35  | Pro        | Ile        | Val        | Gln        | Ser<br>40  | Ser        | Gln        | Ser        | Lys        | Phe<br>45  | His        | Cys       | Pro        |
| Cys        | Gly<br>50  | Val        | Cys        | Lys        | Asn        | Glu<br>55  | Lys        | His        | Ile        | Ile        | Ser<br>60  | Gly        | Arg        | Arg       | Val        |
| Ser<br>65  | Ser        | His        | Leu        | Phe        | Ser<br>70  | Glu        | Glu        | Phe        | Met        | Pro<br>75  | Asp        | Tyr        | Tyr        | Val       | Trp<br>80  |
| Tyr        | Lys        | His        | Gly<br>85  | Glu        | Glu        | Met        | Asn        | Ile        | Asp<br>90  | Ile        | Gly        | Thr        | Ser        | Ser       | Met        |
| Asp        | Arg        | Thr        | Tyr<br>100 | Phe        | Ser        | Ser        | Asn        | His<br>105 | Glu        | Glu        | Val        | Gly        | Asn<br>110 | Val       | Val        |
| Glu        | Asp        | Pro<br>115 | Tyr        | Val        | Asp        | Met        | Val<br>120 | Asn        | Asp        | Ala        | Phe        | Asn<br>125 | Phe        | Asn       | Val        |
| Gly        | Tyr<br>130 | Asp        | Asp        | Asn        | Tyr        | His<br>135 | His        | Asp        | Asp        | Ser        | Tyr<br>140 | Gln        | Asn        | Val       | Glu        |
| Glu<br>145 | Pro        | Val        | Tyr        | Asn        | His<br>150 | Leu        | Asn        | Lys        | Phe<br>155 | Tyr        | Asp        | Leu        | Leu        | Glu       | Gly<br>160 |
| Ala        | Asn        | Asn        | Pro<br>165 | Ser        | Tyr        | Asp        | Asp        | Cys        | Arg<br>170 | Glu        | Glu        | Gln        | Ser        | Gln       | Leu        |
| Ser        | Leu        | Ala        | Ser<br>180 | Arg        | Leu        | Met        | His<br>185 | Asn        | Lys        | Ala        | Glu        | Tyr        | Asn<br>190 | Met       | Ser        |
| Glu        | Lys<br>195 | Leu        | Val        | Asp        | Ser        | Ile        | Cys<br>200 | Glu        | Met        | Phe        | Thr        | Asp<br>205 | Phe        | Leu       | Pro        |
| Glu        | Gly<br>210 | Asn        | Gln        | Ala        | Thr        | Thr<br>215 | Ser        | His        | Tyr        | Gln        | Ile<br>220 | Glu        | Lys        | Leu       | Met        |
| Arg<br>225 | Asn        | Leu        | Gly        | Leu        | Pro<br>230 | Tyr        | His        | Thr        | Ile        | Asp<br>235 | Val        | Cys        | Gln        | Asn       | Asn<br>240 |
| Cys        | Met        | Leu        | Phe<br>245 | Trp        | Lys        | Glu        | Asp        | Glu        | Lys<br>250 | Glu        | Asp        | Gln        | Cys        | Arg       | Phe<br>255 |
| Cys        | Gly        | Ala        | Gln<br>260 | Arg        | Trp        | Lys        | Pro        | Glu<br>265 | Asp        | Asp        | Arg        | Arg        | Arg        | Thr       | Lys        |
| Val        | Pro<br>275 | Tyr        | Ser        | Arg        | Met        | Trp        | Tyr<br>280 | Leu        | Pro        | Ile        | Gly        | Asp<br>285 | Arg        | Leu       | Lys        |
| Arg        | Met<br>290 | Tyr        | Gln        | Ser        | His<br>295 | Lys        | Thr        | Ala        | Ala        | Val        | Met<br>300 | Arg        | Trp        | His       | Val        |
| Glu<br>305 | His        | Gln        | Ser        | Lys<br>310 | Glu        | Gly        | Glu        | Met        | Asn<br>315 | Asn        | Pro        | Leu        | Asp        | Ala       | Val<br>320 |
| Glu        | Trp        | Arg        | Tyr<br>325 | Phe        | Gln        | Glu        | Leu        | His        | Pro<br>330 | Arg        | Phe        | Ala        | Glu        | Glu       | Pro<br>335 |
| Arg        | Asn        | Val        | Tyr<br>340 | Leu        | Gly        | Leu        | Cys        | Thr<br>345 | Asp        | Gly        | Phe        | Asn        | Pro<br>350 | Phe       | Gly        |
| Met        | Ser<br>355 | Arg        | Asn        | His        | Ser        | Leu        | Trp<br>360 | Pro        | Val        | Ile        | Leu        | Asn<br>365 | Pro        | Tyr       | Asn        |
| Leu        | Pro<br>370 | Pro        | Val        | Leu        | Ser        | Glu<br>375 | His        | Ala        | Glu        | Asn        | Arg        | Ser        | Asn        | Asn       | Arg        |
| Ile<br>385 | Thr        | Lys        | Ile        | Thr<br>390 | Arg        | Pro        | Gln        | Gln        | Ala<br>395 | Asp        | Xaa        | Arg        | Ser        | Arg       | Met<br>400 |
| Trp        | Ser        | Ser        | Asn<br>405 | Arg        | Ser        | Ser        | Asn        | Arg        | Gln<br>410 | Asp        | Thr        | Lys        | Gln        | Leu       | Tyr<br>415 |

| Table 1. Demographic characteristics of the study population |      |
|--------------------------------------------------------------|------|
| <b>Age (years)</b>                                           |      |
| 18-24                                                        | 10.0 |
| 25-34                                                        | 15.0 |
| 35-44                                                        | 15.0 |
| 45-54                                                        | 15.0 |
| 55-64                                                        | 15.0 |
| 65-74                                                        | 15.0 |
| 75-84                                                        | 15.0 |
| 85-94                                                        | 15.0 |
| 95-104                                                       | 15.0 |
| 105-114                                                      | 15.0 |
| 115-124                                                      | 15.0 |
| 125-134                                                      | 15.0 |
| 135-144                                                      | 15.0 |
| 145-154                                                      | 15.0 |
| 155-164                                                      | 15.0 |
| 165-174                                                      | 15.0 |
| 175-184                                                      | 15.0 |
| 185-194                                                      | 15.0 |
| 195-204                                                      | 15.0 |
| 205-214                                                      | 15.0 |
| 215-224                                                      | 15.0 |
| 225-234                                                      | 15.0 |
| 235-244                                                      | 15.0 |
| 245-254                                                      | 15.0 |
| 255-264                                                      | 15.0 |
| 265-274                                                      | 15.0 |
| 275-284                                                      | 15.0 |
| 285-294                                                      | 15.0 |
| 295-304                                                      | 15.0 |
| 305-314                                                      | 15.0 |
| 315-324                                                      | 15.0 |
| 325-334                                                      | 15.0 |
| 335-344                                                      | 15.0 |
| 345-354                                                      | 15.0 |
| 355-364                                                      | 15.0 |
| 365-374                                                      | 15.0 |
| 375-384                                                      | 15.0 |
| 385-394                                                      | 15.0 |
| 395-404                                                      | 15.0 |
| 405-414                                                      | 15.0 |
| 415-424                                                      | 15.0 |
| 425-434                                                      | 15.0 |
| 435-444                                                      | 15.0 |
| 445-454                                                      | 15.0 |
| 455-464                                                      | 15.0 |
| 465-474                                                      | 15.0 |
| 475-484                                                      | 15.0 |
| 485-494                                                      | 15.0 |
| 495-504                                                      | 15.0 |
| 505-514                                                      | 15.0 |
| 515-524                                                      | 15.0 |
| 525-534                                                      | 15.0 |
| 535-544                                                      | 15.0 |
| 545-554                                                      | 15.0 |
| 555-564                                                      | 15.0 |
| 565-574                                                      | 15.0 |
| 575-584                                                      | 15.0 |
| 585-594                                                      | 15.0 |
| 595-604                                                      | 15.0 |
| 605-614                                                      | 15.0 |
| 615-624                                                      | 15.0 |
| 625-634                                                      | 15.0 |
| 635-644                                                      | 15.0 |
| 645-654                                                      | 15.0 |
| 655-664                                                      | 15.0 |
| 665-674                                                      | 15.0 |
| 675-684                                                      | 15.0 |
| 685-694                                                      | 15.0 |
| 695-704                                                      | 15.0 |
| 705-714                                                      | 15.0 |
| 715-724                                                      | 15.0 |
| 725-734                                                      | 15.0 |
| 735-744                                                      | 15.0 |
| 745-754                                                      | 15.0 |
| 755-764                                                      | 15.0 |
| 765-774                                                      | 15.0 |
| 775-784                                                      | 15.0 |
| 785-794                                                      | 15.0 |
| 795-804                                                      | 15.0 |
| 805-814                                                      | 15.0 |
| 815-824                                                      | 15.0 |
| 825-834                                                      | 15.0 |
| 835-844                                                      | 15.0 |
| 845-854                                                      | 15.0 |
| 855-864                                                      | 15.0 |
| 865-874                                                      | 15.0 |
| 875-884                                                      | 15.0 |
| 885-894                                                      | 15.0 |
| 895-904                                                      | 15.0 |
| 905-914                                                      | 15.0 |
| 915-924                                                      | 15.0 |
| 925-934                                                      | 15.0 |
| 935-944                                                      | 15.0 |
| 945-954                                                      | 15.0 |
| 955-964                                                      | 15.0 |
| 965-974                                                      | 15.0 |
| 975-984                                                      | 15.0 |
| 985-994                                                      | 15.0 |
| 995-1004                                                     | 15.0 |
| 1005-1014                                                    | 15.0 |
| 1015-1024                                                    | 15.0 |
| 1025-1034                                                    | 15.0 |
| 1035-1044                                                    | 15.0 |
| 1045-1054                                                    | 15.0 |
| 1055-1064                                                    | 15.0 |
| 1065-1074                                                    | 15.0 |
| 1075-1084                                                    | 15.0 |
| 1085-1094                                                    | 15.0 |
| 1095-1104                                                    | 15.0 |
| 1105-1114                                                    | 15.0 |
| 1115-1124                                                    | 15.0 |
| 1125-1134                                                    | 15.0 |
| 1135-1144                                                    | 15.0 |
| 1145-1154                                                    | 15.0 |
| 1155-1164                                                    | 15.0 |
| 1165-1174                                                    | 15.0 |
| 1175-1184                                                    | 15.0 |
| 1185-1194                                                    | 15.0 |
| 1195-1204                                                    | 15.0 |
| 1205-1214                                                    | 15.0 |
| 1215-1224                                                    | 15.0 |
| 1225-1234                                                    | 15.0 |
| 1235-1244                                                    | 15.0 |
| 1245-1254                                                    | 15.0 |
| 1255-1264                                                    | 15.0 |
| 1265-1274                                                    | 15.0 |
| 1275-1284                                                    | 15.0 |
| 1285-1294                                                    | 15.0 |
| 1295-1304                                                    | 15.0 |
| 1305-1314                                                    | 15.0 |
| 1315-1324                                                    | 15.0 |
| 1325-1334                                                    | 15.0 |
| 1335-1344                                                    |      |

Ser Thr Ala Gln Ser Val Ala Arg His Trp Val Trp Ser Lys Trp Cys  
420 425 430  
Pro Ser Leu Phe Glu Trp Leu Thr Ser Ala Ile Lys Leu Ser Leu Asp  
435 440 445  
Asn Arg Phe Asn Asn Arg Pro Ile His Ser Arg Asp Arg Asn Pro Gln  
450 455 460  
Ala Lys Leu Ala Gln Thr Asn Ser His  
465 470

(2) INFORMATION FOR SEQ ID NO:774:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 445 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..445

(D) OTHER INFORMATION: / Ceres Seq. ID 1593710

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

Met Thr Phe Ala Asn Ser Gln Pro Ile Val Gln Ser Ser Gln Ser Lys  
1 5 10 15  
Phe His Cys Pro Cys Gly Val Cys Lys Asn Glu Lys His Ile Ile Ser  
20 25 30  
Gly Arg Arg Val Ser Ser His Leu Phe Ser Glu Glu Phe Met Pro Asp  
35 40 45  
Tyr Tyr Val Trp Tyr Lys His Gly Glu Glu Met Asn Ile Asp Ile Gly  
50 55 60  
Thr Ser Ser Met Asp Arg Thr Tyr Phe Ser Ser Asn His Glu Glu Val  
65 70 75 80  
Gly Asn Val Val Glu Asp Pro Tyr Val Asp Met Val Asn Asp Ala Phe  
85 90 95  
Asn Phe Asn Val Gly Tyr Asp Asp Asn Tyr His His Asp Asp Ser Tyr  
100 105 110  
Gln Asn Val Glu Glu Pro Val Tyr Asn His Leu Asn Lys Phe Tyr Asp  
115 120 125  
Leu Leu Glu Gly Ala Asn Asn Pro Ser Tyr Asp Asp Cys Arg Glu Glu  
130 135 140  
Gln Ser Gln Leu Ser Leu Ala Ser Arg Leu Met His Asn Lys Ala Glu  
145 150 155 160  
Tyr Asn Met Ser Glu Lys Leu Val Asp Ser Ile Cys Glu Met Phe Thr  
165 170 175  
Asp Phe Leu Pro Glu Gly Asn Gln Ala Thr Thr Ser His Tyr Gln Ile  
180 185 190  
Glu Lys Leu Met Arg Asn Leu Gly Leu Pro Tyr His Thr Ile Asp Val  
195 200 205  
Cys Gln Asn Asn Cys Met Leu Phe Trp Lys Glu Asp Glu Lys Glu Asp  
210 215 220  
Gln Cys Arg Phe Cys Gly Ala Gln Arg Trp Lys Pro Glu Asp Asp Arg  
225 230 235 240  
Arg Arg Thr Lys Val Pro Tyr Ser Arg Met Trp Tyr Leu Pro Ile Gly  
245 250 255  
Asp Arg Leu Lys Arg Met Tyr Gln Ser His Lys Thr Ala Ala Val Met  
260 265 270  
Arg Trp His Val Glu His Gln Ser Lys Glu Gly Glu Met Asn Asn Pro  
275 280 285  
Leu Asp Ala Val Glu Trp Arg Tyr Phe Gln Glu Leu His Pro Arg Phe  
290 295 300  
Ala Glu Glu Pro Arg Asn Val Tyr Leu Gly Leu Cys Thr Asp Gly Phe  
305 310 315 320  
Asn Pro Phe Gly Met Ser Arg Asn His Ser Leu Trp Pro Val Ile Leu

09669930 1030

325 330 335  
Asn Pro Tyr Asn Leu Pro Pro Val Leu Ser Glu His Ala Glu Asn Arg  
340 345 350  
Ser Asn Asn Arg Ile Thr Lys Ile Thr Arg Pro Gln Gln Ala Asp Xaa  
355 360 365  
Arg Ser Arg Met Trp Ser Ser Asn Arg Ser Ser Asn Arg Gln Asp Thr  
370 375 380  
Lys Gln Leu Tyr Ser Thr Ala Gln Ser Val Ala Arg His Trp Val Trp  
385 390 395 400  
Ser Lys Trp Cys Pro Ser Leu Phe Glu Trp Leu Thr Ser Ala Ile Lys  
405 410 415  
Leu Ser Leu Asp Asn Arg Phe Asn Asn Arg Pro Ile His Ser Arg Asp  
420 425 430  
Arg Asn Pro Gln Ala Lys Leu Ala Gln Thr Asn Ser His  
435 440 445

(2) INFORMATION FOR SEQ ID NO:775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..753
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

|             |            |             |             |            |            |     |
|-------------|------------|-------------|-------------|------------|------------|-----|
| gacttatata  | tggttgattc | aattgtatcg  | ttcgggtgttg | aaaagctttg | gaaactcctg | 60  |
| agccaagaat  | atgagcgatt | ccagggagtt  | gaagagcaaa  | ttactgagct | aagagatgat | 120 |
| ctgaagatgt  | taatggcctt | tctatctgat  | gcagatgcaa  | agaaacaaac | cgtgcccctt | 180 |
| gcaagaaatt  | gctcgaaga  | gataaaggaa  | atcacttatg  | atgctgagga | tataatcgaa | 240 |
| acctttcttc  | taaaaggcag | tggcaacaag  | agtcacatga  | gaagccttgc | ttgctttcca | 300 |
| agtggtcgta  | gggagattgc | cttgcaaadc  | acaagcatca  | gtaagaggat | ctccaagggt | 360 |
| atccaactta  | tgcagacttt | aggcataaaa  | tcagacatta  | tggacggtgt | ggatttgcaa | 420 |
| gctcaactgg  | aaaggagaag | ggagtcgcgt  | catacatttt  | ctagtgaatc | tgagagcaat | 480 |
| cttggttggtt | tggagaaaaa | tggttgagaaa | ttggttgaag  | aattggtggg | aaacgatagc | 540 |
| agtcattggg  | tatctattac | tggtttgggt  | ggtcttggca  | aaaccaccct | tgcacggcaa | 600 |
| gtttttgatc  | atgataagat | aaaaactcat  | tttgatggac  | ttgcgtgggt | gtgtgtatca | 660 |
| caagagttaa  | cacggaagga | tgtgtggcag  | accattttgg  | ggcatcctag | tcctgcagat | 720 |
| aaagattcaa  | aattgccgga | agacgatatt  | cag         |            |            |     |

(2) INFORMATION FOR SEQ ID NO:776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..251
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593712

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

Asp Leu Tyr Met Val Asp Ser Ile Val Ser Phe Gly Val Glu Lys Leu  
1 5 10 15  
Trp Lys Leu Leu Ser Gln Glu Tyr Glu Arg Phe Gln Gly Val Glu Glu  
20 25 30  
Gln Ile Thr Glu Leu Arg Asp Asp Leu Lys Met Leu Met Ala Phe Leu  
35 40 45  
Ser Asp Ala Asp Ala Lys Lys Gln Thr Arg Ala Leu Ala Arg Asn Cys  
50 55 60  
Leu Glu Glu Ile Lys Glu Ile Thr Tyr Asp Ala Glu Asp Ile Ile Glu

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Phe | Leu | Leu | Lys | Gly | Ser | Gly | Asn | Lys | Ser | His | Met | Arg | Ser | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Cys | Phe | Pro | Ser | Gly | Arg | Arg | Glu | Ile | Ala | Leu | Gln | Ile | Thr | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Ser | Lys | Arg | Ile | Ser | Lys | Val | Ile | Gln | Leu | Met | Gln | Thr | Leu | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Lys | Ser | Asp | Ile | Met | Asp | Gly | Val | Asp | Leu | Gln | Ala | Gln | Leu | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Arg | Arg | Glu | Ser | Arg | His | Thr | Phe | Ser | Ser | Glu | Ser | Glu | Ser | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Val | Gly | Leu | Glu | Lys | Asn | Val | Glu | Lys | Leu | Val | Glu | Glu | Leu | Val |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Asn | Asp | Ser | Ser | His | Gly | Val | Ser | Ile | Thr | Gly | Leu | Gly | Gly | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Lys | Thr | Thr | Leu | Ala | Arg | Gln | Val | Phe | Asp | His | Asp | Lys | Ile | Lys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | His | Phe | Asp | Gly | Leu | Ala | Trp | Val | Cys | Val | Ser | Gln | Glu | Phe | Thr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Arg | Lys | Asp | Val | Trp | Gln | Thr | Ile | Leu | Gly | His | Leu | Ser | Pro | Ala | Asp |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Lys | Asp | Ser | Lys | Leu | Pro | Glu | Asp | Asp | Ile | Gln |     |     |     |     |     |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:777:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..248

(D) OTHER INFORMATION: / Ceres Seq. ID 1593713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Asp | Ser | Ile | Val | Ser | Phe | Gly | Val | Glu | Lys | Leu | Trp | Lys | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Ser | Gln | Glu | Tyr | Glu | Arg | Phe | Gln | Gly | Val | Glu | Glu | Gln | Ile | Thr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Leu | Arg | Asp | Asp | Leu | Lys | Met | Leu | Met | Ala | Phe | Leu | Ser | Asp | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ala | Lys | Lys | Gln | Thr | Arg | Ala | Leu | Ala | Arg | Asn | Cys | Leu | Glu | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ile | Lys | Glu | Ile | Thr | Tyr | Asp | Ala | Glu | Asp | Ile | Ile | Glu | Thr | Phe | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Lys | Gly | Ser | Gly | Asn | Lys | Ser | His | Met | Arg | Ser | Leu | Ala | Cys | Phe |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Ser | Gly | Arg | Arg | Glu | Ile | Ala | Leu | Gln | Ile | Thr | Ser | Ile | Ser | Lys |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Ile | Ser | Lys | Val | Ile | Gln | Leu | Met | Gln | Thr | Leu | Gly | Ile | Lys | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Ile | Met | Asp | Gly | Val | Asp | Leu | Gln | Ala | Gln | Leu | Glu | Arg | Arg | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Ser | Arg | His | Thr | Phe | Ser | Ser | Glu | Ser | Glu | Ser | Asn | Leu | Val | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Glu | Lys | Asn | Val | Glu | Lys | Leu | Val | Glu | Glu | Leu | Val | Gly | Asn | Asp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ser | Ser | His | Gly | Val | Ser | Ile | Thr | Gly | Leu | Gly | Gly | Leu | Gly | Lys | Thr |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Leu | Ala | Arg | Gln | Val | Phe | Asp | His | Asp | Lys | Ile | Lys | Thr | His | Phe |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |

09669900 10300



Asp Lys Pro His Asp Asp Ala Pro Val  
50 55

(i) SEQUENCE CHARACTERISTICS:

- (1) **LENGTH** 266 1

- (A) LENGTH: 366 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..366

- (D) OTHER INFORMATION: / Ceres Seq. ID 1593769

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gaagagaagt | tgggaagacc | ggtccatctt | ggtgaggtgt | tcatccaaac | acacactaag | 60  |
| tcggatggct | catttattga | tcagaaggcg | gagaagattg | ctcaagctta | tgagcagaat | 120 |
| gtgagagata | ggctgtcagc | actagaggcg | gctgcttctg | ctgtctttga | tggtctttca | 180 |
| cgacctccgg | agctcacact | agatgattat | atagccatct | ttctcgagtc | cacagaaagg | 240 |
| gattcaagag | gcaatcctta | tggactttga | tgtctaaaag | acactctagg | cagtgccaac | 300 |
| cgccaacact | ccggttcttc | atcatccttt | caagccctag | aaaaatggct | gcaggaagct | 360 |
| caaaagc    |            |            |            |            |            |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino ac

- (A) LENGTH: 122 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..122

- (D) OTHER INFORMATION: / Ceres Seq. ID 1593770

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Glu | Lys | Leu | Gly | Arg | Pro | Val | His | Leu | Gly | Glu | Val | Phe | Ile | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | His | Thr | Lys | Ser | Asp | Gly | Ser | Phe | Ile | Asp | Gln | Lys | Ala | Glu | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ala | Gln | Ala | Tyr | Glu | Gln | Asn | Val | Arg | Asp | Arg | Leu | Ser | Ala | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Ala | Ala | Ala | Ser | Ala | Val | Phe | Asp | Gly | Ser | Ser | Arg | Pro | Pro | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Thr | Leu | Asp | Asp | Tyr | Ile | Ala | Ile | Phe | Leu | Glu | Ser | Thr | Glu | Arg |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Ser | Arg | Gly | Asn | Pro | Tyr | Gly | Leu | Val | Cys | Leu | Lys | Asp | Thr | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Ser | Ala | Asn | Arg | Gln | His | Ser | Gly | Ser | Ser | Ser | Ser | Phe | Gln | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Glu | Lys | Trp | Leu | Gln | Glu | Ala | Gln | Arg |     |     |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..748

- (D) OTHER INFORMATION: / Ceres Seq. ID 1593773

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atacgcctct | togtcgtggt | gtcttgacga | attggcggag | attatgaagt | gcaaggaaga | 60  |
| ttttggtcaa | acagtgatgg | ccattttcta | cgaagtggat | ccaactgatg | tagagaagca | 120 |

| Table 1. Demographic characteristics of the study population |             |
|--------------------------------------------------------------|-------------|
| Age (years)                                                  | 65.0 ± 10.0 |
| Gender                                                       |             |
| Male                                                         | 50 (50.0%)  |
| Female                                                       | 50 (50.0%)  |
| Education (years)                                            | 12.0 ± 2.0  |
| Marital status                                               |             |
| Married                                                      | 40 (80.0%)  |
| Single                                                       | 10 (20.0%)  |
| Occupation                                                   |             |
| Retired                                                      | 30 (60.0%)  |
| Unemployed                                                   | 20 (40.0%)  |
| Income (USD/month)                                           | 1,000 ± 200 |
| Health status                                                |             |
| Good                                                         | 30 (60.0%)  |
| Poor                                                         | 20 (40.0%)  |
| Comorbidities                                                |             |
| Hypertension                                                 | 15 (30.0%)  |
| Diabetes                                                     | 10 (20.0%)  |
| Cholesterol                                                  | 12 (24.0%)  |
| Smoking status                                               |             |
| Smoker                                                       | 10 (20.0%)  |
| Non-smoker                                                   | 40 (80.0%)  |
| Alcohol consumption                                          |             |
| Regular                                                      | 5 (10.0%)   |
| Occasional                                                   | 15 (30.0%)  |
| Never                                                        | 30 (60.0%)  |

gaccggaggt tttggggaag tcttcacaga aacttgtaaa ggtaaaacag ctgaggacat 180  
tgagaaatgg agtcaagctc ttgcaaaagt ggcaactgtc attagttacc tttcaagcag 240  
ctgggatact gaaacagaaa tgatcgaaga aattgccact gatgtttcga atatgttgac 300  
taagtcaacg caatcaaggg atttcgtcgg ctttaattgga atgggatctc atatggagaa 360  
gatgaaaccg ttgctatgcc tagagtcaga ggaagtgagg atatttgctg caggagatat 420  
ttgtcaagta ctgagtgatg atacagcagg tagcagcact gttataggaa tagatctcac 480  
attacctgag aaggccgacg aggacgaaga attttatata agtgaaagag catttgaaaa 540  
tatgactaac ctccaattct taaaaattag tgggtgattgc agtagattgt actttccgcc 600  
acgtctgaac tccatatctc gaaaacttat attactatct tggggtcagt ttccgatgac 660  
acttttgctt tctaatttta atccacagtc cctggtcaat ctaaccatga ggagaagcaa 720  
gcttgagaag ttgtgggacg gaaataaa

(2) INFORMATION FOR SEQ ID NO:786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..249

(D) OTHER INFORMATION: / Ceres Seq. ID 1593774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

Tyr Ala Ser Ser Ser Trp Cys Leu Asp Glu Leu Ala Glu Ile Met Lys  
1 5 10 15  
Cys Lys Glu Asp Phe Gly Gln Thr Val Met Ala Ile Phe Tyr Glu Val  
20 25 30  
Asp Pro Thr Asp Val Glu Lys Gln Thr Gly Gly Phe Gly Glu Val Phe  
35 40 45  
Thr Glu Thr Cys Lys Gly Lys Thr Ala Glu Asp Ile Glu Lys Trp Ser  
50 55 60  
Gln Ala Leu Ala Lys Val Ala Thr Val Ile Ser Tyr Leu Ser Ser Ser  
65 70 75 80  
Trp Asp Thr Glu Thr Glu Met Ile Glu Glu Ile Ala Thr Asp Val Ser  
85 90 95  
Asn Met Leu Thr Lys Ser Thr Gln Ser Arg Asp Phe Val Gly Leu Ile  
100 105 110  
Gly Met Gly Ser His Met Glu Lys Met Lys Pro Leu Leu Cys Leu Glu  
115 120 125  
Ser Glu Glu Val Arg Ile Phe Ala Ala Gly Asp Ile Cys Gln Val Leu  
130 135 140  
Ser Asp Asp Thr Ala Gly Ser Ser Thr Val Ile Gly Ile Asp Leu Thr  
145 150 155 160  
Leu Pro Glu Lys Ala Asp Glu Asp Glu Glu Phe Tyr Ile Ser Glu Arg  
165 170 175  
Ala Phe Glu Asn Met Thr Asn Leu Gln Phe Leu Lys Ile Ser Gly Asp  
180 185 190  
Cys Ser Arg Leu Tyr Phe Pro Pro Arg Leu Asn Ser Ile Ser Arg Lys  
195 200 205  
Leu Ile Leu Leu Ser Trp Gly Gln Phe Pro Met Thr Leu Leu Pro Ser  
210 215 220  
Asn Phe Asn Pro Gln Ser Leu Val Asn Leu Thr Met Arg Arg Ser Lys  
225 230 235 240  
Leu Glu Lys Leu Trp Asp Gly Asn Lys  
245

(2) INFORMATION FOR SEQ ID NO:787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

00559900 101300



- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..235  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1593775  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

Met Lys Cys Lys Glu Asp Phe Gly Gln Thr Val Met Ala Ile Phe Tyr  
1                  5                  10                  15  
Glu Val Asp Pro Thr Asp Val Glu Lys Gln Thr Gly Gly Phe Gly Glu  
                  20                  25                  30  
Val Phe Thr Glu Thr Cys Lys Gly Lys Thr Ala Glu Asp Ile Glu Lys  
                  35                  40                  45  
Trp Ser Gln Ala Leu Ala Lys Val Ala Thr Val Ile Ser Tyr Leu Ser  
50                  55                  60  
Ser Ser Trp Asp Thr Glu Thr Glu Met Ile Glu Glu Ile Ala Thr Asp  
65                  70                  75                  80  
Val Ser Asn Met Leu Thr Lys Ser Thr Gln Ser Arg Asp Phe Val Gly  
                  85                  90                  95  
Leu Ile Gly Met Gly Ser His Met Glu Lys Met Lys Pro Leu Leu Cys  
                  100                 105                 110  
Leu Glu Ser Glu Glu Val Arg Ile Phe Ala Ala Gly Asp Ile Cys Gln  
                 115                 120                 125  
Val Leu Ser Asp Asp Thr Ala Gly Ser Ser Thr Val Ile Gly Ile Asp  
130                 135                 140  
Leu Thr Leu Pro Glu Lys Ala Asp Glu Asp Glu Glu Phe Tyr Ile Ser  
145                 150                 155                 160  
Glu Arg Ala Phe Glu Asn Met Thr Asn Leu Gln Phe Leu Lys Ile Ser  
                 165                 170                 175  
Gly Asp Cys Ser Arg Leu Tyr Phe Pro Pro Arg Leu Asn Ser Ile Ser  
                 180                 185                 190  
Arg Lys Leu Ile Leu Leu Ser Trp Gly Gln Phe Pro Met Thr Leu Leu  
                 195                 200                 205  
Pro Ser Asn Phe Asn Pro Gln Ser Leu Val Asn Leu Thr Met Arg Arg  
210                 215                 220  
Ser Lys Leu Glu Lys Leu Trp Asp Gly Asn Lys  
225                 230                 235

(2) INFORMATION FOR SEQ ID NO:788:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 224 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..224  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1593776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

Met Ala Ile Phe Tyr Glu Val Asp Pro Thr Asp Val Glu Lys Gln Thr  
1                  5                  10                  15  
Gly Gly Phe Gly Glu Val Phe Thr Glu Thr Cys Lys Gly Lys Thr Ala  
                  20                  25                  30  
Glu Asp Ile Glu Lys Trp Ser Gln Ala Leu Ala Lys Val Ala Thr Val  
                  35                  40                  45  
Ile Ser Tyr Leu Ser Ser Ser Trp Asp Thr Glu Thr Glu Met Ile Glu  
50                  55                  60  
Glu Ile Ala Thr Asp Val Ser Asn Met Leu Thr Lys Ser Thr Gln Ser  
65                  70                  75                  80  
Arg Asp Phe Val Gly Leu Ile Gly Met Gly Ser His Met Glu Lys Met  
                  85                  90                  95  
Lys Pro Leu Leu Cys Leu Glu Ser Glu Glu Val Arg Ile Phe Ala Ala

DOCKET# 08663660

[illegible]

(i) SEOUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

- (B) LOCATION: 1..795

- (D) OTHER INFORMATION: / Ceres Seq. ID 1593781

|             |             |             |            |            |             |     |
|-------------|-------------|-------------|------------|------------|-------------|-----|
| tcaaccacac  | caccaaaagaa | acattacgta  | tacaagtctc | ctctctctcc | ggttaagcac  | 60  |
| tactctcccc  | ctccggttta  | ccactcacca  | ccaccaccaa | aaaaacatta | cgtttacaag  | 120 |
| tctctctctc  | ctccggtttaa | gcactactct  | ccccctccgg | tttaccattc | cccaccccca  | 180 |
| cctaaaaagc  | attacgtcta  | caaattctcca | ccaccaccgg | tgaagcacta | ctcacctcct  | 240 |
| ccggttttacc | attccccacc  | acccccaaag  | aaacactacg | tgtacaaatc | tctctctcct  | 300 |
| ccggttaagc  | actactctct  | tctctccggt  | taccattccc | caccaccacc | aaagaaacac  | 360 |
| tacgtgtaca  | aatctctctc  | tctctcaggt  | aagcactact | ctctctctcc | ggtttaccat  | 420 |
| tccccacccc  | caccaaagaa  | acactacgtg  | tacaaatctc | caccaccacc | ggatgaagcac | 480 |
| tactctcccc  | ctccagttta  | ccattcccca  | ccaccaccaa | agaaacatta | cgtatacaag  | 540 |
| tccccctctc  | ctccggtttaa | gcactactct  | ccccctccag | tctactattc | cccaccacca  | 600 |
| ccaaagaaac  | attacgtata  | caagtccctt  | ctctctccgg | ttaagcacta | ctctctctct  | 660 |
| ccggttttacc | actctccacc  | ancaccaaaa  | gaaaagtacg | tgtacaaatc | acctctctct  | 720 |
| cctccagtag  | accactactc  | tccaccacac  | catccttacc | tctacaaatc | tctctctctt  | 780 |
| cctccactact | attag       |             |            |            |             |     |

(i) SEOUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

- (B) LOCATION: 1..264

- (D) OTHER INFORMATION: / Ceres Seq. ID 1593782

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Pro | Pro | Pro | 5   | Lys | Lys | His | Tyr | Val | Tyr | Lys | Ser | Pro | Pro | Pro |
| 1   |     |     |     | 10  |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Val | Lys | His | Tyr | Ser | Pro | Pro | Pro | Val | Tyr | His | Ser | Pro | Pro | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Lys | Lys | His | Tyr | Val | Tyr | Lys | Ser | Pro | Pro | Pro | Pro | Val | Lys | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

Tyr Ser Pro Pro Pro Val Tyr His Ser Pro Pro Pro Pro Lys Lys His  
50 55 60  
Tyr Val Tyr Lys Ser Pro Pro Pro Val Lys His Tyr Ser Pro Pro  
65 70 75 80  
Pro Val Tyr His Ser Pro Pro Pro Pro Lys Lys His Tyr Val Tyr Lys  
85 90 95  
Ser Pro Pro Pro Pro Val Lys His Tyr Ser Pro Pro Pro Val Tyr His  
100 105 110  
Ser Pro Pro Pro Pro Lys Lys His Tyr Val Tyr Lys Ser Pro Pro Pro  
115 120 125  
Pro Val Lys His Tyr Ser Pro Pro Pro Val Tyr His Ser Pro Pro Pro  
130 135 140  
Pro Lys Lys His Tyr Val Tyr Lys Ser Pro Pro Pro Val Lys His  
145 150 155 160  
Tyr Ser Pro Pro Pro Val Tyr His Ser Pro Pro Pro Pro Lys Lys His  
165 170 175  
Tyr Val Tyr Lys Ser Pro Pro Pro Pro Val Lys His Tyr Ser Pro Pro  
180 185 190  
Pro Val Tyr Tyr Ser Pro Pro Pro Pro Lys Lys His Tyr Val Tyr Lys  
195 200 205  
Ser Pro Pro Pro Pro Val Lys His Tyr Ser Pro Pro Pro Val Tyr His  
210 215 220  
Ser Pro Pro Xaa Pro Lys Glu Lys Tyr Val Tyr Lys Ser Pro Pro Pro  
225 230 235 240  
Pro Pro Val His His Tyr Ser Pro Pro His His Pro Tyr Leu Tyr Lys  
245 250 255  
Ser Pro Pro Pro Pro Tyr His Tyr  
260

(2) INFORMATION FOR SEQ ID NO:791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 701 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..701
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| tcgttgaata tctcggagct attggtagac gttcccgaat cagccacggt tggctcactg  | 60  |
| aaactagcgg tattggaggc ggtaacgaga ttctcaagga tggattaaac attggagtgc  | 120 |
| tctttcaagg taaaaccatc gttgatgact ccaaaacgct tcttcagatt gggatcccat  | 180 |
| acgatgatga cgatgacgaa aacctcgggt ctttgggatt catgctagaa ccgcaaaaaat | 240 |
| cagaaacaac aacaataaca acgttaacca ctgtttcccc gagaacacga cttagacaaa  | 300 |
| atcaggtcct agggtcctg gatagcactg aggcagtagc agctaaatcc gtggttccag   | 360 |
| tacgtatgaa accggcctg cagccagaga tggttcaacg gagaataaga cggccattca   | 420 |
| ctgtctcaga agtagaagct ttggttcagg ccgtagagag gctcggcacc ggaagggtggc | 480 |
| gcgacgtgaa gtctcatgca ttttaaccatg taaatcatcg tacctacgtt gacctcaaga | 540 |
| acagaaatga tctagttttc aaaggagag aattcacagc cccgcaagt atccttaagg    | 600 |
| caacagagga catggatgca tggataatc gtaaggaacc acaaccccaa gtgacaagct   | 660 |
| ctacacgtga tcggtgtgta aaatggcnac ccccttctca c                      |     |

(2) INFORMATION FOR SEQ ID NO:792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

DOCKET# 08668860

(B) LOCATION: 1..233

(D) OTHER INFORMATION: / Ceres Seq. ID 1593810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

Val Glu Tyr Leu Gly Ala Ile Gly Arg Arg Ser Arg Ile Ser His Gly  
1 5 10 15  
Trp Leu Thr Glu Thr Ser Gly Ile Gly Gly Gly Asn Glu Ile Leu Lys  
20 25 30  
Asp Gly Leu Asn Ile Gly Val Leu Phe Gln Gly Lys Thr Ile Val Asp  
35 40 45  
Asp Ser Lys Thr Leu Leu Gln Ile Gly Ile Pro Tyr Asp Asp Asp Asp  
50 55 60  
Asp Glu Asn Leu Gly Ser Leu Gly Phe Met Leu Glu Pro Gln Lys Ser  
65 70 75 80  
Glu Thr Thr Thr Ile Thr Thr Leu Thr Thr Val Ser Pro Arg Thr Arg  
85 90 95  
Leu Arg Gln Asn Gln Val Leu Gly Ser Val Asp Ser Thr Glu Ala Val  
100 105 110  
Ala Ala Lys Ser Val Val Pro Val Arg Met Lys Pro Ala Trp Gln Pro  
115 120 125  
Glu Met Val Gln Arg Arg Ile Arg Arg Pro Phe Thr Val Ser Glu Val  
130 135 140  
Glu Ala Leu Val Gln Ala Val Glu Arg Leu Gly Thr Gly Arg Trp Arg  
145 150 155 160  
Asp Val Lys Ser His Ala Phe Asn His Val Asn His Arg Thr Tyr Val  
165 170 175  
Asp Leu Lys Asn Arg Asn Asp Leu Val Phe Lys Gly Arg Glu Phe Thr  
180 185 190  
Ala Pro Gln Val Ile Leu Lys Ala Thr Glu Asp Met Asp Ala Trp Asn  
195 200 205  
Asn Arg Lys Glu Pro Gln Pro Gln Val Thr Ser Ser Thr Arg Asp Arg  
210 215 220  
Cys Val Lys Trp Xaa Pro Pro Ser His  
225 230

(2) INFORMATION FOR SEQ ID NO:793:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1593811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

Met Leu Glu Pro Gln Lys Ser Glu Thr Thr Thr Ile Thr Thr Leu Thr  
1 5 10 15  
Thr Val Ser Pro Arg Thr Arg Leu Arg Gln Asn Gln Val Leu Gly Ser  
20 25 30  
Val Asp Ser Thr Glu Ala Val Ala Ala Lys Ser Val Val Pro Val Arg  
35 40 45  
Met Lys Pro Ala Trp Gln Pro Glu Met Val Gln Arg Arg Ile Arg Arg  
50 55 60  
Pro Phe Thr Val Ser Glu Val Glu Ala Leu Val Gln Ala Val Glu Arg  
65 70 75 80  
Leu Gly Thr Gly Arg Trp Arg Asp Val Lys Ser His Ala Phe Asn His  
85 90 95  
Val Asn His Arg Thr Tyr Val Asp Leu Lys Asn Arg Asn Asp Leu Val  
100 105 110  
Phe Lys Gly Arg Glu Phe Thr Ala Pro Gln Val Ile Leu Lys Ala Thr  
115 120 125

00669980-101300

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Asp | Met | Asp | Ala | Trp | Asn | Asn | Arg | Lys | Glu | Pro | Gln | Pro | Gln | Val |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Ser | Ser | Thr | Arg | Asp | Arg | Cys | Val | Lys | Trp | Xaa | Pro | Pro | Ser | His |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

(2) INFORMATION FOR SEQ ID NO:794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..675
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

|             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| gcttcaggat  | tggtctatct | ccatgaggaa | tgggancaa  | ttgtgattca  | ccgtgacgtg | 60  |
| aaagctagca  | atgttctgtt | agatgctgat | ttcaatggta | gactcgggtga | ttttgggttg | 120 |
| gctcggttgt  | atgatcacgg | ctcggatcct | cagaccactc | acgttggttg  | aacattgggt | 180 |
| tacttagcac  | ctgaacattc | ccggactgga | cgtgccacta | ccgcgactga  | tgtctatgcg | 240 |
| tttggtgcgt  | ttcttttaga | agttgtttcc | ggtagacgac | ccatcgagtt  | ccatagtgca | 300 |
| agcgatgata  | cgttcttgct | tgtggaatgg | gttttcagtt | tgtggctcag  | aggtaacata | 360 |
| atggaagcga  | aagatccgaa | gctcggttct | tcaggttatg | atcttgaaga  | ggttgaaatg | 420 |
| gtattgaaac  | tccgtctgtt | gtgttcgcat | tcagaccctc | gggctagacc  | aagtatgagg | 480 |
| caggctcttac | aatatctaag | aggagacatg | gcactgcctg | aattaacgcc  | cttggatttg | 540 |
| tccggcgggga | gcgtgatgaa | tctgggaggc | cgggacggct | ttagcgggat  | tgcaatgact | 600 |
| gattttttcca | ctgtgtttta | agggtttacc | ggaggatctt | ccattgctga  | ctctctactc | 660 |
| tccgggtggga | ggtga      |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..224
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ser | Gly | Leu | Phe | Tyr | Leu | His | Glu | Glu | Trp | Xaa | Gln | Val | Val | Ile |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| His | Arg | Asp | Val | Lys | Ala | Ser | Asn | Val | Leu | Leu | Asp | Ala | Asp | Phe | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Arg | Leu | Gly | Asp | Phe | Gly | Leu | Ala | Arg | Leu | Tyr | Asp | His | Gly | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Pro | Gln | Thr | Thr | His | Val | Val | Gly | Thr | Leu | Gly | Tyr | Leu | Ala | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | His | Ser | Arg | Thr | Gly | Arg | Ala | Thr | Thr | Ala | Thr | Asp | Val | Tyr | Ala |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Phe | Gly | Ala | Phe | Leu | Glu | Val | Val | Ser | Gly | Arg | Arg | Pro | Ile | Glu |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Phe | His | Ser | Ala | Ser | Asp | Asp | Thr | Phe | Leu | Leu | Val | Glu | Trp | Val | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Leu | Trp | Leu | Arg | Gly | Asn | Ile | Met | Glu | Ala | Lys | Asp | Pro | Lys | Leu |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Ser | Ser | Gly | Tyr | Asp | Leu | Glu | Glu | Val | Glu | Met | Val | Leu | Lys | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Leu | Leu | Cys | Ser | His | Ser | Asp | Pro | Arg | Ala | Arg | Pro | Ser | Met | Arg |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 |     | 150 |     | 155 |     | 160 |     |     |     |     |     |     |     |     |     |
| Gln | Val | Leu | Gln | Tyr | Leu | Arg | Gly | Asp | Met | Ala | Leu | Pro | Glu | Leu | Thr |
|     |     | 165 |     |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Pro | Leu | Asp | Leu | Ser | Ala | Gly | Ser | Val | Met | Asn | Leu | Gly | Gly | Arg | Asp |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Phe | Ser | Gly | Ile | Ala | Met | Thr | Asp | Phe | Ser | Thr | Val | Phe | Lys | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Phe | Thr | Gly | Gly | Ser | Ser | Ile | Ala | Asp | Ser | Leu | Leu | Ser | Gly | Gly | Arg |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..739

(D) OTHER INFORMATION: / Ceres Seq. ID 1593817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

|            |             |             |             |            |            |     |
|------------|-------------|-------------|-------------|------------|------------|-----|
| tgatcttgag | tgggtcaggc  | tgggtgctgac | ggctgatcca  | ggtcttagaa | tggaaagtat | 60  |
| tactgatccg | aaaaccccac  | gtcgaaagga  | acatcgctcg  | gtttcaagta | tagttgccta | 120 |
| cgaggaagta | agggctgctg  | cagcgaaggg  | agaggcacct  | ccaggtcttc | ctctcaaagg | 180 |
| ggctggtcag | gattcatcag  | atgcacaacc  | aatggccaat  | ggtggcatgc | tgaaagcagg | 240 |
| tgatgcctta | tctgggtgaat | tttgggaggg  | gaagcgacta  | agaattcgta | aagattcaat | 300 |
| atatggcaac | ctaccagggt  | gggacttgcg  | ctctatcatt  | gtgaagagcg | gtgatgactg | 360 |
| tcggcaggaa | catcttgccg  | ttcaacttat  | atctcatttt  | tttgatatat | tccaggaagc | 420 |
| agggcttccc | ctctggttac  | gtccttatga  | agtcttggtg  | acatcttcat | acactgccct | 480 |
| tatagaaaca | attccagata  | cggcttctat  | tcattctatt  | aaaagtagat | accctaacat | 540 |
| cacaagcctg | cgtgattttt  | ttgatgccaa  | gtttaaagag  | aactctccaa | gttttaagct | 600 |
| tgctcaggta | cattttatgg  | ttttatggct  | caagtccaca  | agcaagttgg | ctgttttctt | 660 |
| tcagaaactt | tctgttaaac  | atgatgttgt  | tctaattgaga | gctgtggaat | atatgttaaa | 720 |
| ttttctctcc | caaaaattc   |             |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..246

(D) OTHER INFORMATION: / Ceres Seq. ID 1593818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Leu | Glu | Trp | Val | Arg | Leu | Val | Leu | Thr | Ala | Asp | Pro | Gly | Leu | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Glu | Ser | Ile | Thr | Asp | Pro | Lys | Thr | Pro | Arg | Arg | Lys | Glu | His | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Val | Ser | Ser | Ile | Val | Ala | Tyr | Glu | Glu | Val | Arg | Ala | Ala | Ala | Ala |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Lys | Gly | Glu | Ala | Pro | Pro | Gly | Leu | Pro | Leu | Lys | Gly | Ala | Gly | Gln | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ser | Ser | Asp | Ala | Gln | Pro | Met | Ala | Asn | Gly | Gly | Met | Leu | Lys | Ala | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Ala | Leu | Ser | Gly | Glu | Phe | Trp | Glu | Gly | Lys | Arg | Leu | Arg | Ile | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Asp | Ser | Ile | Tyr | Gly | Asn | Leu | Pro | Gly | Trp | Asp | Leu | Arg | Ser | Ile |



(2) INFORMATION FOR SEQ ID NO:799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1593820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

Met Ala Asn Gly Gly Met Leu Lys Ala Gly Asp Ala Leu Ser Gly Glu  
1 5 10 15  
Phe Trp Glu Gly Lys Arg Leu Arg Ile Arg Lys Asp Ser Ile Tyr Gly  
20 25 30  
Asn Leu Pro Gly Trp Asp Leu Arg Ser Ile Ile Val Lys Ser Gly Asp  
35 40 45  
Asp Cys Arg Gln Glu His Leu Ala Val Gln Leu Ile Ser His Phe Phe  
50 55 60  
Asp Ile Phe Gln Glu Ala Gly Leu Pro Leu Trp Leu Arg Pro Tyr Glu  
65 70 75 80  
Val Leu Val Thr Ser Ser Tyr Thr Ala Leu Ile Glu Thr Ile Pro Asp  
85 90 95  
Thr Ala Ser Ile His Ser Ile Lys Ser Arg Tyr Pro Asn Ile Thr Ser  
100 105 110  
Leu Arg Asp Phe Phe Asp Ala Lys Phe Lys Glu Asn Ser Pro Ser Phe  
115 120 125  
Lys Leu Ala Gln Val His Phe Met Val Leu Trp Leu Lys Ser Thr Ser  
130 135 140  
Lys Leu Ala Val Phe Phe Gln Lys Leu Ser Val Lys His Asp Val Val  
145 150 155 160  
Leu Met Arg Ala Val Glu Tyr Met Leu Asn Phe Leu Ser Gln Lys Phe  
165 170 175

(2) INFORMATION FOR SEQ ID NO:800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..813

(D) OTHER INFORMATION: / Ceres Seq. ID 1593869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

atggcgatca tggccgttgc cgctctcttt cagcgccgct tccctcttct cctccgtcgc 60  
agtatcccggt tactgtcggc tcctacttct gttattttaca atcacagaac tcttctatcc 120  
gatggactca gtactcgatt atgctcgatt ctccggttatt catcgctctga cggcgctcaac 180  
ggcgggaagta gcggtggcga ttctcggtaac gataacgatt ccggttagtgt tgtttcggat 240  
gttcagagtc ctaattactt aaaattcacc gatgaagaat tgatgaagca atgtagatta 300  
gagacattta gagtttcagg acctggagga caacaccgga acaagcgtga ctccgccgtg 360  
cgtctgaaac atctccccac cggaatcgta gctcaagccg tcgaagatcg ttcacagcac 420  
aagaaccgtg cttctgctct aaaccgttct cgtacgctcc tcgccattaa agtgagaaac 480  
aaagtggaca ttgaagctta tgctcctcct ccagagcttc ttcagattct acctcctaag 540  
tctaccatta gaacttcttc tggttcacag attgggtccca acaatcctaa atttgtacct 600  
ggaatgcaag ctttgcttga tgttatttct gottctgaag gttctatcgc tgattctgcc 660  
aaattgctgg gtttgagcac tgggtgctta tctcgtttga tactctccca tgatggtctt 720  
cgtatggctg tcaatagcat gagagcagcc aaggtactgt ttgttgatta ccaatccaaa 780

0965930 10100





Arg Ser Ile Pro Leu Leu Ser Ala Pro Thr Ser Val Ile Tyr Asn His  
20 25 30  
Arg Thr Leu Leu Ser Asp Gly Leu Ser Thr Arg Leu Cys Ser Ile Leu  
35 40 45  
Arg Tyr Ser Ser Ser Asp Gly Val Asn Gly Gly Ser Ser Gly Gly Asp  
50 55 60  
Phe Gly Asn Asp Asn Asp Ser Val Ser Val Val Ser Asp Val Gln Ser  
65 70 75 80  
Pro Asn Tyr Leu Lys Phe Thr Asp Glu Glu Leu Met Lys Gln Cys Arg  
85 90 95  
Leu Glu Thr Phe Arg Val Ser Gly Pro Gly Gly Gln His Arg Asn Lys  
100 105 110  
Arg Asp Ser Ala Val Arg Leu Lys His Leu Pro Thr Gly Ile Val Ala  
115 120 125  
Gln Ala Val Glu Asp Arg Ser Gln His Lys Asn Arg Ala Ser Ala Leu  
130 135 140  
Asn Arg Leu Arg Thr Leu Leu Ala Ile Lys Val Arg Asn Lys Val Asp  
145 150 155 160  
Ile Glu Ala Tyr Ala Pro Pro Pro Glu Leu Leu Gln Ile Leu Pro Pro  
165 170 175  
Lys Ser Thr Ile Arg Thr Ser Ser Gly Ser Gln Ile Gly Pro Asn Asn  
180 185 190  
Pro Lys Phe Val Pro Gly Met Gln Ala Leu Leu Asp Val Ile Ser Ala  
195 200 205  
Ser Asp Gly Ser Ile Ala Asp Ser Ala Lys Leu Leu Gly Leu Ser Thr  
210 215 220  
Gly Gly Leu Ser Arg Leu Ile Leu Ser His Asp Gly Leu Arg Met Ala  
225 230 235 240  
Val Asn Ser Met Arg Ala Ala Lys Val Leu Phe Val Asp Tyr Gln Ser  
245 250 255  
Lys Tyr Phe Val Ile Lys Ile Met Pro Ile Arg  
260 265

(2) INFORMATION FOR SEQ ID NO:803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..408
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| atgagtaacg tgggtgtgac agtacgagat cgagagcggc ttattcgtac ggttcattgc   | 60  |
| agacttcctt caccgcoqgt gatggagaga atgaacatga gcgaagagga ggagcaatgc   | 120 |
| aaaagaaacc aagaggcatt caagagattc ttcgagcaaa tccccaggac tgcggtgata   | 180 |
| ggcatgcttt ccttcttcct ccacggccag atgagtaagt tcgagaaagc tccaagcaag   | 240 |
| cctctttcca atgctttcgc cttcgccctcc gtgggctacg ttgtgttgca ggtcgcacac  | 300 |
| ggctttgctc gagctaatacgc tctttcatct ttcgctttcg acttctcttc tgttctctgt | 360 |
| ggacttgcac ccgttgccat tctcttcaact gccatcttca acgactga               |     |

(2) INFORMATION FOR SEQ ID NO:804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135

09639930 101300



ggcatgcttt ccttcttcct ccacggccag atgagtcgca cacggctttg ctogagctaa 240

(2) INFORMATION FOR SEQ ID NO:807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

Met Ser Asn Val Gly Val Thr Val Arg Asp Arg Glu Arg Leu Ile Arg  
1 5 10 15  
Thr Val His Cys Arg Leu Pro Ser Pro Pro Leu Met Glu Arg Met Asn  
20 25 30  
Met Ser Glu Glu Glu Gln Cys Lys Arg Asn Gln Glu Ala Phe Lys  
35 40 45  
Arg Phe Phe Glu Gln Ile Pro Arg Thr Ala Val Ile Gly Met Leu Ser  
50 55 60  
Phe Phe Leu His Gly Gln Met Ser Arg Thr Arg Leu Cys Ser Ser  
65 70 75

(2) INFORMATION FOR SEQ ID NO:808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: / Ceres Seq. ID 1593891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

Met Glu Arg Met Asn Met Ser Glu Glu Glu Glu Gln Cys Lys Arg Asn  
1 5 10 15  
Gln Glu Ala Phe Lys Arg Phe Phe Glu Gln Ile Pro Arg Thr Ala Val  
20 25 30  
Ile Gly Met Leu Ser Phe Phe Leu His Gly Gln Met Ser Arg Thr Arg  
35 40 45  
Leu Cys Ser Ser  
50

(2) INFORMATION FOR SEQ ID NO:809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

atgatgtctt tgctcccaaa tccgaccgc attactgtac cctggctcct caagctttgc 60  
tcctttcttc cgccacggag gctcttctct ctcaggctca ggcgcttcac ccgaaagtca 120  
tcattctctt ttcggttggt cgtgttttcg tctctctccg ctactgncgc aaaacctacc 180  
agatggagag agaagccgga attggcggaa agcgactcaa tttccctcct caacgagagg 240  
attcggcgtg acctcggcaa gagagagact gctagaccgg ccatggactc tgaggaggcc 300

09669930 10300











|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ser | Lys | Glu | Glu | Ile | Arg | Val | Ser | Gly | Ser | Leu | Arg | Gly | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Leu | Cys | Ala | Lys | Phe | Glu | Lys | Gln | Lys | Glu | Ile | Ser | Ser | Ala | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | His | Asp | Ile | Thr | Leu | Ser | Ser | Tyr | Lys | Gln | Gln | Glu | Gln | Thr |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Arg | Met | Val | Ser | Ser | Ile | Lys | Pro | Pro | Lys | Arg | Leu | Gln | Gln | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Pro | Val | Ile | Ala | Ala | Gly | Ala | Pro | Asp | Leu | Cys | Lys | Val | Gln | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Ala | Cys | Arg | Val | Ala | Leu | Asp | Pro | Ser | Leu | Cys | Leu | Phe | Lys | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Gly | Cys | Val | Val | Leu | Leu | Cys | Lys | Phe | Gly | Ile | Arg | Ala | Ser | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Leu | Pro | Arg | Ser | Glu | Lys | Ile | Cys | Ser | Arg | Cys | Leu | Arg | Ala | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Arg | Trp | Arg | Ser | Ser | Thr | Glu | Met | Gly | Ile | Thr | Ser | Cys | Gly | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Ser | Tyr | Trp | Leu | Ile | Trp | Arg | Cys | Trp | Asp | Phe | Trp | Arg | Val | Ser |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Lys | Lys | Arg | Lys | Gln | Trp | Leu | Lys | Ile | Leu | Pro | Leu | Arg | Leu | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Met | Glu | Glu | Thr | Lys | Thr | Gln | Lys | Leu | Gln | Leu | Leu | Asn | Trp | Lys | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Ser | Ser | Lys | Lys | Lys | Arg | Gly | Lys | Ala | Arg | Ser | Thr | Ile | Ile | Leu |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Leu | Gly | Asn | Asn | Val | Leu | Arg | Lys | Val | Ile | Lys | Gln | Lys | Thr | Ala |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Gly | Met | Ile | Lys | Val | Leu | Asp | Gln | Leu | Phe | Met | Ala | Lys | Ser | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Pro | Asn | Arg | Ile | Tyr | Leu | Lys | Gln | Arg | Leu | Tyr | Gly | Tyr | Lys | Met | Ser |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Asn | Met | Thr | Met | Glu | Glu | Asn | Val | Asn | Asp | Phe | Phe | Lys | Leu | Ile |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Asp | Leu | Glu | Asn | Val | Lys | Val | Val | Val | Pro | Asp | Glu | Asp | Gln | Ala |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Val | Leu | Leu | Met | Ser | Leu | Pro | Arg | Gln | Phe | Asp | Gln | Leu | Lys | Glu |
| 290 |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Thr | Leu | Lys | Tyr | Cys | Lys | Thr | Thr | Leu | His | Leu | Glu | Glu | Ile | Thr | Ser |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ala | Ile | Arg | Ser | Lys | Ile | Leu | Glu | Leu | Gly | Ala | Ser | Glu | Ala | Asp | Gln |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Lys | Pro | Gly | Gly | Asn | Asp | Arg | Thr | Arg | Thr | Arg | Ala | Asp | Leu | Ser | Gln |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Arg | Glu | Gln | Glu | Lys | Arg | Val | Gly | Ser | Val | Ala | Arg | Arg | Glu | Arg | Asn |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Lys | Gln | Gly | Ser | Thr | Ser | Glu | Arg | Gly | Glu | Ala | Ser | Thr | Val | Thr | Ala |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Gln | Val | Thr | Asp | Ala | Ala | Ala | Leu | Val | Val | Ser | Arg | Ala | Leu | Leu | Gly |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Phe | Ala | Glu | Val | Thr | Pro | Asp | Thr | Trp | Ile | Leu | Asp | Thr | Gly | Cys | Ser |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Phe | His | Met | Thr | Cys | Arg | Lys | Asp | Trp | Ile | Ile | Asp | Phe | Lys | Glu | Thr |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Ala | Ser | Gly | Lys | Val | Arg | Met | Gly | Asn | Asp | Thr | Tyr | Ser | Glu | Val | Lys |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Gly | Ile | Gly | Asp | Val | Arg | Ile | Lys | Asn | Glu | Asp | Gly | Ser | Thr | Ile | Leu |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Leu | Thr | Asp | Val | Arg | Leu | Gly | His | Ile | Gly | Ala | Lys | Arg | Leu | Gln | Val |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Leu | Val | Ser | Lys | Gly | His | Leu | Asp | Lys | Asn | Met | Ile | Lys | Glu | Leu | Gln |

DOCKET# 08662950

| Aggregates - 1990 |       |
|-------------------|-------|
| Year              | Value |
| 1990              | 1.00  |
| 1991              | 1.00  |
| 1992              | 1.00  |
| 1993              | 1.00  |
| 1994              | 1.00  |
| 1995              | 1.00  |
| 1996              | 1.00  |
| 1997              | 1.00  |
| 1998              | 1.00  |
| 1999              | 1.00  |
| 2000              | 1.00  |
| 2001              | 1.00  |
| 2002              | 1.00  |
| 2003              | 1.00  |
| 2004              | 1.00  |
| 2005              | 1.00  |
| 2006              | 1.00  |
| 2007              | 1.00  |
| 2008              | 1.00  |
| 2009              | 1.00  |
| 2010              | 1.00  |
| 2011              | 1.00  |
| 2012              | 1.00  |
| 2013              | 1.00  |
| 2014              | 1.00  |
| 2015              | 1.00  |
| 2016              | 1.00  |
| 2017              | 1.00  |
| 2018              | 1.00  |
| 2019              | 1.00  |
| 2020              | 1.00  |
| 2021              | 1.00  |
| 2022              | 1.00  |
| 2023              | 1.00  |
| 2024              | 1.00  |
| 2025              | 1.00  |
| 2026              | 1.00  |
| 2027              | 1.00  |
| 2028              | 1.00  |
| 2029              | 1.00  |
| 2030              | 1.00  |
| 2031              | 1.00  |
| 2032              | 1.00  |
| 2033              | 1.00  |
| 2034              | 1.00  |
| 2035              | 1.00  |
| 2036              | 1.00  |
| 2037              | 1.00  |
| 2038              | 1.00  |
| 2039              | 1.00  |
| 2040              | 1.00  |
| 2041              | 1.00  |
| 2042              | 1.00  |
| 2043              | 1.00  |
| 2044              | 1.00  |
| 2045              | 1.00  |
| 2046              | 1.00  |
| 2047              | 1.00  |
| 2048              | 1.00  |
| 2049              | 1.00  |
| 2050              | 1.00  |
| 2051              | 1.00  |
| 2052              | 1.00  |
| 2053              | 1.00  |
| 2054              | 1.00  |
| 2055              | 1.00  |
| 2056              | 1.00  |
| 2057              | 1.00  |
| 2058              | 1.00  |
| 2059              | 1.00  |
| 2060              | 1.00  |
| 2061              | 1.00  |
| 2062              | 1.00  |
| 2063              | 1.00  |
| 2064              | 1.00  |
| 2065              | 1.00  |
| 2066              | 1.00  |
| 2067              | 1.00  |
| 2068              | 1.00  |
| 2069              | 1.00  |
| 2070              | 1.00  |
| 2071              | 1.00  |
| 2072              | 1.00  |
| 2073              | 1.00  |
| 2074              | 1.00  |
| 2075              | 1.00  |
| 2076              | 1.00  |
| 2077              | 1.00  |
| 2078              | 1.00  |
| 2079              | 1.00  |
| 2080              | 1.00  |
| 2081              | 1.00  |
| 2082              | 1.00  |
| 2083              | 1.00  |
| 2084              | 1.00  |
| 2085              | 1.00  |
| 2086              | 1.00  |
| 2087              | 1.00  |
| 2088              | 1.00  |
| 2089              | 1.00  |
| 2090              | 1.00  |
| 2091              | 1.00  |
| 2092              | 1.00  |
| 2093              | 1.00  |
| 2094              | 1.00  |
| 2095              | 1.00  |
| 2096              | 1.00  |
| 2097              | 1.00  |
| 2098              | 1.00  |
| 2099              | 1.00  |
| 2100              | 1.00  |
| 2101              | 1.00  |
| 2102              | 1.00  |
| 2103              | 1.00  |
| 2104              | 1.00  |
| 2105              | 1.00  |
| 2106              | 1.00  |
| 2107              | 1.00  |
| 2108              | 1.00  |
| 2109              | 1.00  |
| 2110              | 1.00  |
| 2111              | 1.00  |
| 2112              | 1.00  |
| 2113              | 1.00  |
| 2114              | 1.00  |
| 2115              | 1.00  |
| 2116              | 1.00  |
| 2117              | 1.00  |
| 2118              | 1.00  |
| 2119              | 1.00  |
| 2120              | 1.00  |
| 2121              | 1.00  |
| 2122              | 1.00  |
| 2123              | 1.00  |
| 2124              | 1.00  |
| 2125              | 1.00  |
| 2126              | 1.00  |
| 2127              | 1.00  |
| 2128              | 1.00  |
| 2129              | 1.00  |
| 2130              | 1.00  |
| 2131              | 1.00  |
| 2132              | 1.00  |
| 2133              | 1.00  |
| 2134              | 1.00  |
| 2135              | 1.00  |
| 2136              | 1.00  |
| 2137              | 1.00  |
| 2138              | 1.00  |
| 2139              |       |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 738 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..738

(D) OTHER INFORMATION: / Ceres Seq. ID 1594133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ser | Ser | Ile | Lys | Pro | Pro | Lys | Arg | Leu | Gln | Gln | Phe | Arg | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ile | Ala | Ala | Gly | Ala | Pro | Asp | Leu | Cys | Lys | Val | Gln | Ala | Arg | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Arg | Val | Ala | Leu | Asp | Pro | Ser | Leu | Cys | Leu | Phe | Lys | Gly | Val | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Val | Val | Leu | Leu | Cys | Lys | Phe | Gly | Ile | Arg | Ala | Ser | Arg | Leu | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Arg | Ser | Glu | Lys | Ile | Cys | Ser | Arg | Cys | Leu | Arg | Ala | Glu | Gln | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |







|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |     |
| Ser | Met | Ser | Gln | Lys | Ile | Asn | Ser | Thr | Met | Cys | Ile | Leu | Ile | Tyr | Gly |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Asp | His | Arg | Met | Tyr | His | Ser | Pro | Leu | Ile | Glu | Asn | Gln | Gln | Asp | Lys |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Lys | Leu | Lys | Ile | Leu | Lys | Thr | Asp | Asn | Gly | Leu | Glu | Phe | Cys | Asn | Gln |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Glu | Phe | Asp | Ser | Phe | Cys | Arg | Lys | Glu | Gly | Val | Ile | Arg | His | Met | Thr |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Cys | Ala | Tyr | Thr | Pro | Gln | Gln | Asn | Gly | Val | Ala | Glu | Arg | Met | Asn | Arg |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Thr | Ile | Met | Asn | Lys | Gly | Trp | Gly | Asn | Ser | Ser | Gly | Gln | Lys | Gln | Arg |
|     |     |     | 485 |     |     |     |     | 490 |     |     |     |     |     | 495 |     |
| Leu | Leu | Pro | Cys | Ser | Ser | Ser | Thr | Lys | Ala | Gln | Ala | Leu | Gln |     |     |
|     |     | 500 |     |     |     |     |     | 505 |     |     |     |     | 510 |     |     |

(2) INFORMATION FOR SEQ ID NO:820:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 460 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..460

(D) OTHER INFORMATION: / Ceres Seq. ID 1594137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ser | Ser | Ile | Lys | Pro | Pro | Lys | Arg | Leu | Gln | Gln | Phe | Arg | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ile | Ala | Ala | Gly | Ala | Pro | Asp | Leu | Cys | Lys | Val | Gln | Ala | Arg | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Arg | Val | Ala | Leu | Asp | Pro | Ser | Leu | Cys | Leu | Phe | Lys | Gly | Val | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Val | Val | Leu | Leu | Cys | Lys | Phe | Gly | Ile | Arg | Ala | Ser | Arg | Leu | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Arg | Ser | Glu | Lys | Ile | Cys | Ser | Arg | Cys | Leu | Arg | Ala | Glu | Gln | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Trp | Arg | Ser | Ser | Thr | Glu | Met | Gly | Ile | Thr | Ser | Cys | Gly | Lys | Lys | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Trp | Leu | Ile | Trp | Arg | Cys | Trp | Asp | Phe | Trp | Arg | Val | Ser | Gly | Lys |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Arg | Lys | Gln | Trp | Leu | Lys | Ile | Leu | Pro | Leu | Arg | Leu | Val | Met | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Thr | Lys | Thr | Gln | Lys | Leu | Gln | Leu | Leu | Asn | Trp | Lys | Thr | Arg | Ser |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Lys | Lys | Lys | Arg | Gly | Lys | Ala | Arg | Ser | Thr | Ile | Ile | Leu | Ser | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Asn | Asn | Val | Leu | Arg | Lys | Val | Ile | Lys | Gln | Lys | Thr | Ala | Ala | Glu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Asp | Gln | Lys | Pro | Gly | Gly | Asn | Asp | Arg | Thr | Arg | Thr | Arg | Ala | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Ser | Gln | Arg | Glu | Gln | Glu | Lys | Arg | Val | Gly | Ser | Val | Ala | Arg | Arg |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Arg | Asn | Lys | Gln | Gly | Ser | Thr | Ser | Glu | Arg | Gly | Glu | Ala | Ser | Thr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Thr | Ala | Gln | Val | Thr | Asp | Ala | Ala | Ala | Leu | Val | Val | Ser | Arg | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Leu | Leu | Gly | Phe | Ala | Glu | Val | Thr | Pro | Asp | Thr | Trp | Ile | Leu | Asp | Thr |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Cys | Ser | Phe | His | Met | Thr | Cys | Arg | Lys | Asp | Trp | Ile | Ile | Asp | Phe |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |

00669800 001000

Lys Glu Thr Ala Ser Gly Lys Val Arg Met Gly Asn Asp Thr Tyr Ser  
275 280 285  
Glu Val Lys Gly Ile Gly Asp Val Arg Ile Lys Asn Glu Asp Gly Ser  
290 295 300  
Thr Ile Leu Leu Thr Asp Val Arg Leu Gly His Ile Gly Ala Lys Arg  
305 310 315 320  
Leu Gln Val Leu Val Ser Lys Gly His Leu Asp Lys Asn Met Ile Lys  
325 330 335  
Glu Leu Gln Phe Cys Glu Asp Trp Leu Ala Leu Glu Leu Gln Ser Met  
340 345 350  
Ser Gln Lys Ile Asn Ser Thr Met Cys Ile Leu Ile Tyr Gly Asp His  
355 360 365  
Arg Met Tyr His Ser Pro Leu Ile Glu Asn Gln Gln Asp Lys Lys Leu  
370 375 380  
Lys Ile Leu Lys Thr Asp Asn Gly Leu Glu Phe Cys Asn Gln Glu Phe  
385 390 395 400  
Asp Ser Phe Cys Arg Lys Glu Gly Val Ile Arg His Met Thr Cys Ala  
405 410 415  
Tyr Thr Pro Gln Gln Asn Gly Val Ala Glu Arg Met Asn Arg Thr Ile  
420 425 430  
Met Asn Lys Gly Trp Gly Asn Ser Ser Gly Gln Lys Gln Arg Leu Leu  
435 440 445  
Pro Cys Ser Ser Ser Thr Lys Ala Gln Ala Leu Gln  
450 455 460

(2) INFORMATION FOR SEQ ID NO:821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1371
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

|            |            |            |             |             |            |      |
|------------|------------|------------|-------------|-------------|------------|------|
| atggaagctc | taaactctat | cttaaccggc | tacgcgctg   | cagccctatc  | agtctacgct | 60   |
| ctttggttct | acttctctgc | ccgaagacta | accgggtccca | aagtcttacc  | gttcgtagga | 120  |
| agcttaccgt | atctaatacg | taaccggagc | cgaattcacg  | attggatcgc  | tgataatctc | 180  |
| cgagcaactg | gtggtacgta | tcaaacatgc | accatggtga  | tacctttcgt  | agccaaggcg | 240  |
| caagggtttt | acactgtgac | gtgtcaccca | aaaaacgtcg  | agcatatcct  | taagacacgg | 300  |
| ttcgacaact | atccgaaaag | tccgatgtgg | cgcgctgctt  | tccacgacct  | gttaggacaa | 360  |
| ggaatcttca | acagcgacgg | tgacacgtgg | ctcatgcaac  | gtaagactgc  | agcgcttgag | 420  |
| ttcacaacta | gaactcttag | acaagccatg | gctcgggtgg  | ttaacgggac  | tatcaagaac | 480  |
| cggttatggc | ttatattaga | ccgtgcggtt | caaaacaaca  | aaccggttga  | tcttcaagat | 540  |
| ttgtttttga | ggttaacttt | tgacaacatt | tgtggtctga  | cttttggtta  | agaccgggag | 600  |
| acgctctctc | tggatctacc | ggataatccc | ttctctgtcg  | cttttgacac  | cgcgacagag | 660  |
| gctactctaa | agagacttct | ctacaccggg | ttcttggtga  | ggattcagaa  | agctatgggg | 720  |
| attggatcag | aagataagct | caagaagagt | cttgaagtgc  | ttgagactta  | catgaacgat | 780  |
| gcaatcgacg | ctcggaaaaa | ctctccctcc | gatgatcttt  | tgtcacgttt  | cttgaagaaa | 840  |
| cgtgacgtta | acggtaacgt | tcttccaaca | gatgttcttc  | agcgtatcgc  | gcttaacttt | 900  |
| gttctcgcgg | gccgtgacac | ttcttcggtg | gccttgagct  | ggttcttctg  | gctcgtcatg | 960  |
| aataaccggg | aggtggaaac | gaagatcggt | aacgagttgt  | cgatggttct  | gaaggagaca | 1020 |
| cgtggcaatg | atcaggagaa | atggacggag | gagccggttag | agttcgacga  | ggcagatagg | 1080 |
| ctcgtttacc | tcaaggctgc | tttggttgaa | acgctgcgtt  | tatacccttc  | tgtgcctcag | 1140 |
| natgacgttt | tgccggacgg | gactttcgtg | ncaagaggnt  | cgacgggtgac | ctactcgatt | 1200 |
| tactcgatcg | gacgtatgaa | aacaatttgg | ggcgaagatt  | gtctcgagtt  | ccgtccggaa | 1260 |
| cggtggtcga | cagncgacgg | tgaacggttt | gagactnccc  | aaagatgggt  | acaagttcgt | 1320 |
| agcgttcnac | gccgnccaa  | ggacttgctt | gggaaaggac  | ttgggttata  | a          |      |

(2) INFORMATION FOR SEQ ID NO:822:

(i) SEQUENCE CHARACTERISTICS:







Thr Ile Trp Gly Glu Asp Cys Leu Glu Phe Arg Pro Glu Arg Trp Leu  
340 345 350  
Thr Xaa Asp Gly Glu Arg Phe Glu Thr Xaa Gln Arg Trp Leu Gln Val  
355 360 365  
Arg Ser Val Xaa Arg Arg Xaa Lys Asp Leu Leu Gly Lys Gly Leu Gly  
370 375 380  
Leu  
385

(2) INFORMATION FOR SEQ ID NO:824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

ctgctcgcca agtgtttcaa gactatcaag tttctaacag ataagttgag ttgttcctcc 60  
tccaccactg ctattccaca aggacaacct cctatggaga tgccatcgag gagatttgat 120  
gagccttag

(2) INFORMATION FOR SEQ ID NO:825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

Leu Leu Ala Lys Cys Phe Lys Thr Ile Lys Phe Leu Thr Asp Lys Leu  
1 5 10 15  
Ser Cys Ser Ser Ser Thr Thr Ala Ile Pro Gln Gly Gln Pro Pro Met  
20 25 30  
Glu Met Pro Ser Arg Arg Phe Asp Glu Pro  
35 40

(2) INFORMATION FOR SEQ ID NO:826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..336
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

atggcatatc ctctctctac aaactctcgt tggatcatcg acgaaaaagg gcaaagagtg 60  
aagctggcgt gtgtgaattg gccatcacat ttgcagcctg tgggtggcgga agggctgagc 120  
aagcagagtg tagatgactt ggccaagaag ataatggcaa tgggtttcaa ctgtgttagg 180  
tttacttggc cacttgatct agctacaaat gagacgttgg ctaataatgt tactgtgaga 240  
caatcttttc aaagtcttgg tcttaatgat gatatttctg gtttcgaaac aaagaacca 300  
tccatgattg atcttccctt cattgaagct tacaag

(2) INFORMATION FOR SEQ ID NO:827:

(i) SEQUENCE CHARACTERISTICS:



ccatacgggtg agaacttggt ctggggaagt ggctcagact ttacatcgac ttctgcagtg 240  
gagtcattgga ctgtggaggc taagtcctac aaccacatga ccaacacgtg tgaaggagat 300  
ggtatgtgtg gtcactacac tcagatcgtg tggcgtgaaa ccaggcgctt aggttgcgct 360  
agagttgtct gcgagaacgg cgcaggagtt ttcattcactt gcaactacga ccctccgggt 420  
aactacgttg gggagaagcc ttactaa

(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

Met Tyr Ile Lys Tyr Leu Leu Ala Trp Leu Lys Tyr Leu Gln Asp Tyr  
1 5 10 15  
Asn Ser Leu Ala Phe Xaa Lys Ala Lys Gln Ser Gly Leu Pro Pro Leu  
20 25 30  
Val Trp Asp Val Lys Ile Ala Ser Tyr Ala Thr Trp Trp Ala Asn Gln  
35 40 45  
Arg Arg Tyr Asp Cys Ser Leu Thr His Ser Thr Gly Pro Tyr Gly Glu  
50 55 60  
Asn Leu Phe Trp Gly Ser Gly Ser Asp Phe Thr Ser Thr Phe Ala Val  
65 70 75 80  
Glu Ser Trp Thr Val Glu Ala Lys Ser Tyr Asn His Met Thr Asn Thr  
85 90 95  
Cys Glu Gly Asp Gly Met Cys Gly His Tyr Thr Gln Ile Val Trp Arg  
100 105 110  
Glu Thr Arg Arg Leu Gly Cys Ala Arg Val Val Cys Glu Asn Gly Ala  
115 120 125  
Gly Val Phe Ile Thr Cys Asn Tyr Asp Pro Pro Gly Asn Tyr Val Gly  
130 135 140  
Glu Lys Pro Tyr  
145

(2) INFORMATION FOR SEQ ID NO:831:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..573
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

atgagctcat cctatttacg agtaaatatta ctcttaggtg cccttaatgt cgccgtttct 60  
ttatcaataa ccaactcatt aataaccaa tccgcaacac ttggtcagggt gttccgaatc 120  
tgtaagaatt tgtgtccggg atgtgaccac gactccttgc agttcttgtt ccgacacaac 180  
ctgggtccgtg ccgcaagatt cgaacctcct ttgatattggg accgcagact ccagaactac 240  
gcccagggtt gggctaatac aagaaggagg gatttgtgctt tgagacactc tgtctcaaac 300  
ggagagttta atctcggcga gaacatctac tggggatacgc gcgccaaactg gtctccggcc 360  
gacgcggttg ttgcatgggc cagcgagaag aggttttata attacggctc caacacgtgc 420  
gacgctggtc agatgtgtgg tcattacaca cagatttgtg ggaagagcac taggagggtc 480  
ggatgtgcac gtgtggtgtg cgacaatggt gggatottca tgacttgtaa ctatgatcct 540  
cccggtaact acatcggcca gaaaccctat taa

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS:



gggatgaagg ggacacaaga gatgcttgag ttctgtgcc agcataaaat cgtttcggat 960  
attgagctca taaagatgag tgatatcaac tctgcgatgg accgtttggc taaatctgat 1020  
gtcaggtacc ggttcgtgat cgatgtggcc aactctttac tccctgaatc gtcagctgag 1080  
attttaacgg agcaggtgga ccattggagtc tcgatcacgt ctgattctg a

(2) INFORMATION FOR SEQ ID NO:834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..376
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Asp | Gln | Asn | Lys | Ala | Phe | Gly | Trp | Ala | Ala | Asn | Asp | Glu | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Val | Leu | Ser | Pro | Phe | His | Phe | Ser | Arg | Arg | Glu | Asn | Gly | Glu | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Val | Thr | Val | Lys | Ile | Leu | Phe | Cys | Gly | Val | Cys | His | Ser | Asp | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Thr | Ile | Lys | Asn | His | Trp | Gly | Phe | Ser | Arg | Tyr | Pro | Ile | Ile | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | His | Glu | Ile | Val | Gly | Ile | Ala | Thr | Lys | Val | Gly | Lys | Asn | Val | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Phe | Lys | Glu | Gly | Asp | Arg | Val | Gly | Val | Gly | Val | Ile | Ile | Gly | Ser |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Cys | Gln | Ser | Cys | Glu | Ser | Cys | Asn | Gln | Asp | Leu | Glu | Asn | Tyr | Cys | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Val | Val | Phe | Thr | Tyr | Asn | Ser | Arg | Ser | Ser | Asp | Gly | Thr | Ser | Arg |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Asn | Gln | Gly | Gly | Tyr | Ser | Asp | Val | Ile | Val | Val | Asp | His | Arg | Phe | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Ser | Ile | Pro | Asp | Gly | Leu | Pro | Ser | Asp | Ser | Gly | Ala | Pro | Leu | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Cys | Ala | Gly | Ile | Thr | Val | Tyr | Ser | Pro | Met | Lys | Tyr | Tyr | Gly | Met | Thr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Glu | Ser | Gly | Lys | Arg | Leu | Gly | Val | Asn | Gly | Leu | Gly | Gly | Leu | Gly |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| His | Ile | Ala | Val | Lys | Ile | Gly | Lys | Ala | Phe | Gly | Leu | Arg | Val | Thr | Val |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ile | Ser | Arg | Ser | Ser | Lys | Lys | Glu | Arg | Glu | Ala | Ile | Asp | Arg | Leu | Gly |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Ala | Asp | Ser | Phe | Leu | Val | Thr | Thr | Asp | Ser | Gln | Lys | Met | Lys | Glu | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Val | Gly | Thr | Met | Asp | Phe | Ile | Ile | Asp | Thr | Val | Ser | Ala | Glu | His | Ala |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Leu | Pro | Leu | Phe | Ser | Leu | Leu | Lys | Val | Asn | Gly | Lys | Leu | Val | Ala |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Leu | Gly | Leu | Pro | Glu | Lys | Pro | Leu | Asp | Leu | Pro | Ile | Phe | Ser | Leu | Val |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Leu | Gly | Arg | Lys | Met | Val | Gly | Gly | Ser | Gln | Ile | Gly | Gly | Met | Lys | Gly |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Thr | Gln | Glu | Met | Leu | Glu | Phe | Cys | Ala | Lys | His | Lys | Ile | Val | Ser | Asp |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Ile | Glu | Leu | Ile | Lys | Met | Ser | Asp | Ile | Asn | Ser | Ala | Met | Asp | Arg | Leu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ala | Lys | Ser | Asp | Val | Arg | Tyr | Arg | Phe | Val | Ile | Asp | Val | Ala | Asn | Ser |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Leu | Leu | Pro | Glu | Ser | Ser | Ala | Glu | Ile | Leu | Thr | Glu | Gln | Val | Asp | His |

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agattggaag aggaagctga tgttgacgtt gaagaatcaa ctgcgtcgtga aattggacaa 540
gaggaagagg aagctttagg tgaaacgtct tgtggcggag aagaggaagc tcacgatgaa 600
gctcaagaat caggcgttga tgtgacagat gcagtcgaag ttcgtgctcc acttagacga 660
agtaaacgaa ggagaatcag agatgaagaa gaggaggatt tagaggctga agttcctgct 720
cttgatgaak wmgatgactg tgcagtccaa ggagatgaag actgcgatga ggttgatgat 780
gcagtagata ctaatagaga agaagatgat actgctggat taggtgtcga agaagatggt 840
aacttagaca tggaaagaga ttttccagag gctaattggag aagaagaagc tagtgacaat 900
gacagggtag atgatatatg ggatgaagac aagattccag atcctttgtc ctctgacgat 960
gaagatgatg atagagtaga ggcagctcga aatgatcttg gtgatcctga gattttacta 1020
gcattggaga agacttataa ctctcctgaa gatttcaagc ttgctctttt gatgtattcc 1080
ctaaagacaa ggtatgacat taaactttat aaatctgaag ctatggttgt tgctgctaag 1140
tgtgtgtatg ttagtgatga ggggtgttga tgtccgtgga gagtccgttg ctcttatgag 1200
aagagaaaac ataagatgca aatacgaact tattacaatg agcatacttg tgtgaggtca 1260
ggacattcga agatgttaaa ggtgtcatct attgggtttt tgtttgaaga aagggtgaga 1320
gtgaatccaa aactcactaa acatgagatg gttgctgaga tcttaagaga atacaagttg 1380
gaagtgactc cagaccaatg tgctaaggca aagacaaaag ttttgagagc tagacgtgct 1440
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ccggggacag agttcaacat agagacagtt gcaggagcag tgattggaag caagcagaga 1560
ttttaccggt tatatatattg ttttcaagct caaagggagt catggaaaca aacttgcaga 1620
cctataatag ggatagatgg agcttttctg aaatgggaca taaaaggaca tctattagcc 1680
acagtttgaa gagatggtga caatcgaatt gtccgtattg ctgggtctgt agtcgagata 1740
gaaaatgatg acaattggga ctggttcttg agacagctct ctacaagctt ggggctatgc 1800
gaaatgactg atctagcaat catttcagat aaacaatctg gtttagtcaa ggctatccat 1860
accattcttc cgcaagctga gcatcgacaa tgttcaaaac acatcatgga taattggaaa 1920
agggacaacc aggacattga gctacaacgg aaaaaaaaga aggttgaaag ctatgtgaac 1980
gactactaca caagaaatag gtggcgagaa acatatattcc gtggctgcoct gtcttgccac 2040
caccatggga gaagaggcaa taccggaagg ccaagcaatt atgcaagaag gaaaggaaga 2100
aatgaagttg cctcttcttc aaatccgaac aaaatgtcaa gggaaaagag gatcatgaca 2160
tgctctaact gcttgcaaga agggcacaaac aagaaatcat gcaaaaatgc tactgtttta 2220
agtccaccaa agagaccaag aggtcgacca aggataaatg agccacaagg gcatgtagaa 2280
ggatcagatg gacatgataa tggctcacaa gggcagggtg atgtgttaca agggcaggaa 2340
aatatgttac aaggacagaa taatgtgtca caagggcagg ataatggctc acaagggcag 2400
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cgtggaacac aaagacaaaag gggaacaact cgtggagcac aaagacagag gggaagaggt 2520
cgtggaacat cacaagtgtc tgaacaacca caaggagaag cacaaccgca aggacttgct 2580
ggacttgcac catggtttga atgttctcgt ggaacatga

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(2) INFORMATION FOR SEQ ID NO:837:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 872 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..872

(D) OTHER INFORMATION: / Ceres Seq. ID 1594438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

```

Met Pro Leu Val Arg Lys Asn Gly Val Val Met Arg Ile Gly Ser Pro
1 5 10 15
Met Leu His Glu Ser Glu Asn Leu Val Gly Asp Gly Val Glu Ala Xaa
20 25 30
Pro Arg Gly Glu Arg Asp Glu Ile Gly Glu Glu Val Gly Gly Glu Thr
35 40 45
Asn Val Val Ser Glu Ser Cys Gly Gly Glu Asp Gly Ala Gln Asp Ala
50 55 60
Ala Lys Pro Thr Pro Glu Arg Glu Ala Asp Arg Ile Gly Glu Glu Ala
65 70 75 80
Arg Gly Gln Ala Asn Val Val Ser Asn Val Asp Val Ala Asp Val Ala
85 90 95
Glu Val Arg Ser Pro Leu Arg Arg Ser Lys Arg Arg Gln Ile Arg Leu

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00000000 00000000



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Glu | Glu | Glu | Ala | His | Asp | Ala | Val | Glu | Pro | Met | Pro | Glu | Gly | Glu | Ala |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Asn | Gln | Ile | Gly | Glu | Glu | Ala | Arg | Gly | Gln | Ser | Val | Asp | Val | Ala | Asp |  |
|     | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |  |
| Ala | Thr | Ala | Val | Cys | Ser | Pro | Leu | Arg | Arg | Ser | Lys | Arg | Arg | Gln | Asn |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Arg | Leu | Glu | Glu | Glu | Ala | Asp | Val | Ala | Val | Glu | Glu | Ser | Thr | Arg | Arg |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Glu | Ile | Gly | Gln | Glu | Glu | Glu | Glu | Ala | Leu | Gly | Glu | Thr | Ser | Cys | Gly |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Gly | Glu | Glu | Glu | Ala | His | Asp | Glu | Ala | Gln | Glu | Ser | Gly | Val | Asp | Val |  |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Thr | Asp | Ala | Val | Glu | Val | Arg | Ala | Pro | Leu | Arg | Arg | Ser | Lys | Arg | Arg |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Arg | Ile | Arg | Asp | Glu | Glu | Glu | Glu | Asp | Leu | Glu | Ala | Glu | Val | Pro | Ala |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Leu | Asp | Glu | Xaa | Asp | Asp | Cys | Ala | Val | Gln | Gly | Asp | Glu | Asp | Cys | Asp |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Glu | Val | Asp | Asp | Ala | Val | Asp | Thr | Asn | Arg | Glu | Glu | Asp | Asp | Thr | Ala |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Gly | Leu | Gly | Val | Glu | Glu | Asp | Gly | Asn | Leu | Asp | Met | Glu | Arg | Asp | Phe |  |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Pro | Glu | Ala | Asn | Gly | Glu | Glu | Glu | Ala | Ser | Asp | Asn | Asp | Arg | Val | Asp |  |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |  |
| Asp | Ile | Trp | Asp | Glu | Asp | Lys | Ile | Pro | Asp | Pro | Leu | Ser | Ser | Asp | Asp |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Glu | Asp | Asp | Asp | Arg | Val | Glu | Ala | Ala | Arg | Asn | Asp | Leu | Gly | Asp | Pro |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Glu | Ile | Leu | Leu | Ala | Leu | Glu | Lys | Thr | Tyr | Asn | Ser | Pro | Glu | Asp | Phe |  |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     |     | 350 |     |     |  |
| Lys | Leu | Ala | Leu | Leu | Met | Tyr | Ser | Leu | Lys | Thr | Arg | Tyr | Asp | Ile | Lys |  |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |  |
| Leu | Tyr | Lys | Ser | Glu | Ala | Met | Val | Val | Ala | Ala | Lys | Cys | Val | Tyr | Val |  |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |
| Ser | Asp | Glu | Gly | Val | Glu | Cys | Pro | Trp | Arg | Val | Arg | Cys | Ser | Tyr | Glu |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |
| Lys | Arg | Lys | His | Lys | Met | Gln | Ile | Arg | Thr | Tyr | Tyr | Asn | Glu | His | Thr |  |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |  |
| Cys | Val | Arg | Ser | Gly | His | Ser | Lys | Met | Leu | Lys | Val | Ser | Ser | Ile | Gly |  |
|     |     | 420 |     |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |
| Phe | Leu | Phe | Glu | Glu | Arg | Leu | Arg | Val | Asn | Pro | Lys | Leu | Thr | Lys | His |  |
|     | 435 |     |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |
| Glu | Met | Val | Ala | Glu | Ile | Leu | Arg | Glu | Tyr | Lys | Leu | Glu | Val | Thr | Pro |  |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |
| Asp | Gln | Cys | Ala | Lys | Ala | Lys | Thr | Lys | Val | Leu | Arg | Ala | Arg | Arg | Ala |  |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |  |
| Ser | His | Asp | Ser | His | Phe | Ala | Arg | Ile | Trp | Asp | Tyr | Gln | Ala | Glu | Val |  |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |  |
| Leu | Leu | Arg | Asn | Pro | Gly | Thr | Glu | Phe | Asn | Ile | Glu | Thr | Val | Ala | Gly |  |
|     |     | 500 |     |     |     |     |     | 505 |     |     |     |     | 510 |     |     |  |
| Ala | Val | Ile | Gly | Ser | Lys | Gln | Arg | Phe | Tyr | Arg | Leu | Tyr | Ile | Cys | Phe |  |
|     | 515 |     |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |  |
| Gln | Ala | Gln | Arg | Glu | Ser | Trp | Lys | Gln | Thr | Cys | Arg | Pro | Ile | Ile | Gly |  |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |  |
| Ile | Asp | Gly | Ala | Phe | Leu | Lys | Trp | Asp | Ile | Lys | Gly | His | Leu | Leu | Ala |  |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |  |
| Thr | Val | Gly | Arg | Asp | Gly | Asp | Asn | Arg | Ile | Val | Arg | Ile | Ala | Trp | Ser |  |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |  |
| Val | Val | Glu | Ile | Glu | Asn | Asp | Asp | Asn | Trp | Asp | Trp | Phe | Leu | Arg | Gln |  |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |  |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Met | Pro | Glu | Gly | Glu | Ala | Asn | Gln | Ile | Gly | Glu | Glu | Ala | Arg | Gly | Gln |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ser | Val | Asp | Val | Ala | Asp | Ala | Thr | Ala | Val | Cys | Ser | Pro | Leu | Arg | Arg |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ser | Lys | Arg | Arg | Gln | Asn | Arg | Leu | Glu | Glu | Glu | Ala | Asp | Val | Ala | Val |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Glu | Glu | Ser | Thr | Arg | Arg | Glu | Ile | Gly | Gln | Glu | Glu | Glu | Glu | Ala | Leu |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |  |
| Gly | Glu | Thr | Ser | Cys | Gly | Gly | Glu | Glu | Glu | Ala | His | Asp | Glu | Ala | Gln |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Glu | Ser | Gly | Val | Asp | Val | Thr | Asp | Ala | Val | Glu | Val | Arg | Ala | Pro | Leu |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Arg | Arg | Ser | Lys | Arg | Arg | Arg | Ile | Arg | Asp | Glu | Glu | Glu | Glu | Asp | Leu |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Glu | Ala | Glu | Val | Pro | Ala | Leu | Asp | Glu | Xaa | Asp | Asp | Cys | Ala | Val | Gln |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Gly | Asp | Glu | Asp | Cys | Asp | Glu | Val | Asp | Asp | Ala | Val | Asp | Thr | Asn | Arg |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Glu | Glu | Asp | Asp | Thr | Ala | Gly | Leu | Gly | Val | Glu | Glu | Asp | Gly | Asn | Leu |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Asp | Met | Glu | Arg | Asp | Phe | Pro | Glu | Ala | Asn | Gly | Glu | Glu | Glu | Ala | Ser |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Asp | Asn | Asp | Arg | Val | Asp | Asp | Ile | Trp | Asp | Glu | Asp | Lys | Ile | Pro | Asp |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Pro | Leu | Ser | Ser | Asp | Asp | Glu | Asp | Asp | Asp | Arg | Val | Glu | Ala | Ala | Arg |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Asn | Asp | Leu | Gly | Asp | Pro | Glu | Ile | Leu | Leu | Ala | Leu | Glu | Lys | Thr | Tyr |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |  |
| Asn | Ser | Pro | Glu | Asp | Phe | Lys | Leu | Ala | Leu | Leu | Met | Tyr | Ser | Leu | Lys |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |
| Thr | Arg | Tyr | Asp | Ile | Lys | Leu | Tyr | Lys | Ser | Glu | Ala | Met | Val | Val | Ala |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |
| Ala | Lys | Cys | Val | Tyr | Val | Ser | Asp | Glu | Gly | Val | Glu | Cys | Pro | Trp | Arg |  |
|     | 370 |     |     |     |     |     | 375 |     |     |     | 380 |     |     |     |     |  |
| Val | Arg | Cys | Ser | Tyr | Glu | Lys | Arg | Lys | His | Lys | Met | Gln | Ile | Arg | Thr |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |
| Tyr | Tyr | Asn | Glu | His | Thr | Cys | Val | Arg | Ser | Gly | His | Ser | Lys | Met | Leu |  |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |  |
| Lys | Val | Ser | Ser | Ile | Gly | Phe | Leu | Phe | Glu | Glu | Arg | Leu | Arg | Val | Asn |  |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |
| Pro | Lys | Leu | Thr | Lys | His | Glu | Met | Val | Ala | Glu | Ile | Leu | Arg | Glu | Tyr |  |
|     |     | 435 |     |     |     |     |     |     |     |     |     |     |     |     |     |  |







(B) LOCATION: 1..1800

(D) OTHER INFORMATION: / Ceres Seq. ID 1594517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

|            |             |             |            |            |             |      |
|------------|-------------|-------------|------------|------------|-------------|------|
| atgcctaacg | ccggtcgtgg  | aggatctcga  | aagaggaaga | ccacaccaaa | cgtgactcaa  | 60   |
| agagtcggag | gttcaacgcc  | tgctggaaga  | ccctcttcgc | taccgcagca | gtacgctttc  | 120  |
| accccgcgcg | cagcgacggg  | tcaagttcct  | gcattgattc | cgctctagg  | agccggtgcc  | 180  |
| ggcgctcat  | cctctgcccc  | ccactactgt  | aactaccac  | caccgcagca | actcttccaa  | 240  |
| cactccacca | atcaaccaca  | gcgtgtagat  | ccgttgccac | cacaagagac | tgctcagcaa  | 300  |
| gaccctctct | tttcgccaga  | tccagaaact  | gcctctcaca | gtcatccctc | gttgctaggc  | 360  |
| aacaacttcg | aagagggcat  | tcctgcagtg  | ttgtcggagc | tccaagaaga | ctccgtgggt  | 420  |
| gctctgaatg | acattctctc  | tgctgctggc  | agagaagcgt | ggtgttgtgt | gttgtcttcc  | 480  |
| attccctggc | cgaaaaccga  | atkgtttact  | cgagacagag | gatctcgctt | ggtttaggaag | 540  |
| atcactagaa | ttttttttaca | aaaattcgat  | gctcccttct | ataactggtc | atgtgtgcta  | 600  |
| gytgataaaa | gagaaagatt  | attttttagag | tttgcgaaaa | ctcaccagtg | ggatccctta  | 660  |
| ataacaggga | cagtcacgta  | ttacttcaat  | gagatcgta  | agaggcgctt | gaaggacatg  | 720  |
| gttagcaccg | caaggacaac  | tcgagagcag  | cctccatgga | ttggagaaac | gatgtgggga  | 780  |
| acaatgtgtg | cttactggga  | cacagaagca  | gcacataaaa | ggagtcagac | ctattccaaa  | 840  |
| gctcatctct | ctgaccgtaa  | cggtatcagt  | cctcacgtcc | actactctgg | gccaaaatct  | 900  |
| tttcaagaaa | tcccagatga  | attggaagag  | aagttgggaa | gaccggtcca | tcttggtgag  | 960  |
| gtgttcatcc | aaacacacac  | taagtcggat  | ggctcatttg | ttgatcagaa | gtcggagaag  | 1020 |
| attgctcaag | cttatcagca  | gaatgaagag  | aagttgggaa | gaccggtcca | tcttggtgag  | 1080 |
| gtgttcatcc | aaacacacac  | taagtcggat  | ggctcatttg | ttgatcagaa | gtcggagaag  | 1140 |
| attgctcaag | cttatcagca  | gaatgaagag  | aagttgggaa | gaccggtcca | tcttggtgag  | 1200 |
| gtgttcatcc | aaacacacac  | taagtcggat  | ggctcatttg | ttgatcagaa | gtcggagaag  | 1260 |
| attgctcaag | cttatcagca  | gaatgaagag  | aagttgggaa | gaccggtcca | tcttggtgag  | 1320 |
| gtgttcatcc | aaacacacac  | taagtcggat  | ggctcatttg | ttgatcagaa | gtcggagaag  | 1380 |
| attgctcaag | cttatcagca  | gaatgtgaga  | tataggctgt | cagcactaga | ggcggatgct  | 1440 |
| tctgctatct | ctgatggctc  | ttcacgacct  | ccagagctca | cactagatga | ttatacagcc  | 1500 |
| atctttctcg | agtccacaga  | aagggattca  | agaggcaatc | cttatggact | tggatgtcta  | 1560 |
| aaagacactc | taagcagtg   | caaccgccat  | cactccggtt | cctcatcatc | ctttcaagcc  | 1620 |
| ctagaagaac | ggctgcagga  | agctcaaagg  | aaaatagaag | agcaggctgc | atataatgag  | 1680 |
| aagagagatg | ctgagattgc  | tgcccagaga  | gctgagtcac | cccaggtcac | aactgagcaa  | 1740 |
| aaggacaaga | tcgagcaatt  | gtcttttaggc | gagaagtatc | tccgccaaac | cgatccgtag  | 1800 |

(2) INFORMATION FOR SEQ ID NO:847:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 599 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..599

(D) OTHER INFORMATION: / Ceres Seq. ID 1594518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Asn | Ala | Gly | Arg | Gly | Gly | Ser | Arg | Lys | Arg | Lys | Thr | Thr | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Asn | Val | Thr | Gln | Arg | Val | Gly | Gly | Ser | Thr | Pro | Ala | Gly | Arg | Pro | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Leu | Pro | Gln | Gln | Tyr | Ala | Phe | Thr | Pro | Ala | Ala | Ala | Thr | Val | Gln |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Val | Pro | Ala | Leu | Ile | Pro | Pro | Leu | Gly | Ala | Gly | Ala | Gly | Ala | Ser | Ser |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Ser | Ala | Pro | His | Tyr | Cys | Asn | Tyr | Pro | Pro | Pro | Gln | Gln | Leu | Phe | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| His | Ser | Thr | Asn | Gln | Pro | Gln | Arg | Val | Asp | Pro | Leu | Pro | Pro | Gln | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Thr | Ala | Gln | Gln | Asp | Pro | Pro | Leu | Ser | Pro | Asp | Pro | Glu | Thr | Ala | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Ser | His | Pro | Ser | Leu | Leu | Gly | Asn | Asn | Phe | Glu | Glu | Gly | Ile | Pro |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 115                                                             | 120 | 125 |
| Ala Val Leu Ser Glu Leu Gln Glu Asp Ser Val Val Ala Leu Asn Asp |     |     |
| 130                                                             | 135 | 140 |
| Ile Leu Ser Val Pro Gly Arg Glu Ala Trp Cys Cys Val Leu Ser Ser |     |     |
| 145                                                             | 150 | 155 |
| Ile Pro Trp Pro Lys Thr Glu Xaa Phe Thr Arg Asp Arg Gly Ser Arg |     |     |
| 165                                                             | 170 | 175 |
| Leu Val Arg Lys Ile Thr Arg Ile Phe Leu Gln Lys Phe Asp Ala Pro |     |     |
| 180                                                             | 185 | 190 |
| Phe Tyr Asn Trp Ser Cys Val Leu Xaa Asp Lys Arg Glu Arg Leu Phe |     |     |
| 195                                                             | 200 | 205 |
| Leu Glu Phe Ala Lys Thr His Gln Trp Asp Pro Leu Ile Thr Gly Thr |     |     |
| 210                                                             | 215 | 220 |
| Val Gln Tyr Tyr Phe Asn Glu Ile Val Lys Arg Arg Leu Lys Asp Met |     |     |
| 225                                                             | 230 | 235 |
| Val Ser Thr Ala Arg Thr Thr Arg Glu Gln Pro Pro Trp Ile Gly Glu |     |     |
| 245                                                             | 250 | 255 |
| Thr Met Trp Gly Thr Met Cys Ala Tyr Trp Asp Thr Glu Ala Ala His |     |     |
| 260                                                             | 265 | 270 |
| Lys Arg Ser Gln Thr Tyr Ser Lys Ala His Leu Ser Asp Arg Asn Gly |     |     |
| 275                                                             | 280 | 285 |
| Ile Ser Pro His Val His Tyr Ser Gly Pro Lys Ser Phe Gln Glu Ile |     |     |
| 290                                                             | 295 | 300 |
| Pro Asp Glu Leu Glu Glu Lys Leu Gly Arg Pro Val His Leu Gly Glu |     |     |
| 305                                                             | 310 | 315 |
| Val Phe Ile Gln Thr His Thr Lys Ser Asp Gly Ser Phe Val Asp Gln |     |     |
| 325                                                             | 330 | 335 |
| Lys Ser Glu Lys Ile Ala Gln Ala Tyr Gln Gln Asn Glu Glu Lys Leu |     |     |
| 340                                                             | 345 | 350 |
| Gly Arg Pro Val His Leu Gly Glu Val Phe Ile Gln Thr His Thr Lys |     |     |
| 355                                                             | 360 | 365 |
| Ser Asp Gly Ser Phe Val Asp Gln Lys Ser Glu Lys Ile Ala Gln Ala |     |     |
| 370                                                             | 375 | 380 |
| Tyr Gln Gln Asn Glu Glu Lys Leu Gly Arg Pro Val His Leu Gly Glu |     |     |
| 385                                                             | 390 | 395 |
| Val Phe Ile Gln Thr His Thr Lys Ser Asp Gly Ser Phe Val Asp Gln |     |     |
| 405                                                             | 410 | 415 |
| Lys Ser Glu Lys Ile Ala Gln Ala Tyr Gln Gln Asn Glu Glu Lys Leu |     |     |
| 420                                                             | 425 | 430 |
| Gly Arg Pro Val His Leu Gly Glu Val Phe Ile Gln Thr His Thr Lys |     |     |
| 435                                                             | 440 | 445 |
| Ser Asp Gly Ser Phe Val Asp Gln Lys Ser Glu Lys Ile Ala Gln Ala |     |     |
| 450                                                             | 455 | 460 |
| Tyr Gln Gln Asn Val Arg Tyr Arg Leu Ser Ala Leu Glu Ala Asp Ala |     |     |
| 465                                                             | 470 | 475 |
| Ser Ala Ile Ser Asp Gly Ser Ser Arg Pro Pro Glu Leu Thr Leu Asp |     |     |
| 485                                                             | 490 | 495 |
| Asp Tyr Thr Ala Ile Phe Leu Glu Ser Thr Glu Arg Asp Ser Arg Gly |     |     |
| 500                                                             | 505 | 510 |
| Asn Pro Tyr Gly Leu Gly Cys Leu Lys Asp Thr Leu Ser Ser Ala Asn |     |     |
| 515                                                             | 520 | 525 |
| Arg His His Ser Gly Ser Ser Ser Ser Phe Gln Ala Leu Glu Glu Arg |     |     |
| 530                                                             | 535 | 540 |
| Leu Gln Glu Ala Gln Arg Lys Ile Glu Glu Gln Ala Ala Tyr Asn Glu |     |     |
| 545                                                             | 550 | 555 |
| Lys Arg Asp Ala Glu Ile Ala Ala Arg Glu Ala Glu Ser Ser Arg Val |     |     |
| 565                                                             | 570 | 575 |
| Thr Thr Glu Gln Lys Asp Lys Ile Glu Gln Leu Ser Leu Gly Glu Lys |     |     |
| 580                                                             | 585 | 590 |
| Tyr Leu Arg Gln Thr Asp Pro                                     |     |     |
| 595                                                             |     |     |

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- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..823  
(D) OTHER INFORMATION: / Ceres Seq. ID 1594543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| atggttgacg | caattgtatc  | gttcggtgtt | gaaaagcttt | gggagctcgt | gagcaaaaat | 60  |
| tatgaccgat | ttcagggagt  | tgaagagcaa | attactgttc | tagaaagtga | tctgaagatg | 120 |
| ttaatgtcct | ttctgagtga  | tgcggtgca  | aggcaacaaa | caactgaact | tgctagaaac | 180 |
| tgtgtggacg | acgtaaagga  | aatcacttac | gatgctgagg | atataattga | aacatatctt | 240 |
| ctgaagcgag | aacggagtga  | aagcagtggc | atcaagaatc | acatgagaag | tcttgcttgc | 300 |
| attcaaagtg | gtcgtaggaa  | gactgcctta | gaaatcacaa | gcattagtaa | gagaatctcc | 360 |
| aaagtgatcc | aggttatgca  | gactttaggc | atacaatcga | acattattga | aggtggatat | 420 |
| ttgcaggctc | tacaagatag  | gaaaagagag | atgcgtcata | catttcctat | tgagactgaa | 480 |
| agcaatcttg | ttggtttgga  | gacaaatgtt | gagaaattgg | ttgaagcttt | ggtgggaaat | 540 |
| gatagcagtc | atgggggtatc | cataactggc | ttgggtggtc | ttggcaaaac | cacccttgca | 600 |
| cggcaggttt | ttaatcatac  | taaggttaaa | gatcattttg | atgcacttgc | gtgggtgtgc | 660 |
| gtatcacaa  | agtttacacg  | gaagcatgtg | tgggagacca | tcttgaagaa | acttagtcac | 720 |
| ggagattacg | ttgctgacac  | gaatgaaggc | gaacttcaag | agaaactcat | tcagttgttg | 780 |
| gaaacaaaaa | aggctttgat  | cgtctttgat | gacgtatgga | aaa        |            |     |

(2) INFORMATION FOR SEQ ID NO:850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..274  
(D) OTHER INFORMATION: / Ceres Seq. ID 1594544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Asp | Ala | Ile | Val | Ser | Phe | Gly | Val | Glu | Lys | Leu | Trp | Glu | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ser | Lys | Asn | Tyr | Asp | Arg | Phe | Gln | Gly | Val | Glu | Glu | Gln | Ile | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Leu | Glu | Ser | Asp | Leu | Lys | Met | Leu | Met | Ser | Phe | Leu | Ser | Asp | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ala | Arg | Gln | Gln | Thr | Thr | Glu | Leu | Ala | Arg | Asn | Cys | Val | Asp | Asp |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Val | Lys | Glu | Ile | Thr | Tyr | Asp | Ala | Glu | Asp | Ile | Ile | Glu | Thr | Tyr | Leu |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Lys | Arg | Glu | Arg | Ser | Glu | Ser | Ser | Gly | Ile | Lys | Asn | His | Met | Arg |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Leu | Ala | Cys | Ile | Gln | Ser | Gly | Arg | Arg | Lys | Thr | Ala | Leu | Glu | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Ser | Ile | Ser | Lys | Arg | Ile | Ser | Lys | Val | Ile | Gln | Val | Met | Gln | Thr |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Leu | Gly | Ile | Gln | Ser | Asn | Ile | Ile | Glu | Gly | Gly | Tyr | Leu | Gln | Ala | Leu |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Gln | Asp | Arg | Lys | Arg | Glu | Met | Arg | His | Thr | Phe | Pro | Ile | Glu | Thr | Glu |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Asn | Leu | Val | Gly | Leu | Glu | Thr | Asn | Val | Glu | Lys | Leu | Val | Glu | Ala |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Leu | Val | Gly | Asn | Asp | Ser | Ser | His | Gly | Val | Ser | Ile | Thr | Gly | Leu | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Leu | Gly | Lys | Thr | Thr | Leu | Ala | Arg | Gln | Val | Phe | Asn | His | Thr | Lys |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     |     |     |     | 205 |



(B) LOCATION: 1..1712

(D) OTHER INFORMATION: / Ceres Seq. ID 1594562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

|            |             |             |             |             |             |      |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| ctggcgattc | tctagggttt  | aaaccgcgat  | ccactatccg  | aattgggtcga | atcggtccgtg | 60   |
| gtaatgaaat | cgccatcaaa  | gacgcgggaa  | tctccaccaa  | gcacctccgg  | atcgtttccg  | 120  |
| attccgagaa | ctggataatc  | cacgatcttg  | gtttcttccaa | cggcaccata  | ttgaactctg  | 180  |
| acactatcga | ctcagatacg  | cccgtcaatc  | ttagccatgg  | agacgaaatt  | aagcttggtg  | 240  |
| agtacacttc | catttttggtg | aactttggga  | gtgatgttgt  | tcaggcgccg  | caggagcata  | 300  |
| agcttccgcc | caggccaagg  | aggaacaaca  | agcggtctgc  | tgcttcggat  | ccgatccgg   | 360  |
| atcctattga | gtcggttcag  | gagaaaccaa  | agcgcacgcg  | tggatcgctg  | aagcaagagg  | 420  |
| aaaatgaact | gccaagagt   | actagggtct  | cgaggaaaaa  | gaatctggac  | gatatcgccg  | 480  |
| ataaagaaga | ggaattggat  | gtggaaattg  | agaaggtggt  | caaagctagg  | gttgggaggc  | 540  |
| ctcggaagaa | cgcaggcagt  | gcaattgcga  | aggaagaaga  | agttgtggag  | gagaaaaaaa  | 600  |
| gggttgggag | gccccggaag  | aacgcaagta  | gtgcaattac  | ggaggaagaa  | gaagttgtgg  | 660  |
| aggagaaaaa | aggcaactct  | agggctcgga  | gaggtaagaa  | cagtgagatt  | gtccagaaat  | 720  |
| caatcaaatt | ggaagttgag  | gatactccca  | aggcagtggg  | aatctcagag  | gtgaaaagca  | 780  |
| ggaagagagt | gacaaggagc  | aagcagatag  | aaaatgaatg  | ttttggattg  | gaggttaaa   | 840  |
| atgagaagag | aactacaagg  | tctaccagaa  | gcaagacgac  | tgaaattggt  | ggagagtctt  | 900  |
| ttctggagtt | ggagatggtc  | ctgaaccaag  | cccggaaaaa  | ccgtgcaaa   | aggaagaaaa  | 960  |
| tggatgagga | gccatccaag  | gagactagaa  | atgatgatgc  | cggagaagag  | gttttgaaga  | 1020 |
| actgtcatgt | tgaagaagat  | aaggaaaatg  | aagctcagga  | aggttgcagt  | ggaagaagtg  | 1080 |
| atgacatatg | tgatcaagaa  | gatgagaagg  | aatgcgatgg  | atctaagagg  | gtagagcagg  | 1140 |
| tggagattga | gttaagggaag | aaaagcacag  | tagaaggcct  | gaaatgcact  | gataaagaag  | 1200 |
| atggagaaac | agagaactca  | caagatattg  | aaagagaaag  | agaaaatgaa  | aatgaaaatg  | 1260 |
| aagctcaaga | aggttgcagt  | gaaagaagtg  | ataaagaata  | tgagagggtt  | ggtggtgggg  | 1320 |
| ctaagagggt | agagcaggtg  | gagattgagt  | taaggaagaa  | aagcaccgta  | ggagaagatg  | 1380 |
| acctgaactg | tactgttaga  | gaagatggag  | agacagaaaa  | cttacaagaa  | attgaagaag  | 1440 |
| agtgtcacga | cgaggaaagt  | gactgcaagg  | tcgaggaggc  | tggatttgcg  | acattagatg  | 1500 |
| aggaaaaggt | tgggcaggga  | tggaaacaata | agaaagtaga  | gagggtagaa  | gtatatttag  | 1560 |
| aaaaaatgaa | actaagagaa  | tggtttgatg  | ccatagaggt  | tcaactgcca  | aaacagacaa  | 1620 |
| ttgaagaaac | agagaagatg  | attgagccca  | tgagaagtaa  | gagtatgaga  | gttcacaagc  | 1680 |
| atattgcaga | gcaaaaggaa  | aagggcgact  | aa          |             |             |      |

(2) INFORMATION FOR SEQ ID NO:853:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 569 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..569

(D) OTHER INFORMATION: / Ceres Seq. ID 1594563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Asp | Ser | Leu | Gly | Phe | Lys | Pro | Gly | Ser | Thr | Ile | Arg | Ile | Gly | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Val | Arg | Gly | Asn | Glu | Ile | Ala | Ile | Lys | Asp | Ala | Gly | Ile | Ser | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | His | Leu | Arg | Ile | Val | Ser | Asp | Ser | Glu | Asn | Trp | Ile | Ile | His | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Gly | Ser | Ser | Asn | Gly | Thr | Ile | Leu | Asn | Ser | Asp | Thr | Ile | Asp | Ser |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Asp | Thr | Pro | Val | Asn | Leu | Ser | His | Gly | Asp | Glu | Ile | Lys | Leu | Gly | Glu |
|     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |     |     | 80  |     |
| Tyr | Thr | Ser | Ile | Leu | Val | Asn | Phe | Gly | Ser | Asp | Val | Val | Gln | Ala | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gln | Glu | His | Lys | Leu | Pro | Pro | Arg | Pro | Arg | Arg | Asn | Asn | Lys | Arg | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Ala | Ser | Asp | Pro | Asp | Pro | Asp | Pro | Ile | Glu | Ser | Val | Gln | Glu | Lys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Lys | Arg | Thr | Arg | Gly | Ser | Ser | Lys | Gln | Glu | Glu | Asn | Glu | Leu | Pro |

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|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 130                                                             | 135 | 140 |
| Lys Ser Thr Arg Ala Ser Arg Lys Lys Asn Leu Asp Asp Ile Ala Asp |     |     |
| 145                                                             | 150 | 155 |
| Lys Glu Glu Glu Leu Asp Val Glu Ile Glu Lys Val Val Lys Ala Arg |     |     |
|                                                                 | 165 | 170 |
| Val Gly Arg Pro Arg Lys Asn Ala Gly Ser Ala Ile Ala Lys Glu Glu |     |     |
|                                                                 | 180 | 185 |
| Glu Val Val Glu Glu Lys Lys Arg Val Gly Arg Pro Arg Lys Asn Ala |     |     |
|                                                                 | 195 | 200 |
| Ser Ser Ala Ile Thr Glu Glu Glu Glu Val Val Glu Glu Lys Lys Gly |     |     |
|                                                                 | 210 | 215 |
| Asn Ser Arg Ala Arg Arg Glu Lys Asn Ser Glu Ile Val Gln Lys Ser |     |     |
| 225                                                             | 230 | 235 |
| Ile Lys Leu Glu Val Glu Asp Thr Pro Lys Ala Val Glu Ile Ser Glu |     |     |
|                                                                 | 245 | 250 |
| Val Lys Ser Arg Lys Arg Val Thr Arg Ser Lys Gln Ile Glu Asn Glu |     |     |
|                                                                 | 260 | 265 |
| Cys Phe Gly Leu Glu Val Lys Asp Glu Lys Arg Thr Thr Arg Ser Thr |     |     |
|                                                                 | 275 | 280 |
| Arg Ser Lys Thr Thr Glu Ile Gly Gly Glu Ser Phe Leu Glu Leu Glu |     |     |
|                                                                 | 290 | 295 |
| Met Val Leu Asn Gln Ala Arg Lys Ser Arg Ala Lys Arg Lys Lys Met |     |     |
| 305                                                             | 310 | 315 |
| Asp Glu Glu Pro Ser Lys Glu Thr Arg Asn Asp Asp Ala Gly Glu Glu |     |     |
|                                                                 | 325 | 330 |
| Val Leu Lys Asn Cys His Val Glu Glu Asp Lys Glu Asn Glu Ala Gln |     |     |
|                                                                 | 340 | 345 |
| Glu Gly Cys Ser Gly Arg Ser Asp Asp Ile Cys Asp Gln Glu Asp Glu |     |     |
|                                                                 | 355 | 360 |
| Lys Glu Cys Asp Gly Ser Lys Arg Val Glu Gln Val Glu Ile Glu Leu |     |     |
|                                                                 | 370 | 375 |
| Arg Lys Lys Ser Thr Val Glu Gly Leu Lys Cys Thr Asp Lys Glu Asp |     |     |
|                                                                 | 385 | 390 |
| Gly Glu Thr Glu Asn Ser Gln Asp Ile Glu Arg Glu Arg Glu Asn Glu |     |     |
|                                                                 | 405 | 410 |
| Asn Glu Asn Glu Ala Gln Glu Gly Cys Ser Glu Arg Ser Asp Lys Glu |     |     |
|                                                                 | 420 | 425 |
| Tyr Glu Arg Val Gly Gly Gly Ala Lys Arg Val Glu Gln Val Glu Ile |     |     |
|                                                                 | 435 | 440 |
| Glu Leu Arg Lys Lys Ser Thr Val Gly Glu Asp Asp Leu Asn Cys Thr |     |     |
|                                                                 | 450 | 455 |
| Val Arg Glu Asp Gly Glu Thr Glu Asn Leu Gln Glu Ile Glu Glu Glu |     |     |
|                                                                 | 465 | 470 |
| Cys His Asp Glu Glu Ser Asp Cys Lys Val Glu Glu Ala Gly Phe Ala |     |     |
|                                                                 | 485 | 490 |
| Thr Leu Asp Glu Glu Lys Val Gly Gln Gly Trp Asn Asn Lys Lys Val |     |     |
|                                                                 | 500 | 505 |
| Glu Arg Val Glu Val Tyr Leu Glu Lys Met Lys Leu Arg Glu Trp Phe |     |     |
|                                                                 | 515 | 520 |
| Asp Ala Ile Glu Val Gln Leu Pro Lys Gln Thr Ile Glu Glu Thr Glu |     |     |
|                                                                 | 530 | 535 |
| Lys Met Ile Glu Pro Met Arg Ser Lys Ser Met Arg Val His Lys His |     |     |
|                                                                 | 545 | 550 |
| Ile Ala Glu Gln Lys Glu Lys Gly Asp                             |     |     |
|                                                                 | 565 |     |

(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1789

(D) OTHER INFORMATION: / Ceres Seq. ID 1594667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

atggcttctt gcttccaccc ttctgctatg gctacaagcc accgcgagga agactccatc 60  
attctttttt cagcatcaaa ctctcctgat gaattctcct ctgcttcctc ttctttttt 120  
tcttcaccac tcccaacccc taaccgctac tctttaaccg tcactaacct atcctacacc 180  
atcaatcaca ccccaatact caattccggt tcattagctg ctgaatcctc taaaatccta 240  
gccgtgggtg gaccgagtg aacaggaaaa tccactcttt taaagatcat ttcaggaaga 300  
gtgaaccaca aggcactaga tccgtcttcc gcggttttga tgaacaatcg taaaatcact 360  
gactataacc aactacgaag gctatgcggg tttgtcccgc aggcagatga cctactgcct 420  
ctacttaccg tgaaagagac gttaatgtat agcgccaaat tcagtttgag agattcaacg 480  
gctaaggaaa gagaagagag agtggagagc ttgttgagt atctcgggtc tgttctcgtc 540  
caagacagct tcgtgggaga aggagacgaa gaggatcgt gcgtttcggg tggagagagg 600  
aagagagtct ctatagccgt tgagatgatt cgtgatccac caattctgct tcttgacgaa 660  
ccaacctctg gtttgatag tcgaaactcg cttcaggttg ttgagctttt ggctactatg 720  
gcgaaatcca aacagagaac cgtcctcttc tccatccacc aaccaagtta taggatcctc 780  
gattacatct ccgattacct gattctttct cgcggtatcg ttatccactt gggaagtctt 840  
gaacatctcg aggactcgat agcgaaacta gggtttcaga ttccagaaca gctgaatcct 900  
atagaattcg ccattggaaat agttgagtc ttgagaactt ttaagccaaa ctcggtagct 960  
gtcgtagaat catcatcaat gtggcctgaa aacaacgaaa acgatgggat tatctctaag 1020  
aaagaagcgt ttctgttct agacgtcacc gagatctcat acctctgctc aagattctgc 1080  
aagatcatct atagaacaaa gcagttgttc ctggcgcgaa caatgcaagc ggttgtagct 1140  
ggattaggtc taggtagcgt ctacacaaga ctcaagcgtg acgaagaagg cgttgacagag 1200  
cggtctggac tctttgcctt cagcttaagc ttctcctct cttcaacagt cgaagcactt 1260  
cccatttacc tccgagaacg tcgcgttctg atgaaagaat catctcgtgg atcctaccga 1320  
atctcatcct acatgatagc caacaccatc gcatttgtac cgttcctctt cggtgtatct 1380  
ctcctcttct ccattccagt ctactggatc gtaggcctaa acccatcgat tcaagccttc 1440  
tcttcttttg tctcttggtt ttggctcatt atttcatggt ccagttctct ggtgcttttc 1500  
ctcagcgctg tttctcctga cttcatctct ggtaactccc tcatatgcac tgttcttgga 1560  
gccttcttcc tttctccgg ctactttatc ccaaagaga agatcccaaa accatggatg 1620  
ttcatgtact atgtgtcctt gtaccgttac ccgctggagt cnnnggtggt gaatgagtac 1680  
tgagcatgac gagaggaatg cttctccagt gggaacatgg gctgcttgat gaccggagag 1740  
gatgtgtga aggagagagg gcttgacaag gatacgagat ggatcaacg

(2) INFORMATION FOR SEQ ID NO:855:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 596 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..596

(D) OTHER INFORMATION: / Ceres Seq. ID 1594668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

Met Ala Ser Cys Phe His Pro Ser Ala Met Ala Thr Ser His Arg Glu  
1 5 10 15  
Glu Asp Ser Ile Ile Leu Phe Ser Ala Ser Asn Ser Pro Asp Glu Phe  
20 25 30  
Ser Ser Ala Ser Ser Ser Phe Ser Ser Ser Pro Leu Pro Thr Pro Asn  
35 40 45  
Arg Tyr Ser Leu Thr Val Thr Asn Leu Ser Tyr Thr Ile Asn His Thr  
50 55 60  
Pro Ile Leu Asn Ser Val Ser Leu Ala Ala Glu Ser Ser Lys Ile Leu  
65 70 75 80  
Ala Val Val Gly Pro Ser Gly Thr Gly Lys Ser Thr Leu Leu Lys Ile  
85 90 95  
Ile Ser Gly Arg Val Asn His Lys Ala Leu Asp Pro Ser Ser Ala Val

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|             |                                                         |  |     |  |     |
|-------------|---------------------------------------------------------|--|-----|--|-----|
|             | 100                                                     |  | 105 |  | 110 |
| Leu Met     | Asn Asn Arg Lys Ile Thr Asp Tyr Asn Gln Leu Arg Arg Leu |  |     |  |     |
|             | 115                                                     |  | 120 |  | 125 |
| Cys Gly     | Phe Val Pro Gln Asp Asp Leu Leu Pro Leu Leu Thr Val     |  |     |  |     |
|             | 130                                                     |  | 135 |  | 140 |
| Lys Glu Thr | Leu Met Tyr Ser Ala Lys Phe Ser Leu Arg Asp Ser Thr     |  |     |  |     |
|             | 145                                                     |  | 150 |  | 155 |
| Ala Lys Glu | Arg Glu Glu Arg Val Glu Ser Leu Leu Ser Asp Leu Gly     |  |     |  |     |
|             | 165                                                     |  | 170 |  | 175 |
| Leu Val Leu | Val Gln Asp Ser Phe Val Gly Glu Gly Asp Glu Glu Asp     |  |     |  |     |
|             | 180                                                     |  | 185 |  | 190 |
| Arg Gly Val | Ser Gly Gly Glu Arg Lys Arg Val Ser Ile Ala Val Glu     |  |     |  |     |
|             | 195                                                     |  | 200 |  | 205 |
| Met Ile Arg | Asp Pro Pro Ile Leu Leu Leu Asp Glu Pro Thr Ser Gly     |  |     |  |     |
|             | 210                                                     |  | 215 |  | 220 |
| Leu Asp Ser | Arg Asn Ser Leu Gln Val Val Glu Leu Leu Ala Thr Met     |  |     |  |     |
|             | 225                                                     |  | 230 |  | 235 |
| Ala Lys Ser | Lys Gln Arg Thr Val Leu Phe Ser Ile His Gln Pro Ser     |  |     |  |     |
|             | 245                                                     |  | 250 |  | 255 |
| Tyr Arg Ile | Leu Asp Tyr Ile Ser Asp Tyr Leu Ile Leu Ser Arg Gly     |  |     |  |     |
|             | 260                                                     |  | 265 |  | 270 |
| Ser Val Ile | His Leu Gly Ser Leu Glu His Leu Glu Asp Ser Ile Ala     |  |     |  |     |
|             | 275                                                     |  | 280 |  | 285 |
| Lys Leu Gly | Phe Gln Ile Pro Glu Gln Leu Asn Pro Ile Glu Phe Ala     |  |     |  |     |
|             | 290                                                     |  | 295 |  | 300 |
| Met Glu Ile | Val Glu Ser Leu Arg Thr Phe Lys Pro Asn Ser Val Ala     |  |     |  |     |
|             | 305                                                     |  | 310 |  | 315 |
| Val Val Glu | Ser Ser Ser Met Trp Pro Glu Asn Asn Glu Asn Asp Gly     |  |     |  |     |
|             | 325                                                     |  | 330 |  | 335 |
| Ile Ile Ser | Lys Lys Glu Ala Phe Arg Val Leu Asp Val Thr Glu Ile     |  |     |  |     |
|             | 340                                                     |  | 345 |  | 350 |
| Ser Tyr Leu | Cys Ser Arg Phe Cys Lys Ile Ile Tyr Arg Thr Lys Gln     |  |     |  |     |
|             | 355                                                     |  | 360 |  | 365 |
| Leu Phe Leu | Ala Arg Thr Met Gln Ala Val Val Ala Gly Leu Gly Leu     |  |     |  |     |
|             | 370                                                     |  | 375 |  | 380 |
| Gly Ser Val | Tyr Thr Arg Leu Lys Arg Asp Glu Glu Gly Val Ala Glu     |  |     |  |     |
|             | 385                                                     |  | 390 |  | 395 |
| Arg Leu Gly | Leu Phe Ala Phe Ser Leu Ser Phe Leu Leu Ser Ser Thr     |  |     |  |     |
|             | 405                                                     |  | 410 |  | 415 |
| Val Glu Ala | Leu Pro Ile Tyr Leu Arg Glu Arg Arg Val Leu Met Lys     |  |     |  |     |
|             | 420                                                     |  | 425 |  | 430 |
| Glu Ser Ser | Arg Gly Ser Tyr Arg Ile Ser Ser Tyr Met Ile Ala Asn     |  |     |  |     |
|             | 435                                                     |  | 440 |  | 445 |
| Thr Ile Ala | Phe Val Pro Phe Leu Phe Val Val Ser Leu Leu Phe Ser     |  |     |  |     |
|             | 450                                                     |  | 455 |  | 460 |
| Ile Pro Val | Tyr Trp Ile Val Gly Leu Asn Pro Ser Ile Gln Ala Phe     |  |     |  |     |
|             | 465                                                     |  | 470 |  | 475 |
| Ser Phe Phe | Val Leu Trp Val Trp Leu Ile Ile Leu Met Ala Ser Ser     |  |     |  |     |
|             | 485                                                     |  | 490 |  | 495 |
| Leu Val Leu | Phe Leu Ser Ala Val Ser Pro Asp Phe Ile Ser Gly Asn     |  |     |  |     |
|             | 500                                                     |  | 505 |  | 510 |
| Ser Leu Ile | Cys Thr Val Leu Gly Ala Phe Phe Leu Phe Ser Gly Tyr     |  |     |  |     |
|             | 515                                                     |  | 520 |  | 525 |
| Phe Ile Pro | Lys Glu Lys Ile Pro Lys Pro Trp Met Phe Met Tyr Tyr     |  |     |  |     |
|             | 530                                                     |  | 535 |  | 540 |
| Val Ser Leu | Tyr Arg Tyr Pro Leu Glu Xaa Xaa Val Val Asn Glu Tyr     |  |     |  |     |
|             | 545                                                     |  | 550 |  | 555 |
| Trp Ser Met | Arg Glu Glu Cys Phe Ser Ser Gly Asn Met Gly Cys Leu     |  |     |  |     |
|             | 565                                                     |  | 570 |  | 575 |
| Met Thr Gly | Glu Asp Val Leu Lys Glu Arg Gly Leu Asp Lys Asp Thr     |  |     |  |     |
|             | 580                                                     |  | 585 |  | 590 |

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Arg Trp Ile Asn  
595

(2) INFORMATION FOR SEQ ID NO:856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..587
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Thr | Ser | His | Arg | Glu | Glu | Asp | Ser | Ile | Ile | Leu | Phe | Ser | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Asn | Ser | Pro | Asp | Glu | Phe | Ser | Ser | Ala | Ser | Ser | Ser | Phe | Ser | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Pro | Leu | Pro | Thr | Pro | Asn | Arg | Tyr | Ser | Leu | Thr | Val | Thr | Asn | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Tyr | Thr | Ile | Asn | His | Thr | Pro | Ile | Leu | Asn | Ser | Val | Ser | Leu | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ala | Glu | Ser | Ser | Lys | Ile | Leu | Ala | Val | Val | Gly | Pro | Ser | Gly | Thr | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Ser | Thr | Leu | Leu | Lys | Ile | Ile | Ser | Gly | Arg | Val | Asn | His | Lys | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Asp | Pro | Ser | Ser | Ala | Val | Leu | Met | Asn | Asn | Arg | Lys | Ile | Thr | Asp |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Asn | Gln | Leu | Arg | Arg | Leu | Cys | Gly | Phe | Val | Pro | Gln | Asp | Asp | Asp |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Leu | Pro | Leu | Leu | Thr | Val | Lys | Glu | Thr | Leu | Met | Tyr | Ser | Ala | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Ser | Leu | Arg | Asp | Ser | Thr | Ala | Lys | Glu | Arg | Glu | Glu | Arg | Val | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Leu | Leu | Ser | Asp | Leu | Gly | Leu | Val | Leu | Val | Gln | Asp | Ser | Phe | Val |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Glu | Gly | Asp | Glu | Glu | Asp | Arg | Gly | Val | Ser | Gly | Gly | Glu | Arg | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Val | Ser | Ile | Ala | Val | Glu | Met | Ile | Arg | Asp | Pro | Pro | Ile | Leu | Leu |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Asp | Glu | Pro | Thr | Ser | Gly | Leu | Asp | Ser | Arg | Asn | Ser | Leu | Gln | Val |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Glu | Leu | Leu | Ala | Thr | Met | Ala | Lys | Ser | Lys | Gln | Arg | Thr | Val | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Phe | Ser | Ile | His | Gln | Pro | Ser | Tyr | Arg | Ile | Leu | Asp | Tyr | Ile | Ser | Asp |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Tyr | Leu | Ile | Leu | Ser | Arg | Gly | Ser | Val | Ile | His | Leu | Gly | Ser | Leu | Glu |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| His | Leu | Glu | Asp | Ser | Ile | Ala | Lys | Leu | Gly | Phe | Gln | Ile | Pro | Glu | Gln |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Asn | Pro | Ile | Glu | Phe | Ala | Met | Glu | Ile | Val | Glu | Ser | Leu | Arg | Thr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Phe | Lys | Pro | Asn | Ser | Val | Ala | Val | Val | Glu | Ser | Ser | Ser | Met | Trp | Pro |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Glu | Asn | Asn | Glu | Asn | Asp | Gly | Ile | Ile | Ser | Lys | Lys | Glu | Ala | Phe | Arg |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Val | Leu | Asp | Val | Thr | Glu | Ile | Ser | Tyr | Leu | Cys | Ser | Arg | Phe | Cys | Lys |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     |     | 350 |     |     |
| Ile | Ile | Tyr | Arg | Thr | Lys | Gln | Leu | Phe | Leu | Ala | Arg | Thr | Met | Gln | Ala |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Val | Val | Ala | Gly | Leu | Gly | Leu | Gly | Ser | Val | Tyr | Thr | Arg | Leu | Lys | Arg |

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370 375 380  
Asp Glu Glu Gly Val Ala Glu Arg Leu Gly Leu Phe Ala Phe Ser Leu  
385 390 395 400  
Ser Phe Leu Leu Ser Ser Thr Val Glu Ala Leu Pro Ile Tyr Leu Arg  
405 410 415  
Glu Arg Arg Val Leu Met Lys Glu Ser Ser Arg Gly Ser Tyr Arg Ile  
420 425 430  
Ser Ser Tyr Met Ile Ala Asn Thr Ile Ala Phe Val Pro Phe Leu Phe  
435 440 445  
Val Val Ser Leu Leu Phe Ser Ile Pro Val Tyr Trp Ile Val Gly Leu  
450 455 460  
Asn Pro Ser Ile Gln Ala Phe Ser Phe Phe Val Leu Trp Val Trp Leu  
465 470 475 480  
Ile Ile Leu Met Ala Ser Ser Leu Val Leu Phe Leu Ser Ala Val Ser  
485 490 495  
Pro Asp Phe Ile Ser Gly Asn Ser Leu Ile Cys Thr Val Leu Gly Ala  
500 505 510  
Phe Phe Leu Phe Ser Gly Tyr Phe Ile Pro Lys Glu Lys Ile Pro Lys  
515 520 525  
Pro Trp Met Phe Met Tyr Tyr Val Ser Leu Tyr Arg Tyr Pro Leu Glu  
530 535 540  
Xaa Xaa Val Val Asn Glu Tyr Trp Ser Met Arg Glu Glu Cys Phe Ser  
545 550 555 560  
Ser Gly Asn Met Gly Cys Leu Met Thr Gly Glu Asp Val Leu Lys Glu  
565 570 575  
Arg Gly Leu Asp Lys Asp Thr Arg Trp Ile Asn  
580 585

(2) INFORMATION FOR SEQ ID NO:857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1270
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

|             |            |             |            |             |            |      |
|-------------|------------|-------------|------------|-------------|------------|------|
| gattatgtcc  | gaggaacatg | gataccaaag  | gagtgggaag | aaatgcagag  | agaagtttga | 60   |
| gaatctgtac  | aaatactata | ggaagactaa  | agaaggcaaa | gccggaagac  | aagacggaaa | 120  |
| acattacaga  | tttttcgggc | agctcgaagc  | gctatacggg | gattctaata  | acttggtttc | 180  |
| ttgtcccaat  | cataacacgc | agttcatgag  | cagtgtctct | catggtttcc  | atactcaaaa | 240  |
| ccctatgaac  | gttactacaa | caacgtccaa  | catccataac | gttgatagtg  | ttcatggttt | 300  |
| tcataaaagc  | cttagtcttt | ctaacaacta  | caactcctcc | gagcttgagc  | tgatgacttc | 360  |
| ctcttcggaa  | gggaatgatt | ctagtagtag  | aaggaaaaag | aggagttgga  | aagcgaagat | 420  |
| aaaggagttc  | attgatacga | acatgaaaag  | gttgatagag | aggcaagatg  | tttggtttga | 480  |
| gaagttgaca  | aaggttattg | aagacaaaaga | ggaacaacgg | atgatgaaag  | aagaggaatg | 540  |
| gaggaagatt  | gaagctgcaa | ggattgataa  | agagcatttg | ttttgggcta  | aagagagggc | 600  |
| gaggatggaa  | gctagggatg | ttgcgggtgat | tgaggcattg | caatacttga  | caggaaagcc | 660  |
| attgataaag  | ccgctgtgtt | catccccgga  | agagaggaca | aatggtaata  | atgagatccg | 720  |
| aaacaatagt  | gagacacaga | atgagaatgg  | aagcgatcaa | acgatgacta  | acaatgtttg | 780  |
| tgtaaagga   | agtagtagct | gctggggatg  | gcaagagatt | ttaaagctta  | tggagataag | 840  |
| aacgagcatg  | gactcgacct | ttcaagagat  | attaggaggg | tgctcggatg  | agtttctatg | 900  |
| ggaggaaaatc | gcagcgaagt | tgattcagtt  | agggtttgat | cagagaagtg  | ccttattatg | 960  |
| caaggaaaag  | tgggaatgga | taagcaatgg  | aatgaggaaa | gaaaagaagc  | aaatcaacaa | 1020 |
| gaaaagaaag  | gataattcgt | ccagctcgcg  | cgtgtactac | ccgagaaaacg | aagaaaatcc | 1080 |
| aatctacaat  | aatcgagaaa | gtggatataa  | tgataatgat | ccgcatcaaa  | tcaacgaaca | 1140 |
| aggcaatgta  | ggttcttcaa | catcaaacgc  | aaacgcaaac | gcaaacctaa  | ccactggaaa | 1200 |
| tccgancggt  | gcaatggctg | ctactacaaa  | ctgcttcccg | ttcttcatgg  | gagatggaga | 1260 |
| tcagaatttg  |            |             |            |             |            |      |



(2) INFORMATION FOR SEQ ID NO:859:

(A) LENGTH: 422 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..422

(D) OTHER INFORMATION: / Ceres Seq. ID 1594697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

[illegible]

Pro Arg Asn Glu Glu Asn Pro Ile Tyr Asn Asn Arg Glu Ser Gly Tyr  
355 360 365  
Asn Asp Asn Asp Pro His Gln Ile Asn Glu Gln Gly Asn Val Gly Ser  
370 375 380  
Ser Thr Ser Asn Ala Asn Ala Asn Ala Asn Leu Thr Thr Gly Asn Pro  
385 390 395 400  
Xaa Gly Ala Met Ala Ala Thr Thr Asn Cys Phe Pro Phe Phe Met Gly  
405 410 415  
Asp Gly Asp Gln Asn Leu  
420

(2) INFORMATION FOR SEQ ID NO:860:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 355 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..355

(D) OTHER INFORMATION: / Ceres Seq. ID 1594698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

Met Ser Ser Ala Leu His Gly Phe His Thr Gln Asn Pro Met Asn Val  
1 5 10 15  
Thr Thr Thr Thr Ser Asn Ile His Asn Val Asp Ser Val His Gly Phe  
20 25 30  
His Gln Ser Leu Ser Leu Ser Asn Asn Tyr Asn Ser Ser Glu Leu Glu  
35 40 45  
Leu Met Thr Ser Ser Ser Glu Gly Asn Asp Ser Ser Ser Arg Arg Lys  
50 55 60  
Lys Arg Ser Trp Lys Ala Lys Ile Lys Glu Phe Ile Asp Thr Asn Met  
65 70 75 80  
Lys Arg Leu Ile Glu Arg Gln Asp Val Trp Leu Glu Lys Leu Thr Lys  
85 90 95  
Val Ile Glu Asp Lys Glu Glu Gln Arg Met Met Lys Glu Glu Glu Trp  
100 105 110  
Arg Lys Ile Glu Ala Ala Arg Ile Asp Lys Glu His Leu Phe Trp Ala  
115 120 125  
Lys Glu Arg Ala Arg Met Glu Ala Arg Asp Val Ala Val Ile Glu Ala  
130 135 140  
Leu Gln Tyr Leu Thr Gly Lys Pro Leu Ile Lys Pro Leu Cys Ser Ser  
145 150 155 160  
Pro Glu Glu Arg Thr Asn Gly Asn Asn Glu Ile Arg Asn Asn Ser Glu  
165 170 175  
Thr Gln Asn Glu Asn Gly Ser Asp Gln Thr Met Thr Asn Asn Val Cys  
180 185 190  
Val Lys Gly Ser Ser Ser Cys Trp Gly Glu Gln Glu Ile Leu Lys Leu  
195 200 205  
Met Glu Ile Arg Thr Ser Met Asp Ser Thr Phe Gln Glu Ile Leu Gly  
210 215 220  
Gly Cys Ser Asp Glu Phe Leu Trp Glu Glu Ile Ala Ala Lys Leu Ile  
225 230 235 240  
Gln Leu Gly Phe Asp Gln Arg Ser Ala Leu Leu Cys Lys Glu Lys Trp  
245 250 255  
Glu Trp Ile Ser Asn Gly Met Arg Lys Glu Lys Lys Gln Ile Asn Lys  
260 265 270  
Lys Arg Lys Asp Asn Ser Ser Ser Cys Gly Val Tyr Tyr Pro Arg Asn  
275 280 285  
Glu Glu Asn Pro Ile Tyr Asn Asn Arg Glu Ser Gly Tyr Asn Asp Asn  
290 295 300  
Asp Pro His Gln Ile Asn Glu Gln Gly Asn Val Gly Ser Ser Thr Ser

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(2) INFORMATION FOR SEO ID NO:861:

(A) LENGTH: 1185 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (q

(ix) FEATURE:

(A) NAME

(B) LOCATION: 1

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:861:

[illegible]

(2) INFORMATION FOR SEQ ID NO:862:

(A) LENGTH: 394 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAM

(B) LOCATION: 1..394

(D) OTHER INFORMATION: / Ceres Seq. ID 1594700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

| (a1) SEQUENCE DESCRIPTION: SEQ ID NO:1002 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile                                       | Met | Ser | Glu | Glu | His | Gly | Tyr | Gln | Arg | Ser | Gly | Lys | Lys | Cys | Arg |
| 1                                         |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu                                       | Lys | Phe | Glu | Asn | Leu | Tyr | Lys | Tyr | Tyr | Arg | Lys | Thr | Lys | Glu | Gly |
|                                           |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys                                       | Ala | Gly | Arg | Gln | Asp | Gly | Lys | His | Tyr | Arg | Phe | Phe | Arg | Gln | Leu |
|                                           |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu                                       | Ala | Leu | Tyr | Gly | Asp | Ser | Asn | Asn | Leu | Val | Ser | Cys | Pro | Asn | His |
|                                           | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn                                       | Thr | Gln | Phe | Met | Ser | Ser | Ala | Leu | His | Gly | Phe | His | Thr | Gln | Asn |
| 65                                        |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |





Lys Arg Ser Trp Lys Ala Lys Ile Lys Glu Phe Ile Asp Thr Asn Met  
65 70 75 80  
Lys Arg Leu Ile Glu Arg Gln Asp Val Trp Leu Glu Lys Leu Thr Lys  
85 90 95  
Val Ile Glu Asp Lys Glu Glu Gln Arg Met Met Lys Glu Glu Glu Trp  
100 105 110  
Arg Lys Ile Glu Ala Ala Arg Ile Asp Lys Glu His Leu Phe Trp Ala  
115 120 125  
Lys Glu Arg Ala Arg Met Glu Ala Arg Asp Val Ala Val Ile Glu Ala  
130 135 140  
Leu Gln Tyr Leu Thr Gly Lys Pro Leu Ile Lys Pro Leu Cys Ser Ser  
145 150 155 160  
Pro Glu Glu Arg Thr Asn Gly Ser Ser Ser Cys Trp Gly Glu Gln Glu  
165 170 175  
Ile Leu Lys Leu Met Glu Ile Arg Thr Ser Met Asp Ser Thr Phe Gln  
180 185 190  
Glu Ile Leu Gly Gly Cys Ser Asp Glu Phe Leu Trp Glu Glu Ile Ala  
195 200 205  
Ala Lys Leu Ile Gln Leu Gly Phe Asp Gln Arg Ser Ala Leu Leu Cys  
210 215 220  
Lys Glu Lys Trp Glu Trp Ile Ser Asn Gly Met Arg Lys Glu Lys Lys  
225 230 235 240  
Gln Ile Asn Lys Lys Arg Lys Asp Asn Ser Ser Ser Cys Gly Val Tyr  
245 250 255  
Tyr Pro Arg Asn Glu Glu Asn Pro Ile Tyr Asn Asn Arg Glu Ser Gly  
260 265 270  
Tyr Asn Asp Asn Asp Pro His Gln Ile Asn Glu Gln Gly Asn Val Gly  
275 280 285  
Ser Ser Thr Ser Asn Ala Asn Ala Asn Ala Asn Leu Thr Thr Gly Asn  
290 295 300  
Pro Xaa Gly Ala Met Ala Ala Thr Thr Asn Cys Phe Pro Phe Phe Met  
305 310 315 320  
Gly Asp Gly Asp Gln Asn  
325

(2) INFORMATION FOR SEQ ID NO:865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..512
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| gcacgcgaga gctgggaatt atgatgacta caacaatttt ggtgaccctt atcatgcttc | 60  |
| ttatctggca gacgaacatc atagtttcga actggttttc ttctcatccg tnttgttcaa | 120 |
| gtgtggctga tggaagtggg ataactcttg tttttgctac aattatgttt ctcataatgt | 180 |
| ttgtttggaa ctacgggagt aaactgaagt atgaaactga agtccagaaa aagctaccaa | 240 |
| tggacctact acgagaactn ggcagtaacc ttgggacaat tagangcacc cgtatgtccc | 300 |
| tgttccaagt gtgcctcaga ncgagagatt tcttttcaga cgtgtatgcc caagaagcta | 360 |
| tcantttatt ccgctgtgta gccaggatg gatacaaaga tgtgcggaag gaaagtcacc  | 420 |
| aggcgtttga gcagatactg attgagagtc tagaaaaatt tatacgtnag gaagcacag  | 480 |
| agcgtgcact tgnagtgac ggagnaccat aa                                |     |

(2) INFORMATION FOR SEQ ID NO:866:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

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(2) INFORMATION FOR SEQ ID NO:868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

Met Thr Thr Thr Ile Leu Val Thr Leu Ile Met Leu Leu Ile Trp Gln  
1 5 10 15  
Thr Asn Ile Ile Val Ser Asn Trp Phe Ser Ser His Pro Xaa Cys Ser  
20 25 30  
Ser Val Ala Asp Gly Ser Trp Ile Ile Leu Val Phe Ala Thr Ile Met  
35 40 45  
Phe Leu Ile Met Phe Val Trp Asn Tyr Gly Ser Lys Leu Lys Tyr Glu  
50 55 60  
Thr Glu Val Gln Lys Lys Leu Pro Met Asp Leu Leu Arg Glu Xaa Gly  
65 70 75 80  
Ser Asn Leu Gly Thr Ile Arg Xaa Thr Arg Met Ser Leu Phe Gln Val  
85 90 95  
Cys Leu Arg Xaa Arg Asp Phe Phe Ser Asp Val Tyr Ala Gln Glu Ala  
100 105 110  
Ile Xaa Leu Phe Arg Cys Val Ala Arg Tyr Gly Tyr Lys Asp Val Arg  
115 120 125  
Lys Glu Ser His Gln Ala Phe Glu Gln Ile Leu Ile Glu Ser Leu Glu  
130 135 140  
Lys Phe Ile Arg Xaa Glu Ala Gln Glu Arg Ala Leu Xaa Ser Asp Gly  
145 150 155 160  
Xaa Pro

(2) INFORMATION FOR SEQ ID NO:869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1614 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1614
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

atgtctcgct cccagaacga ggagtttcaa caatggtgga acaagcaacg agataggaac 60  
aatcacgacg ttcttttacgc cggcgacgat gaagcattcc tcaccgttga aatccgtact 120  
ccggccaccg ttgaccctga taaggatcgg atccggactc gtaccgttcg tcagctctct 180  
cgtctctacc tctcaagtt caagcaactc gcatcttctt tctcttgat cggtaactct 240  
ttcttttacc ttggatttct cgttgntgtt gtgcttcttc tctgtttcga gcttgccgct 300  
tatttcaagg gatggcactt cacacctccc tctgttgccg ccgccgaggt cgctgtggag 360  
gtggttttacg cttggttggt ggagatcagg gcatcttacc ttgcgccacc gcttcagagc 420  
ttgaccaatg tatgtatagt tctcttcttg attcaatcgg ttgaccgtct ggtgcttggt 480  
cttgatgct tctggatcaa gctccgccgt attaagcctg ttgcatctat ggagtaaccg 540  
actaaattgg ttggagaggg agttagattg gaagattatc caatggtgat tggtcagatt 600  
ccaatgtgca atgaaaagga gggtttaccaa caatctattg gagctgtgtg tatgcttgac 660  
tggtccaagg aaagaatgct agttcagggt cttgatgact ccagtgaatt ggatgttcan 720  
cagcttataa aagcggaagt acaaaaatgg caacaaaggg gtgtccggat agtatttcca 780  
nccacctgcg gatttcttga agaaaactgt gcctcanttt taaggagaat gttaggtgac 840

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|                         |                     |                     |     |     |
|-------------------------|---------------------|---------------------|-----|-----|
| 130                     |                     | 135                 |     | 140 |
| Glu Asp Cys Gly Gly Trp | Leu Glu Arg Thr Thr | Val Glu Asp Met Asp |     |     |
| 145                     | 150                 | 155                 | 160 |     |
| Ile Ala Val Arg Ala His | Xaa Cys Gly Trp Lys | Phe Ile Tyr Leu Asn |     |     |
|                         | 165                 | 170                 | 175 |     |
| Asp Val Lys Val Ser Ala | Ala Lys Lys Ala Asn | Met Xaa Xaa Xaa Ser |     |     |
|                         | 180                 | 185                 | 190 |     |
| Xaa Ser Cys Tyr Gly Ser | Leu Xaa Xaa Pro Phe | Tyr Ser Phe Thr Leu |     |     |
|                         | 195                 | 200                 | 205 |     |
| Phe Cys Val Ile Leu Pro | Leu Thr Met Phe Phe | Pro Glu Ala Asn Leu |     |     |
|                         | 210                 | 215                 | 220 |     |
| Pro Ser Trp Val Val Cys | Tyr Ile Pro Gly Ile | Met Ser Ile Leu Asn |     |     |
| 225                     | 230                 | 235                 | 240 |     |
| Ile Ile Pro Ala Pro Arg | Ser Phe Pro Phe Ile | Val Pro Tyr Leu Leu |     |     |
|                         | 245                 | 250                 | 255 |     |
| Phe Glu Asn Xaa Xaa Xaa | Xaa Xaa Lys Phe Gly | Ala Met Ile Ser Glu |     |     |
|                         | 260                 | 265                 | 270 |     |
| Ser Gly Ser Leu Val Glu | Ser Thr Thr Ile Gln | Arg Ser Ser Ser Asp |     |     |
|                         | 275                 | 280                 | 285 |     |
| Ser Gly Leu Thr Glu Leu | Ser Lys Leu Gly Ala | Ala Lys Lys Ala Gly |     |     |
|                         | 290                 | 295                 | 300 |     |
| Lys Thr Lys Arg Asn Arg | Leu Tyr Arg Thr Glu | Ile Ala Leu Ala Phe |     |     |
| 305                     | 310                 | 315                 | 320 |     |
| Ile Leu Leu Ala Ala Ser | Val Arg Ser Leu Leu | Ser Ala Gln Gly Ile |     |     |
|                         | 325                 | 330                 | 335 |     |
| His Phe Tyr Phe Leu Leu | Phe Gln Gly Ile Thr | Phe Val Ile Val Gly |     |     |
|                         | 340                 | 345                 | 350 |     |
| Leu Asp Leu Ile Gly Glu | Gln Val Ser         |                     |     |     |
|                         | 355                 | 360                 |     |     |

(2) INFORMATION FOR SEQ ID NO:872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..291
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atggggnnngg gtaaccagtt ggaagaagtc agctacatca acaacaacca gggtggctac | 60  |
| aaaggataca acaacttcaa aaccaacaat cccaacctct cctaccgtag caccancgtt  | 120 |
| gctaattctc aggatcaggt gtatcccggt caacaacaac aaggtcagaa caaacctttt  | 180 |
| gttctctaca accaaggttt cgttontaaag cagcaatttn tggggaacta ccagccgcca | 240 |
| ccaccacctg gatttgcaca tcagcaaaaac catggtccta nttgtactg a           |     |

(2) INFORMATION FOR SEQ ID NO:873:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Gly Xaa Gly Asn Gln Leu Glu Glu Val Ser Tyr Ile Asn Asn Asn |  |
| 1 5 10 15                                                       |  |
| Gln Gly Gly Tyr Lys Gly Tyr Asn Asn Phe Lys Thr Asn Asn Pro Asn |  |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 20  |     | 25  |     | 30  |     |     |     |     |     |     |     |     |     |     |
| Leu | Ser | Tyr | Arg | Ser | Thr | Xaa | Val | Ala | Asn | Pro | Gln | Asp | Gln | Val | Tyr |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Val | Gln | Gln | Gln | Gln | Gly | Gln | Asn | Lys | Pro | Phe | Val | Leu | Tyr | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Gly | Phe | Val | Xaa | Lys | Gln | Gln | Phe | Xaa | Gly | Asn | Tyr | Gln | Pro | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Pro | Pro | Gly | Phe | Ala | His | Gln | Gln | Asn | His | Gly | Pro | Xaa | Cys | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

(2) INFORMATION FOR SEQ ID NO:874:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1594763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Xaa | Xaa | Val | Thr | Ser | Trp | Lys | Lys | Ser | Ala | Thr | Ser | Thr | Thr | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Val | Ala | Thr | Lys | Asp | Thr | Thr | Thr | Ser | Lys | Pro | Thr | Ile | Pro | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Pro | Thr | Val | Ala | Pro | Xaa | Leu | Leu | Ile | Leu | Arg | Ile | Arg | Cys | Ile |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Pro | Cys | Asn | Asn | Asn | Lys | Val | Arg | Thr | Asn | Leu | Leu | Phe | Ser | Thr | Thr |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Lys | Val | Ser | Phe | Xaa | Ser | Ser | Asn | Xaa | Trp | Gly | Thr | Thr | Ser | Arg | His |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| His | His | Leu | Asp | Leu | His | Ile | Ser | Lys | Thr | Met | Val | Leu | Xaa | Ala | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

(2) INFORMATION FOR SEQ ID NO:875:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..276

(D) OTHER INFORMATION: / Ceres Seq. ID 1594807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| atgtcgccaa | ccttcaggac | caagttctacg | ctcagcagca | gcagcagcag | aaccaanccc | 60  |
| aaaccgtttg | ttccttacaa | ccaaaaccaa  | gggttcattc | caaagcagca | gtttcaagga | 120 |
| ggatatcaac | aacagcagcc | acaacctggt  | ttcacaccac | aacaacaaca | tgcacctacg | 180 |
| cctcagaatn | cagacataat | gattatgctc  | cagcagctca | ttcaagnaca | agnccacagg | 240 |
| agcaatggaa | atcngctaag | aagttgtgtg  | aagtaa     |            |            |     |

(2) INFORMATION FOR SEQ ID NO:876:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

DOCKET# 08662960

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1594808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

Met Ser Pro Thr Leu Arg Thr Lys Ser Thr Leu Ser Ser Ser Ser Ser  
1 5 10 15  
Arg Thr Xaa Pro Lys Pro Phe Val Pro Tyr Asn Gln Asn Gln Gly Phe  
20 25 30  
Ile Pro Lys Gln Gln Phe Gln Gly Gly Tyr Gln Gln Gln Gln Pro Gln  
35 40 45  
Pro Gly Phe Thr Pro Gln Gln Gln His Ala Pro Thr Pro Gln Asn Xaa  
50 55 60  
Asp Ile Met Ile Met Leu Gln Gln Leu Ile Gln Xaa Gln Xaa His Arg  
65 70 75 80  
Ser Asn Gly Asn Xaa Leu Arg Ser Cys Val Lys  
85 90

(2) INFORMATION FOR SEQ ID NO:877:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1594810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

Val Ala Asn Pro Gln Asp Gln Val Tyr Ala Gln Gln Gln Gln Gln  
1 5 10 15  
Asn Gln Xaa Gln Thr Val Cys Ser Leu Gln Pro Lys Pro Arg Val His  
20 25 30  
Ser Lys Ala Ala Val Ser Arg Arg Ile Ser Thr Thr Ala Ala Thr Thr  
35 40 45  
Trp Phe His Thr Thr Thr Thr Cys Thr Tyr Ala Ser Glu Xaa Arg  
50 55 60  
His Asn Asp Tyr Ala Pro Ala Ala His Ser Xaa Thr Xaa Pro Gln Glu  
65 70 75 80  
Gln Trp Lys Xaa Ala Lys Lys Leu Cys Glu Val  
85 90

(2) INFORMATION FOR SEQ ID NO:878:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 606 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..606

(D) OTHER INFORMATION: / Ceres Seq. ID 1594833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

atgtttccgt ccaatttctg ggaaagaaac agtctccgct tctctcctca actccgagat 60  
ttctcactgt tatcgccatg gctccaccta aaccggagg caaagctaaa aaagttgtng 120  
ggagttatca aacttgcttt agaggcggn aaagcaactc cggcaccacc gggttggtccg 180  
gcgcttggtt ctaaggaggt taacattatg gctttttgca aggattataa tgcaagaact 240  
gctgataaag ctggttatat cattcctgtt gaaatcactg tcttcgatat tggatgatgtg 300  
tttcgagntt ttaggataag agcttcacgt ttattctcaa gacccgcct gcttcgggttt 360  
tggttgcttaa agctgcaggt ttatctctgt agaattgatc ttaagggatc aaaagatcca 420  
cagcaagata aagttggggg gataacaata gaccagctac gcacaattgc agcagagaag 480

00000000 00000000

ctacccgacc tgaactgcac gaccattgaa tccgctatga gaatcattgc aggaactnca 540  
gctaacatgg ggatagacat tgaccctccg attcttgaac ccaaaaagaa agcagtttta 600  
ttgtaa

(2) INFORMATION FOR SEQ ID NO:879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..201

(D) OTHER INFORMATION: / Ceres Seq. ID 1594834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

Met Phe Pro Ser Asn Phe Trp Glu Arg Asn Ser Leu Arg Phe Ser Pro  
1 5 10 15  
Gln Leu Arg Asp Phe Ser Leu Leu Ser Pro Trp Leu His Leu Asn Pro  
20 25 30  
Glu Ala Lys Leu Lys Lys Leu Xaa Gly Val Ile Lys Leu Ala Leu Glu  
35 40 45  
Ala Xaa Lys Ala Thr Pro Ala Pro Pro Val Gly Pro Ala Leu Gly Ser  
50 55 60  
Lys Gly Val Asn Ile Met Ala Phe Cys Lys Asp Tyr Asn Ala Arg Thr  
65 70 75 80  
Ala Asp Lys Ala Gly Tyr Ile Ile Pro Val Glu Ile Thr Val Phe Asp  
85 90 95  
Ile Gly Asp Val Phe Arg Xaa Phe Arg Ile Arg Ala Ser Arg Leu Phe  
100 105 110  
Ser Arg Pro Arg Leu Leu Arg Phe Cys Cys Leu Lys Leu Gln Val Tyr  
115 120 125  
Leu Cys Arg Ile Asp Leu Lys Gly Ser Lys Asp Pro Gln Gln Asp Lys  
130 135 140  
Val Gly Val Ile Thr Ile Asp Gln Leu Arg Thr Ile Ala Ala Glu Lys  
145 150 155 160  
Leu Pro Asp Leu Asn Cys Thr Thr Ile Glu Ser Ala Met Arg Ile Ile  
165 170 175  
Ala Gly Thr Xaa Ala Asn Met Gly Ile Asp Ile Asp Pro Pro Ile Leu  
180 185 190  
Glu Pro Lys Lys Lys Ala Val Leu Leu  
195 200

(2) INFORMATION FOR SEQ ID NO:880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1594836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

Met Ala Phe Cys Lys Asp Tyr Asn Ala Arg Thr Ala Asp Lys Ala Gly  
1 5 10 15  
Tyr Ile Ile Pro Val Glu Ile Thr Val Phe Asp Ile Gly Asp Val Phe  
20 25 30  
Arg Xaa Phe Arg Ile Arg Ala Ser Arg Leu Phe Ser Arg Pro Arg Leu  
35 40 45  
Leu Arg Phe Cys Cys Leu Lys Leu Gln Val Tyr Leu Cys Arg Ile Asp  
50 55 60

09669980-10300





- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..367
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gcatttatcg aaatcggaga tttggtcgtc gaaaatggga aagcagccgg tgaaattgaa  | 60  |
| ggcgggtggtt tacgcgttat cgncgtttca gcagaagatc atgacgggtc tttggaagga | 120 |
| tcttcggag aagattcacc acaaggtctc agagaattgg atcagtacta ttctcctcgt   | 180 |
| cgctcctgtc gtcggaacct actcgtatgc tcagtacttc aaagaacaag agaagctgga  | 240 |
| gcacaggttc taagcatgga gatatcttga ttccaattct ttctcattt ttcattctcc   | 300 |
| aaaatgnggt ttattgacag ttttgtaatn nnnnnnncca aaatagaagc ggaaaagttg  | 360 |
| cttcctt                                                            |     |

(2) INFORMATION FOR SEQ ID NO:884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ala Phe Ile Glu Ile Gly Asp Leu Val Glu Asn Gly Lys Ala Ala     |  |
| 1 5 10 15                                                       |  |
| Gly Glu Ile Glu Gly Gly Gly Leu Arg Val Ile Xaa Val Ser Ala Glu |  |
| 20 25 30                                                        |  |
| Asp His Asp Gly Ser Leu Glu Gly Ser Ser Gly Glu Asp Ser Pro Gln |  |
| 35 40 45                                                        |  |
| Gly Leu Arg Glu Leu Asp Gln Tyr Tyr Ser Pro Arg Arg Ser Cys Arg |  |
| 50 55 60                                                        |  |
| Arg Asn Leu Leu Val Cys Ser Val Leu Gln Arg Thr Arg Glu Ala Gly |  |
| 65 70 75 80                                                     |  |
| Ala Gln Val Leu Ser Met Glu Ile Ser                             |  |
| 85                                                              |  |

(2) INFORMATION FOR SEQ ID NO:885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| His Leu Ser Lys Ser Glu Ile Trp Ser Ser Lys Met Gly Lys Gln Pro |  |
| 1 5 10 15                                                       |  |
| Val Lys Leu Lys Ala Val Val Tyr Ala Leu Ser Xaa Phe Gln Gln Lys |  |
| 20 25 30                                                        |  |
| Ile Met Thr Gly Leu Trp Lys Asp Leu Pro Glu Lys Ile His His Lys |  |
| 35 40 45                                                        |  |
| Val Ser Glu Asn Trp Ile Ser Thr Ile Leu Leu Val Ala Pro Val Val |  |
| 50 55 60                                                        |  |

00000000-1000

Gly Thr Tyr Ser Tyr Ala Gln Tyr Phe Lys Glu Gln Glu Lys Leu Glu  
65 70 75 80  
His Arg Phe

(2) INFORMATION FOR SEQ ID NO:886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

Met Gly Lys Gln Pro Val Lys Leu Lys Ala Val Val Tyr Ala Leu Ser  
1 5 10 15  
Xaa Phe Gln Gln Lys Ile Met Thr Gly Leu Trp Lys Asp Leu Pro Glu  
20 25 30  
Lys Ile His Lys Val Ser Glu Asn Trp Ile Ser Thr Ile Leu Leu  
35 40 45  
Val Ala Pro Val Val Gly Thr Tyr Ser Tyr Ala Gln Tyr Phe Lys Glu  
50 55 60  
Gln Glu Lys Leu Glu His Arg Phe  
65 70

(2) INFORMATION FOR SEQ ID NO:887:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..585
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:

agatatagga gaagggagca gcagtaaggt ggtgatgcat aggtcggtga catgccggcg 60  
gagtgaagccc tggaactcca acgactccaa ccactccgac gacgccacgt aaggataacg 120  
tgtggaggag cgtctttaat ccgggaagca acctcgccac tagagccatc ggtccaacat 180  
ctttgataaa cccacccatc caaattctcc ctccgtctac gactgggtgt acagcgggtga 240  
ctcaaggagt cagcaccgtt aggatgggtcc gatggagtgt gacatgcggg tgatgtaaat 300  
atggtgacct gatcttccgc caccttactt tgtttttttt atattgtttt tgtgtacttt 360  
atcagagtgg ataaagtgc ggggaatggt tttcttttgt acaaaaaact gtcttcccac 420  
ctaagcaatg tgtgttagtt tctgttttgg gctgtgtttt gcaagttttt gtatttcaga 480  
ggtttagtgt agttgcaagt ggcggttgga tctttcacta tcttggttga ttttgatgat 540  
ggttgatgct tttgctttta tgttaaataa ataagcatatc ttttg

(2) INFORMATION FOR SEQ ID NO:888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: / Ceres Seq. ID 1594972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

Asp Ile Gly Glu Gly Ser Ser Ser Lys Val Val Met His Arg Ser Leu

00000000 00000000

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:101:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atcaataaac | acaaaaacaa | aagaagaaga | gaataaacaa | aagaagaaaa | aaaaaagtat | 60  |
| taaaacaaaa | tcaataaaaa | gagaataaaa | aatgggtggg | tctcacaaag | caagcggagt | 120 |





Met Ala Thr Gln Asp Ser Gln Gly Ile Lys Leu Phe Gly Lys Thr Ile  
1 5 10 15  
Thr Phe Asn Ala Asn Ile Thr Gln Thr Ile Lys Lys Glu Glu Gln Gln  
20 25 30  
Gln Gln Gln Gln Pro Glu Leu Gln Ala Thr Thr Ala Val Arg Ser Pro  
35 40 45  
Ser Ser Asp Leu Thr Ala Glu Lys Arg Pro Asp Lys Ile Ile Pro Cys  
50 55 60  
Pro Arg Cys Lys Ser Met Glu Thr Lys Phe Cys Tyr Phe Asn Asn Tyr  
65 70 75 80  
Asn Val Asn Gln Pro Arg His Phe Cys Lys Gly Cys Gln Arg Tyr Trp  
85 90 95  
Thr Ala Gly Gly Ala Leu Arg Asn Val Pro Val Gly Ala Gly Arg Arg  
100 105 110  
Lys Ser Lys Pro Pro Gly Arg Val Gly Gly Phe Ala Glu Leu Leu Gly  
115 120 125  
Ala Ala Thr Gly Ala Val Asp Gln Val Glu Leu Asp Ala Leu Leu Val  
130 135 140  
Glu Glu Trp Arg Ala Ala Thr Ala Ser His Gly Gly Phe Arg His Asp  
145 150 155 160  
Phe Pro Val Lys Arg Leu Arg Cys Phe Pro Leu Phe Asn Ile His Asp  
165 170 175  
Arg Met Arg Glu Trp Glu Arg Lys Arg Lys Arg Glu Arg Glu Arg Glu  
180 185 190  
Arg Ala Tyr Lys His Leu Tyr Ile Phe Ile Ser Asn Phe Phe Val Thr  
195 200 205  
Phe Gly  
210

(2) INFORMATION FOR SEQ ID NO:896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141

(D) OTHER INFORMATION: / Ceres Seq. ID 1595565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

Met Glu Thr Lys Phe Cys Tyr Phe Asn Asn Tyr Asn Val Asn Gln Pro  
1 5 10 15  
Arg His Phe Cys Lys Gly Cys Gln Arg Tyr Trp Thr Ala Gly Gly Ala  
20 25 30  
Leu Arg Asn Val Pro Val Gly Ala Gly Arg Arg Lys Ser Lys Pro Pro  
35 40 45  
Gly Arg Val Gly Gly Phe Ala Glu Leu Leu Gly Ala Ala Thr Gly Ala  
50 55 60  
Val Asp Gln Val Glu Leu Asp Ala Leu Leu Val Glu Glu Trp Arg Ala  
65 70 75 80  
Ala Thr Ala Ser His Gly Gly Phe Arg His Asp Phe Pro Val Lys Arg  
85 90 95  
Leu Arg Cys Phe Pro Leu Phe Asn Ile His Asp Arg Met Arg Glu Trp  
100 105 110  
Glu Arg Lys Arg Lys Arg Glu Arg Glu Arg Glu Arg Ala Tyr Lys His  
115 120 125  
Leu Tyr Ile Phe Ile Ser Asn Phe Phe Val Thr Phe Gly  
130 135 140

(2) INFORMATION FOR SEQ ID NO:897:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1358 base pairs

0563980-10300

| (X1) SEQUENCE DESCRIPTION: S21 (1300000) |             |             |             |             |             |      |
|------------------------------------------|-------------|-------------|-------------|-------------|-------------|------|
| ctaactctctc                              | tgttcatcttt | tttctctctt  | tatttataaa  | tttatctgca  | tagtactctc  | 60   |
| tgaatctata                               | tcttcaaaaa  | aaaaaaacgt  | ccaagatcaa  | atcaagaaac  | ccattaaaaa  | 120  |
| aaaaaatcag                               | gttttggttt  | cagttttaag  | ggtttaaggt  | ttcttgggga  | agaaacgatg  | 180  |
| gagacttttt                               | gtgggtttca  | aaaggaggaa  | gagcagatgg  | atttacctcc  | tgggttcagg  | 240  |
| tttcatccaa                               | cagatgaaga  | actcataact  | cactatctcc  | ataagaaggt  | tcttgacacc  | 300  |
| agcttctcag                               | ctaaagctat  | cgggtgaagtt | gatttaaaaa  | aatcagagcc  | atggggagtta | 360  |
| ccatggatgg                               | caaaaatggg  | tgagaaagaa  | tggatttttt  | ttgtgtggag  | agacagaaaag | 420  |
| tatcccaccg                               | gtttaagaac  | taacccgagca | actgaagccg  | gtttattggaa | ggcgaccggg  | 480  |
| aaggataaag                               | agatataccg  | aggcaaatca  | cttgttggga  | tgaagaagac  | acttgttttc  | 540  |
| tatagaggaa                               | gagctcctaa  | aggtcagaaa  | accaactggg  | tgatgcatga  | gtacaggcct  | 600  |
| gaaaaaaaatt                              | ctctgcccat  | aacttgccga  | aaacgcgcaa  | gaatgaatgg  | gtgatatgca  | 660  |
| gggtgttcca                               | aaagagtgt   | ggagggaaga  | agatcccgat  | ttcgagtcta  | atccgcattc  | 720  |
| gttcaactcg                               | aacgcagctt  | aacccttcgc  | ttttgcctc   | tttaaccgat  | tcttcgcctt  | 780  |
| acaacgataa                               | aaccaaaaca  | gaaccggtct  | acgtgacctg  | ctctccaac   | caaacggatc  | 840  |
| aaaaccgaag                               | aaccacactc  | aattgtttca  | gcagccctgt  | tcttaactcg  | atccaagccg  | 900  |
| acattttttc                               | caggattcca  | ctctatcaaa  | ctcagtcctt  | ccaggtttct  | atgaatctac  | 960  |
| agagcccggt                               | tctcacgcaa  | gaacactcag  | ttctacatgc  | tatgatcgag  | aacaacagaa  | 1020 |
| gacaaagtct                               | caaaacgatg  | agtgtctcac  | aagaaaccgg  | agtttcaact  | gacatgaaca  | 1080 |
| ctgatatctc                               | atcggatttt  | gaatttggtg  | agaggcggtt  | tgattctcaa  | gaagatccgt  | 1140 |
| cttcctctac                               | tggaccgggt  | gatcttgaac  | ctttctggaa  | ttactgaaga  | tgattcaaga  | 1200 |
| ttctcatgtc                               | cattaatttta | ctgtggtgtg  | ttaaagtttg  | tataggctat  | tgatcatatac | 1260 |
| tctcatatac                               | acttcaacta  | tatatattata | caattttaaag | aaacttaaaa  | atatgatttg  | 1320 |
| atatatgact                               | aaagtattat  | aatacaattt  | tgtacccc    |             |             |      |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

| Table 1. Demographic characteristics of the study population |             |
|--------------------------------------------------------------|-------------|
| Age (years)                                                  | Mean (SD)   |
| Male                                                         | 55.2 (10.5) |
| Female                                                       | 56.8 (11.2) |
| Marital status                                               |             |
| Married                                                      | 78.5%       |
| Single                                                       | 12.3%       |
| Divorced                                                     | 8.2%        |
| Widowed                                                      | 1.0%        |
| Education level                                              |             |
| High school or above                                         | 65.4%       |
| Below high school                                            | 34.6%       |
| Occupation                                                   |             |
| White collar                                                 | 45.2%       |
| Blue collar                                                  | 54.8%       |
| Income (USD/month)                                           |             |
| < 1000                                                       | 15.3%       |
| 1000-2000                                                    | 32.1%       |
| 2000-3000                                                    | 28.7%       |
| > 3000                                                       | 23.9%       |
| Health insurance                                             |             |
| Yes                                                          | 89.5%       |
| No                                                           | 10.5%       |
| Smoking status                                               |             |
| Smoker                                                       | 28.4%       |
| Non-smoker                                                   | 71.6%       |
| Alcohol consumption                                          |             |
| Regular                                                      | 12.7%       |
| Occasional                                                   | 35.2%       |
| Never                                                        | 52.1%       |
| Comorbidities                                                |             |
| Hypertension                                                 | 42.3%       |
| Diabetes                                                     | 18.9%       |
| Cholesterol                                                  | 31.5%       |
| Obesity                                                      | 25.7%       |
| Family history of heart disease                              | 38.6%       |



130 135 140  
Ser Leu Pro Ile Thr Cys Arg Lys Pro Gln Arg Met Asn Gly  
145 150 155

(2) INFORMATION FOR SEQ ID NO:899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

Met Asp Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu  
1 5 10 15  
Ile Thr His Tyr Leu His Lys Lys Val Leu Asp Thr Ser Phe Ser Ala  
20 25 30  
Lys Ala Ile Gly Glu Val Asp Leu Asn Lys Ser Glu Pro Trp Glu Leu  
35 40 45  
Pro Trp Met Ala Lys Met Gly Glu Lys Glu Trp Tyr Phe Phe Cys Val  
50 55 60  
Arg Asp Arg Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr Glu  
65 70 75 80  
Ala Gly Tyr Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Tyr Arg Gly  
85 90 95  
Lys Ser Leu Val Gly Met Lys Lys Thr Leu Val Phe Tyr Arg Gly Arg  
100 105 110  
Ala Pro Lys Gly Gln Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu  
115 120 125  
Glu Lys Asn Ser Leu Pro Ile Thr Cys Arg Lys Pro Gln Arg Met Asn  
130 135 140  
Gly  
145

(2) INFORMATION FOR SEQ ID NO:900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

Met Ala Lys Met Gly Glu Lys Glu Trp Tyr Phe Phe Cys Val Arg Asp  
1 5 10 15  
Arg Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr Glu Ala Gly  
20 25 30  
Tyr Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Tyr Arg Gly Lys Ser  
35 40 45  
Leu Val Gly Met Lys Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala Pro  
50 55 60  
Lys Gly Gln Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu Glu Lys  
65 70 75 80  
Asn Ser Leu Pro Ile Thr Cys Arg Lys Pro Gln Arg Met Asn Gly  
85 90 95

(2) INFORMATION FOR SEQ ID NO:901:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1425 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1425  
(D) OTHER INFORMATION: / Ceres Seq. ID 1595585  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:

aatggcgctcg acgaagcccg attccgcaat caaccttgaa gaagaggctg aaggcgacgg 60  
tgtagccgta gacgatccga ttttcatacc ggagaccacg aacttactcg tccggtactc 120  
gccattcgac gacagggaca tcgattgcaa tccttatttc cctttcacag gcccgatttc 180  
agattctgga tcaggttctt actcggattc tgagcccgat cccaacagct gtcccatcga 240  
tttcttcgat cgagattctt ccgatgttga cgtggctgag tacttggaat caggagggct 300  
gaccgcccgt gattataata tttggggctt ttatgacccc aaggaagacg aggaagagga 360  
ggagatagtt ttggggactt ccgggtcggg tctgcaaccg ggtgattcag gggagcaagg 420  
gcttcgagtg accggtatcg attcagattc cgattgtgaa gatggcgtgt ttgattttat 480  
ctctgaggat agtagcggga ataggggaaa tgattcgggt cgggtcagag ttggtacggg 540  
tcttcctcct gtgtgggac atctcttcgg agagggaacc gtgttgctg atgaagaatg 600  
ggagagggtg cagaacgcga ttaactggac agcttttagt ggaccggaag atgaggacga 660  
agaagatgaa ttgtcttcac tatcaaggga tgatgaagaa gaagatcatg aactggactg 720  
gcagggtttg ttaactgtta acaatgttgt taattatata gaacaagctg aaggaatcat 780  
gctaaatcct gatgatatcg atccggatta ttacctgtat ctatctggtt tggatgaatt 840  
tgatgaaaat cagagtggac attatgatgc tgatgctatt cttgggcaaa tgtttgatga 900  
cgagactgga atcaggggaa atcctccagc agccaaaagt gtaattcagg atcttccggt 960  
tgtggagctt gctgtggaag agttagacaa agggaacaat gtttgtgcgg tatgcaaaga 1020  
tgaaatgtta gtggaggaga aagtaaggag gcttccttgt agtcatttct atcatggaga 1080  
gtgtatcata ccttggttg ggataaggaa tacttgcccg gtttgtcgg atgagctgcc 1140  
tactgatgat cttgagtatg aaagacataa gagctcagaa aggggcgata ctggtttggc 1200  
aaggaacgtg ttgccgggta gatatagtta attgaatatt tgaagtgatc tattcttcaa 1260  
gttaatatgac atgggttcag aggcaagatc cttgaaccac tttgtttwtg gtaagcactt 1320  
atcgtgaatg tgataatgtt taagttgtat atattccttt tgttttgtga aataaatcat 1380  
gttaaaccttt gaaccottat cttgaagtgt ttgtgaagtt aattc

(2) INFORMATION FOR SEQ ID NO:902:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 409 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..409  
(D) OTHER INFORMATION: / Ceres Seq. ID 1595586  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

Met Ala Ser Thr Lys Pro Asp Ser Ala Ile Asn Leu Glu Glu Glu Ala  
1 5 10 15  
Glu Gly Asp Gly Val Ala Val Asp Asp Pro Ile Phe Ile Pro Glu Thr  
20 25 30  
Thr Asn Leu Leu Val Arg Tyr Ser Pro Phe Asp Asp Arg Asp Ile Asp  
35 40 45  
Cys Asn Pro Tyr Phe Pro Phe Thr Gly Pro Ile Ser Asp Ser Gly Ser  
50 55 60  
Gly Ser Tyr Ser Asp Ser Glu Pro Asp Pro Asn Ser Cys Pro Ile Asp  
65 70 75 80  
Phe Phe Asp Arg Asp Ser Ser Asp Val Asp Val Ala Glu Tyr Leu Glu  
85 90 95  
Ser Gly Gly Leu Thr Ala Gly Asp Tyr Asn Ile Trp Gly Phe Tyr Asp  
100 105 110  
Pro Lys Glu Asp Glu Glu Glu Glu Glu Ile Val Leu Gly Thr Ser Gly

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|                         |                         |                     |
|-------------------------|-------------------------|---------------------|
| 115                     | 120                     | 125                 |
| Ser Asp Leu Gln Pro Gly | Asp Ser Gly Glu Gln Gly | Leu Arg Val Thr     |
| 130                     | 135                     | 140                 |
| Gly Ile Asp Ser Asp Ser | Asp Cys Glu Asp Gly     | Val Phe Asp Phe Ile |
| 145                     | 150                     | 155                 |
| Ser Glu Asp Ser Ser Gly | Asn Arg Gly Asn Asp Ser | Gly Arg Val Glu     |
| 165                     | 170                     | 175                 |
| Val Gly Thr Gly Leu Pro | Pro Val Trp Asp His Leu | Phe Gly Glu Gly     |
| 180                     | 185                     | 190                 |
| Thr Val Leu Ala Asp Glu | Glu Trp Glu Glu Val Gln | Asn Ala Ile Asn     |
| 195                     | 200                     | 205                 |
| Trp Thr Ala Phe Ser Gly | Pro Glu Asp Glu Asp Glu | Glu Asp Glu Leu     |
| 210                     | 215                     | 220                 |
| Ser Ser Leu Ser Arg Asp | Asp Glu Glu Glu Asp His | Glu Leu Asp Trp     |
| 225                     | 230                     | 235                 |
| Gln Val Leu Leu Thr Val | Asn Asn Val Val Asn Tyr | Ile Glu Gln Ala     |
| 245                     | 250                     | 255                 |
| Glu Gly Ile Met Leu Asn | Pro Asp Asp Ile Asp Pro | Asp Tyr Tyr Leu     |
| 260                     | 265                     | 270                 |
| Tyr Leu Ser Gly Leu Asp | Glu Phe Asp Glu Asn Gln | Ser Gly His Tyr     |
| 275                     | 280                     | 285                 |
| Asp Ala Asp Ala Ile Leu | Gly Gln Met Phe Asp Asp | Glu Thr Gly Ile     |
| 290                     | 295                     | 300                 |
| Arg Gly Asn Pro Pro Ala | Ala Lys Ser Val Ile Gln | Asp Leu Pro Val     |
| 305                     | 310                     | 315                 |
| Val Glu Leu Ala Val Glu | Glu Leu Asp Lys Gly Asn | Asn Val Cys Ala     |
| 325                     | 330                     | 335                 |
| Val Cys Lys Asp Glu Met | Leu Val Glu Lys Val Arg | Arg Leu Pro         |
| 340                     | 345                     | 350                 |
| Cys Ser His Phe Tyr His | Gly Glu Cys Ile Ile Pro | Trp Leu Gly Ile     |
| 355                     | 360                     | 365                 |
| Arg Asn Thr Cys Pro Val | Cys Arg Tyr Glu Leu Pro | Thr Asp Asp Leu     |
| 370                     | 375                     | 380                 |
| Glu Tyr Glu Arg His Lys | Ser Ser Glu Arg Gly Asp | Thr Gly Leu Ala     |
| 385                     | 390                     | 395                 |
| Arg Asn Val Leu Pro Gly | Arg Tyr Ser             |                     |
| 405                     |                         |                     |

(2) INFORMATION FOR SEQ ID NO:903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2547
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

|                                                                      |     |
|----------------------------------------------------------------------|-----|
| atcatcactc tctctctttc gttacagttc cctaatacaag caagttgcat atcaogagct   | 60  |
| ctctcaactc tcaatccaat ccattctctct ctacgcatt ttcgtttggt tcttcgtttt    | 120 |
| cctctttttca gattctttctc ttcgattctt cacattgata aaacttgctc atgggtggttg | 180 |
| ttacgtcgat tgagtagatg aagttcaccg gaaaatcaaa tttgacggct acattaccog    | 240 |
| caactgtccc aaatatcagg gctattcata gaaggagagc gcgaaaaccg agcttcactc    | 300 |
| gtcaacgaag atctggcgtg tctgtcagga ggctaagcag gccggagact cctcaattga    | 360 |
| aatcgaaggt ggaggatcaa aacattgagc gatgcggcgg gtttgaagat gatgataacg    | 420 |
| aggatgatga ttgtaataag atgcgttggt aggaacggag taggagtgtg cggcctgata    | 480 |
| ctgttaggaa acttgctgcc ggagtgtggc aattgcgagt cccggatgcg gtttctagcg    | 540 |
| gcgagataa gaggagcaag gatcggttac ggtttcagga aactgctggt cctgctggaa     | 600 |
| acttgggtcc tctgttttat tatcaccacc atgatgacaa acattctggc tttcaaagca    | 660 |
| acaattcaag aaacaagcat agtggtattct tgtgtaagca tgagccttca gttccatttc   | 720 |

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cccactgcgc gatggaggga gcaacaaaat gggatcccat ctgcttggat acaaggggat 780  
atgtacacca aatctatagc aacgtgaagt ggaataatca acaagtgaat gatgtttcat 840  
tagctttctt tattgaattg aaacttcagg aagctcgtgc ttgcatcaag gatcttgaga 900  
gtgagaagcg atctcagaaa aagaagcttg agcagttcct gaagaaagtt agcgaggaga 960  
gggcagcttg gcgagcaga gagcatgaga aggtccgagc aattattgat gacatgaaag 1020  
ctgacatgaa ccaggaaaag aagactcgtc agagattaga aatcgtcaat tcaaaattag 1080  
tcaatgagct tgcagattca aagttagcag taaagcgta catgcatgat taccaacagg 1140  
aaaggaaggc aagagaattg atcgaagaag tttgtgatga actggcaaag gaaatagaag 1200  
aagataaagc tgagattgaa gcattgaaga gcgaatccat gaatctcaga gaggaagtag 1260  
acgatgaaag aagaatgctg cagatggctg aggtttggcg tgaggaacgt gtccagatga 1320  
agcttattga tgccaaagta acactcgaga acaagtattc acaaatgaac aaactcgtag 1380  
gagatatgga agccttcttc agttcaagaa atactacagg tgtgaaagag gtgaaagttg 1440  
cggattgtt aagagaaaat gctgcatcag ttgataatat ccaagaaatc aaggaattta 1500  
catatgaacc ctcaaagccg gacgatatcc tcatgttgtt tgaacaaatg aacatgggtg 1560  
aaaaccagga tagagaaatc gagcaatatg ttgcctacag tccggtcagc cacgcttcaa 1620  
aagctcacac ggtaagtcca gatgtcaatt tgattaacaa agggagacat tcgaatgctt 1680  
tactgatca gaatggtgaa tttgaagaag atgacagtgg ctgggaaact gtgagccatt 1740  
ctgaagaaca cggatccagt tactctccag atgagagcat ccctaattat agcaacactc 1800  
atcaccgtaa cagcaatgta tcgatgaatg gaacagagta tgaaaagact ctattgagag 1860  
aaataaaaga agtgtgctcg gttccaagac gacaatccaa aaagttaccg tcaatggcaa 1920  
agctctggag ttcattagaa ggtatgaatc gaagggtatc aaacgcgaga aaatcaacca 1980  
ttggatggtt ttcaccagag acaggctcaa acaaaggcgg attcaacaca ttggacctgg 2040  
ttggtcaatg gagctcatca ccagactcgg ctaatgctaa tttaaatcga ggagggagga 2100  
aagggtgcat agagtggcca agaggtgcac ataagaacag cttgaagaca aagctcatag 2160  
aagcacaaat cgagagccaa aaggttcagc tgaagcatgt ccttgagcat aagatctagg 2220  
ccacaacata ttccaaaact accagtccca ggccatacta ctattctttg tggctgagca 2280  
gcagaactgg atttttgatc ccgttctcct gctattgcca ttgtcgcgtg atctagcgt 2340  
ggtcaagcca atcaacgtgg tatattttcg ttagctaaaa gcaaaatgat ctttgtgatt 2400  
gattgctgtc gtagcttggc tgggctagct acagccactt aattaccaac aacctcttg 2460  
ttgctaggaa cagaggcaca atggtgtttt cctttaatga atttgttcc tctttagtcc 2520  
aacgctaggt caataatatt ttctttt

(2) INFORMATION FOR SEQ ID NO:904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 673 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..673
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

Met Lys Phe Thr Gly Lys Ser Asn Leu Thr Ala Thr Leu Pro Ala Thr  
1 5 10 15  
Val Pro Asn Ile Arg Ala Ile His Arg Arg Arg Ala Arg Lys Pro Ser  
20 25 30  
Phe Thr Arg Gln Arg Arg Ser Gly Val Ser Val Arg Arg Leu Ser Arg  
35 40 45  
Pro Glu Thr Pro Gln Leu Lys Ser Lys Val Glu Asp Gln Asn Ile Glu  
50 55 60  
Arg Cys Gly Gly Val Glu Asp Asp Asp Asn Glu Asp Asp Asp Cys Asn  
65 70 75 80  
Lys Met Arg Cys Gln Glu Arg Ser Arg Ser Val Arg Pro Asp Thr Val  
85 90 95  
Arg Lys Leu Ala Ala Gly Val Trp Gln Leu Arg Val Pro Asp Ala Val  
100 105 110  
Ser Ser Gly Gly Asp Lys Arg Ser Lys Asp Arg Leu Arg Phe Gln Glu  
115 120 125  
Thr Ala Gly Pro Ala Gly Asn Leu Gly Pro Leu Phe Tyr Tyr His His  
130 135 140



[illegible]

Leu Arg Glu Thr Ala Ala Ser Val Asp Asn Ile Gln Glu Ile Lys Glu  
340 345 350  
Phe Thr Tyr Glu Pro Ser Lys Pro Asp Asp Ile Leu Met Leu Phe Glu  
355 360 365  
Gln Met Asn Met Gly Glu Asn Gln Asp Arg Glu Ile Glu Gln Tyr Val  
370 375 380  
Ala Tyr Ser Pro Val Ser His Ala Ser Lys Ala His Thr Val Ser Pro  
385 390 395 400  
Asp Val Asn Leu Ile Asn Lys Gly Arg His Ser Asn Ala Phe Thr Asp  
405 410 415  
Gln Asn Gly Glu Phe Glu Glu Asp Asp Ser Gly Trp Glu Thr Val Ser  
420 425 430  
His Ser Glu Glu His Gly Ser Ser Tyr Ser Pro Asp Glu Ser Ile Pro  
435 440 445  
Asn Ile Ser Asn Thr His His Arg Asn Ser Asn Val Ser Met Asn Gly  
450 455 460  
Thr Glu Tyr Glu Lys Thr Leu Leu Arg Glu Ile Lys Glu Val Cys Ser  
465 470 475 480  
Val Pro Arg Arg Gln Ser Lys Lys Leu Pro Ser Met Ala Lys Leu Trp  
485 490 495  
Ser Ser Leu Glu Gly Met Asn Gly Arg Val Ser Asn Ala Arg Lys Ser  
500 505 510  
Thr Met Glu Met Val Ser Pro Glu Thr Gly Ser Asn Lys Gly Gly Phe  
515 520 525  
Asn Thr Leu Asp Leu Val Gly Gln Trp Ser Ser Ser Pro Asp Ser Ala  
530 535 540  
Asn Ala Asn Leu Asn Arg Gly Gly Arg Lys Gly Cys Ile Glu Trp Pro  
545 550 555 560  
Arg Gly Ala His Lys Asn Ser Leu Lys Thr Lys Leu Ile Glu Ala Gln  
565 570 575  
Ile Glu Ser Gln Lys Val Gln Leu Lys His Val Leu Glu His Lys Ile  
580 585 590

(2) INFORMATION FOR SEQ ID NO:906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..495

(D) OTHER INFORMATION: / Ceres Seq. ID 1595602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

Met Glu Gly Ala Thr Lys Trp Asp Pro Ile Cys Leu Asp Thr Arg Asp  
1 5 10 15  
Asp Val His Gln Ile Tyr Ser Asn Val Lys Trp Asn Asn Gln Gln Val  
20 25 30  
Asn Asp Val Ser Leu Ala Ser Ser Ile Glu Leu Lys Leu Gln Glu Ala  
35 40 45  
Arg Ala Cys Ile Lys Asp Leu Glu Ser Glu Lys Arg Ser Gln Lys Lys  
50 55 60  
Lys Leu Glu Gln Phe Leu Lys Lys Val Ser Glu Glu Arg Ala Ala Trp  
65 70 75 80  
Arg Ser Arg Glu His Glu Lys Val Arg Ala Ile Ile Asp Asp Met Lys  
85 90 95  
Ala Asp Met Asn Gln Glu Lys Lys Thr Arg Gln Arg Leu Glu Ile Val  
100 105 110  
Asn Ser Lys Leu Val Asn Glu Leu Ala Asp Ser Lys Leu Ala Val Lys

036659960

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 115                                                             | 120 | 125 |
| Arg Tyr Met His Asp Tyr Gln Gln Glu Arg Lys Ala Arg Glu Leu Ile |     |     |
| 130                                                             | 135 | 140 |
| Glu Glu Val Cys Asp Glu Leu Ala Lys Glu Ile Glu Glu Asp Lys Ala |     |     |
| 145                                                             | 150 | 155 |
| Glu Ile Glu Ala Leu Lys Ser Glu Ser Met Asn Leu Arg Glu Glu Val |     |     |
| 165                                                             | 170 | 175 |
| Asp Asp Glu Arg Arg Met Leu Gln Met Ala Glu Val Trp Arg Glu Glu |     |     |
| 180                                                             | 185 | 190 |
| Arg Val Gln Met Lys Leu Ile Asp Ala Lys Val Thr Leu Glu Asn Lys |     |     |
| 195                                                             | 200 | 205 |
| Tyr Ser Gln Met Asn Lys Leu Val Gly Asp Met Glu Ala Phe Leu Ser |     |     |
| 210                                                             | 215 | 220 |
| Ser Arg Asn Thr Thr Gly Val Lys Glu Val Lys Val Ala Glu Leu Leu |     |     |
| 225                                                             | 230 | 235 |
| Arg Glu Thr Ala Ala Ser Val Asp Asn Ile Gln Glu Ile Lys Glu Phe |     |     |
| 245                                                             | 250 | 255 |
| Thr Tyr Glu Pro Ser Lys Pro Asp Asp Ile Leu Met Leu Phe Glu Gln |     |     |
| 260                                                             | 265 | 270 |
| Met Asn Met Gly Glu Asn Gln Asp Arg Glu Ile Glu Gln Tyr Val Ala |     |     |
| 275                                                             | 280 | 285 |
| Tyr Ser Pro Val Ser His Ala Ser Lys Ala His Thr Val Ser Pro Asp |     |     |
| 290                                                             | 295 | 300 |
| Val Asn Leu Ile Asn Lys Gly Arg His Ser Asn Ala Phe Thr Asp Gln |     |     |
| 305                                                             | 310 | 315 |
| Asn Gly Glu Phe Glu Glu Asp Asp Ser Gly Trp Glu Thr Val Ser His |     |     |
| 325                                                             | 330 | 335 |
| Ser Glu Glu His Gly Ser Ser Tyr Ser Pro Asp Glu Ser Ile Pro Asn |     |     |
| 340                                                             | 345 | 350 |
| Ile Ser Asn Thr His His Arg Asn Ser Asn Val Ser Met Asn Gly Thr |     |     |
| 355                                                             | 360 | 365 |
| Glu Tyr Glu Lys Thr Leu Leu Arg Glu Ile Lys Glu Val Cys Ser Val |     |     |
| 370                                                             | 375 | 380 |
| Pro Arg Arg Gln Ser Lys Lys Leu Pro Ser Met Ala Lys Leu Trp Ser |     |     |
| 385                                                             | 390 | 395 |
| Ser Leu Glu Gly Met Asn Gly Arg Val Ser Asn Ala Arg Lys Ser Thr |     |     |
| 405                                                             | 410 | 415 |
| Met Glu Met Val Ser Pro Glu Thr Gly Ser Asn Lys Gly Gly Phe Asn |     |     |
| 420                                                             | 425 | 430 |
| Thr Leu Asp Leu Val Gly Gln Trp Ser Ser Ser Pro Asp Ser Ala Asn |     |     |
| 435                                                             | 440 | 445 |
| Ala Asn Leu Asn Arg Gly Gly Arg Lys Gly Cys Ile Glu Trp Pro Arg |     |     |
| 450                                                             | 455 | 460 |
| Gly Ala His Lys Asn Ser Leu Lys Thr Lys Leu Ile Glu Ala Gln Ile |     |     |
| 465                                                             | 470 | 475 |
| Glu Ser Gln Lys Val Gln Leu Lys His Val Leu Glu His Lys Ile     |     |     |
| 485                                                             | 490 | 495 |

(2) INFORMATION FOR SEQ ID NO:907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1835 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1835
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595607

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| acacaaccaa agcgttttaga aaaaaaacag cgataaaacc gaaacatcaa gcaaacaaaa | 60  |
| aaaaagagga gaattttttt tttttgtttt cgttttcaaa aacaaaatct ttgaatttta  | 120 |

09689900 101300



tggcaacccg tcttctccga acaaacttta tccggcgatc ttaccgttta cccgctttta 180  
gcccgggtggg tcctccacc gtgactgctt ccaccgcggt cgtcccggag attctctcct 240  
ttggacaaca agcaccggaa ccacctcttc accaccctaaa acccactgag caatctcacg 300  
atgggtctcga tctctccgat caagcccgtc ttttctctc taccocaacc tctgatctcc 360  
tccgttccac cgcggtgttg catgcggcgg cgataggtcc tatggctgac ctagggacgt 420  
gggtcatgag ctctaaactt atggacgctt ccgtgacgcg tggcatgggt ttagggcttg 480  
tgaaaagtac gttttatgac catttttgcg ccggtgaaga tgccgacgca gccgctgagc 540  
gcgtgagaag cgtttatgaa gctaccggtc ttaaagggat gcttgtctat ggcgctgaac 600  
acgccgatga cgctgtatct tgtgatgata acatgcaaca attcattcga accattgaag 660  
ctgccaatc tttaccaaca tctcacttta gctcagtggg tgtgaagata actgccattt 720  
gtccaattag tcttctgaaa cgagtgcggt atctgcttcg gtgggaatac aaaagtccaa 780  
acttcaaact ctcatggaag ctcaaactgt ttccggtttt ctccgattcg agtctctct 840  
accacacaaa ctcaagaacc gaaccgttaa ccgcggaaga agaacgggag ctogaagcag 900  
ctcatggaag gattcaagaa atctgtagga aatgccaaga gtccaatgta ccattgttga 960  
ttgatgcgga agacacaatc ctccaacccg cgatcgatta catggcttat tcatcggcga 1020  
tcatgttcaa tgctgacaaa gaccgaccaa tctgtttaca cacgattcag gcgtacttga 1080  
gagacgccgg tgagagactg catttgccag taaaaatgc tgagaaagag aatgttccta 1140  
tggggttcaa gttggtgaga ggggcttaca tgtctagcga agctagcttg gcggattccc 1200  
tggtgtgcaa gtcgccagtc cagcacacaa ttcaggatac tcaactcttg tacaatgatt 1260  
gtatgacatt cctgatggag aaagcatcaa acggttctgg tttcgggtgc gttctcga 1320  
cacataacgc tgattcgggg agacttgctg cgaggaaagc gagtgaacct gggattgata 1380  
aacagaaccg gaagatagag tttgcacagc tatatggtat gtcggatgca ttgtCcttcg 1440  
gtttaaagag agccgggttc aatgttagca agtacatgcc gtttggaccc gtcgcaaccg 1500  
ctataccgta tcttctccga cgcgcttatg agaaccgggg aatgatggcc accggagctc 1560  
atgaccgtca actcatgagg atggaactta agaggagatt aatcgccggg attgcgtaaa 1620  
gagagagtat ggagccatta aatgaaattg ggaaatgtag atgaataaat ttcttctatg 1680  
tagtttaaga aattgaaaac aaaaaattat aatataagaa atggagtagg taagaacatt 1740  
tctgtgggt aatatTTTT catgaggggac tatgttttta ctatcaatat atcattcaca 1800  
aatgtatatt caccttatca ataaaaatgt ttttt

(2) INFORMATION FOR SEQ ID NO:908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..538
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Thr | Lys | Ala | Phe | Arg | Lys | Lys | Thr | Ala | Ile | Lys | Pro | Lys | His | Gln |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Asn | Lys | Lys | Lys | Glu | Glu | Asn | Phe | Phe | Phe | Leu | Phe | Ser | Phe | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Thr | Lys | Ser | Leu | Asn | Phe | Met | Ala | Thr | Arg | Leu | Leu | Arg | Thr | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Ile | Arg | Arg | Ser | Tyr | Arg | Leu | Pro | Ala | Phe | Ser | Pro | Val | Gly | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Thr | Val | Thr | Ala | Ser | Thr | Ala | Val | Val | Pro | Glu | Ile | Leu | Ser | Phe |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Gln | Gln | Ala | Pro | Glu | Pro | Pro | Leu | His | His | Pro | Lys | Pro | Thr | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gln | Ser | His | Asp | Gly | Leu | Asp | Leu | Ser | Asp | Gln | Ala | Arg | Leu | Phe | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Thr | Pro | Thr | Ser | Asp | Leu | Leu | Arg | Ser | Thr | Ala | Val | Leu | His | Ala |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ala | Ala | Ile | Gly | Pro | Met | Val | Asp | Leu | Gly | Thr | Trp | Val | Met | Ser | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Leu | Met | Asp | Ala | Ser | Val | Thr | Arg | Gly | Met | Val | Leu | Gly | Leu | Val |
|     | 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |

Lys Ser Thr Phe Tyr Asp His Phe Cys Ala Gly Glu Asp Ala Asp Ala  
165 170 175  
Ala Ala Glu Arg Val Arg Ser Val Tyr Glu Ala Thr Gly Leu Lys Gly  
180 185 190  
Met Leu Val Tyr Gly Val Glu His Ala Asp Asp Ala Val Ser Cys Asp  
195 200 205  
Asp Asn Met Gln Gln Phe Ile Arg Thr Ile Glu Ala Ala Lys Ser Leu  
210 215 220  
Pro Thr Ser His Phe Ser Ser Val Val Val Lys Ile Thr Ala Ile Cys  
225 230 235 240  
Pro Ile Ser Leu Leu Lys Arg Val Ser Asp Leu Leu Arg Trp Glu Tyr  
245 250 255  
Lys Ser Pro Asn Phe Lys Leu Ser Trp Lys Leu Lys Ser Phe Pro Val  
260 265 270  
Phe Ser Asp Ser Ser Pro Leu Tyr His Thr Asn Ser Glu Pro Glu Pro  
275 280 285  
Leu Thr Ala Glu Glu Glu Arg Glu Leu Glu Ala Ala His Gly Arg Ile  
290 295 300  
Gln Glu Ile Cys Arg Lys Cys Gln Glu Ser Asn Val Pro Leu Leu Ile  
305 310 315 320  
Asp Ala Glu Asp Thr Ile Leu Gln Pro Ala Ile Asp Tyr Met Ala Tyr  
325 330 335  
Ser Ser Ala Ile Met Phe Asn Ala Asp Lys Asp Arg Pro Ile Val Tyr  
340 345 350  
Asn Thr Ile Gln Ala Tyr Leu Arg Asp Ala Gly Glu Arg Leu His Leu  
355 360 365  
Ala Val Gln Asn Ala Glu Lys Glu Asn Val Pro Met Gly Phe Lys Leu  
370 375 380  
Val Arg Gly Ala Tyr Met Ser Ser Glu Ala Ser Leu Ala Asp Ser Leu  
385 390 395 400  
Gly Cys Lys Ser Pro Val His Asp Thr Ile Gln Asp Thr His Ser Cys  
405 410 415  
Tyr Asn Asp Cys Met Thr Phe Leu Met Glu Lys Ala Ser Asn Gly Ser  
420 425 430  
Gly Phe Gly Val Val Leu Ala Thr His Asn Ala Asp Ser Gly Arg Leu  
435 440 445  
Ala Ser Arg Lys Ala Ser Asp Leu Gly Ile Asp Lys Gln Asn Gly Lys  
450 455 460  
Ile Glu Phe Ala Gln Leu Tyr Gly Met Ser Asp Ala Leu Ser Phe Gly  
465 470 475 480  
Leu Lys Arg Ala Gly Phe Asn Val Ser Lys Tyr Met Pro Phe Gly Pro  
485 490 495  
Val Ala Thr Ala Ile Pro Tyr Leu Leu Arg Arg Ala Tyr Glu Asn Arg  
500 505 510  
Gly Met Met Ala Thr Gly Ala His Asp Arg Gln Leu Met Arg Met Glu  
515 520 525  
Leu Lys Arg Arg Leu Ile Ala Gly Ile Ala  
530 535

(2) INFORMATION FOR SEQ ID NO:909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..499
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

Met Ala Thr Arg Leu Leu Arg Thr Asn Phe Ile Arg Arg Ser Tyr Arg

096998010300





370 375 380  
Gly Ala His Asp Arg Gln Leu Met Arg Met Glu Leu Lys Arg Arg Leu  
385 390 395 400  
Ile Ala Gly Ile Ala  
405

(2) INFORMATION FOR SEQ ID NO:911:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..590
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| aactcatcac | ttacttaaca  | tactaagaga | gttattagaa | cttgcaaaaa  | atggcttcca | 60  |
| aggctttgat | tctgttaggt  | ctcttctcag | ttcttctcgt | cgtctccgaa  | gtgtctgccg | 120 |
| caaggcaatc | gggcatgggtg | aagccagaga | gtgaggaaac | tgtgcaacct  | gaaggttatg | 180 |
| gcggtggcca | cggaggacat  | ggtggtcacg | gagggggagg | aggccacgga  | catggaggac | 240 |
| acaacggagg | agggggccac  | ggacttgacg | gatacggagg | agggtggagga | cactatggag | 300 |
| gaggtggagg | acactacgga  | ggaggtggag | gacactacgg | aggaggtgga  | ggacactacg | 360 |
| gaggaggtgg | tggaggacac  | ggaggtggag | gacactacgg | agggtggtgga | ggaggatacg | 420 |
| gaggtggagg | aggacaccac  | ggaggaggag | gccacgggct | aaacgaacct  | gttcagacta | 480 |
| agccgggtgt | ttaaaactat  | ataatatctt | cactaccatg | catgattgca  | tatatatata | 540 |
| taogcttatg | tattatctat  | atgcctataa | ataaaccatg | gtgagtttgt  |            |     |

(2) INFORMATION FOR SEQ ID NO:912:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Lys | Ala | Leu | Ile | Leu | Leu | Gly | Leu | Phe | Ser | Val | Leu | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Val | Ser | Glu | Val | Ser | Ala | Ala | Arg | Gln | Ser | Gly | Met | Val | Lys | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ser | Glu | Glu | Thr | Val | Gln | Pro | Glu | Gly | Tyr | Gly | Gly | Gly | His | Gly |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Gly | His | Gly | Gly | Gly | His | Gly | Gly | Gly | Gly | His | Gly | His | Gly | Gly | His |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Asn | Gly | Gly | Gly | Gly | His | Gly | Leu | Asp | Gly | Tyr | Gly | Gly | Gly | Gly | Gly |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| His | Tyr | Gly | Gly | Gly | Gly | Gly | His | Tyr | Gly | Gly | Gly | Gly | Gly | His | Tyr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Gly | Gly | Gly | Gly | His | Tyr | Gly | Gly | Gly | Gly | Gly | Gly | His | Gly | Gly |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Gly | Gly | His | Tyr | Gly | Gly | Gly | Gly | Gly | Tyr | Gly | Gly | Gly | Gly | Gly | Gly |
|     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |     |
| His | His | Gly | Gly | Gly | Gly | His | Gly | Leu | Asn | Glu | Pro | Val | Gln | Thr | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Gly | Val |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:913:

(i) SEQUENCE CHARACTERISTICS:

DOCKET# 08669960

- (A) LENGTH: 119 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..119  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1595621  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr Gly  
1                   5                   10                   15  
Gly Gly His Gly Gly His Gly Gly His Gly Gly Gly Gly Gly His Gly  
                  20                   25                   30  
His Gly Gly His Asn Gly Gly Gly Gly His Gly Leu Asp Gly Tyr Gly  
                  35                   40                   45  
Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly  
50                   55                   60  
Gly Gly His Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly  
65                   70                   75                   80  
Gly His Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly Gly Tyr Gly  
                  85                   90                   95  
Gly Gly Gly Gly His His Gly Gly Gly Gly His Gly Leu Asn Glu Pro  
                  100                   105                   110  
Val Gln Thr Lys Pro Gly Val  
                  115

- (2) INFORMATION FOR SEQ ID NO:914:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 94 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..94  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1595622  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

Met Ala Val Ala Thr Glu Asp Met Val Thr Glu Gly Glu Glu Ala  
1                   5                   10                   15  
Thr Asp Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp  
                  20                   25                   30  
Thr Glu Glu Val Glu Asp Thr Met Glu Glu Val Glu Asp Thr Thr Glu  
                  35                   40                   45  
Glu Val Glu Asp Thr Thr Glu Glu Val Glu Asp Thr Thr Glu Glu Val  
50                   55                   60  
Val Glu Asp Thr Glu Val Glu Asp Thr Thr Glu Val Val Glu Glu Asp  
65                   70                   75                   80  
Thr Glu Val Glu Glu Asp Thr Thr Glu Glu Glu Ala Thr Gly  
                  85                   90

- (2) INFORMATION FOR SEQ ID NO:915:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 1460 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..1460  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1595623

005553950







- (A) LENGTH: 1440 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1440  
(D) OTHER INFORMATION: / Ceres Seq. ID 1595627  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

|             |            |            |             |            |             |      |
|-------------|------------|------------|-------------|------------|-------------|------|
| attgggattt  | catttagata | attttttttt | gggtottgat  | ctaagttttg | ttcttttctaa | 60   |
| tttggttaagg | caagaagagc | attaagagca | ttaaaagggt  | tagtgaagct | acaagcattg  | 120  |
| gtgaggggac  | ataatgtgag | aaagcaagct | aaaatgacat  | taaggtgtat | gcaagctctg  | 180  |
| gttcgagtc   | agtctcgtgt | gcttgaccaa | cgcaaacgct  | tgtctcatga | cggtagtcgc  | 240  |
| aaatccgcgt  | tcagtgactc | tcacgctgtt | tttgaatctc  | gctatcttca | agatttgtca  | 300  |
| gatcgacaat  | ccatgtcaag | agaaggaagc | agcgccgcgg  | aagattggga | tgaccgacca  | 360  |
| cacacgatag  | acgcagtga  | agtgatgcta | caacggagac  | gggacacagc | attgagacat  | 420  |
| gacaagacta  | atttgtcaca | agctttctct | caaaagatgt  | ggaggacggt | tggtaaccaa  | 480  |
| tccacggaag  | gacaccacga | ggtagaactt | gaagaggaaa  | ggccaaaatg | gcttgaccgg  | 540  |
| tggtatggcta | ctagaccgtg | ggataaacga | gctagttagta | gagcttcggt | tgaccaaagg  | 600  |
| gtttcagtta  | aaaccgttga | aatcgacact | tctcagcctt  | actcaagaac | aggagcagga  | 660  |
| agcccgagtc  | gtggccaaag | acctagtctc | ccatcaagaa  | ctagccacca | ttaccaatcc  | 720  |
| cgcaataatt  | tctcagccac | tccatctccg | gctaagtcta  | gaccaatact | tattcgggtca | 780  |
| gctagtccac  | ggtgccagag | agacccgagg | gaagaccgtg  | accgagcagc | ttatagttat  | 840  |
| acatcaaaca  | caccaagctt | gagatccaat | tatagtttca  | cagctaggag | tggtatgtaca | 900  |
| ttagtaccac  | aatggttaat | aatgcatcat | tgttgccctaa | ttacatggcg | agtacagagt  | 960  |
| cagctaaagc  | gaggatccgg | tctcatagt  | caccgaggca  | acggccctca | acthccgaga  | 1020 |
| gggaccgtgc  | ggstttAgst | AcaaGAaacg | rytctsgtat  | ccggtaccac | cgccagcgga  | 1080 |
| gtatgaggac  | aataatagct | taaggagtcc | aagctttaag  | agtgtggctg | gttcacattt  | 1140 |
| tggtggaatg  | ttagagcagc | aatcgaatta | ctcttcattg  | tgcaactgag | ctaacggtgt  | 1200 |
| tgagatctct  | ccagcttcta | ctagtgaact | taggaattgg  | cttagatgat | tggtgggtgat | 1260 |
| gccaaatcaa  | ctgtcaagat | ctttcatcat | cctccaggaa  | aagaacgttt | taaaatttta  | 1320 |
| tattccagaa  | gaaaacaaac | acttttatat | tgtgtcgttg  | aggttgattt | gtgtttggaa  | 1380 |
| gataagttaa  | ttgacctatt | gatctgtaac | ttcataagat  | tttgaaacgt | tagaagattc  | 1440 |

(2) INFORMATION FOR SEQ ID NO:920:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 294 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..294  
(D) OTHER INFORMATION: / Ceres Seq. ID 1595628  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Leu | Arg | Cys | Met | Gln | Ala | Leu | Val | Arg | Val | Gln | Ser | Arg | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Asp | Gln | Arg | Lys | Arg | Leu | Ser | His | Asp | Gly | Ser | Arg | Lys | Ser | Ala |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Phe | Ser | Asp | Ser | His | Ala | Val | Phe | Glu | Ser | Arg | Tyr | Leu | Gln | Asp | Leu |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Ser | Asp | Arg | Gln | Ser | Met | Ser | Arg | Glu | Gly | Ser | Ser | Ala | Ala | Glu | Asp |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |
| Trp | Asp | Asp | Arg | Pro | His | Thr | Ile | Asp | Ala | Val | Lys | Val | Met | Leu | Gln |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |
| Arg | Arg | Arg | Asp | Thr | Ala | Leu | Arg | His | Asp | Lys | Thr | Asn | Leu | Ser | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Phe | Ser | Gln | Lys | Met | Trp | Arg | Thr | Val | Gly | Asn | Gln | Ser | Thr | Glu |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |





- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1481  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1595678  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

gcgttacact acaactctct atctctctct cttcttttct gctcattttt gggtaattct 60  
tctggtttta tgttcttggt cctattactg actcacaatc agccaacgca aatcttttct 120  
tgaccatttt taatagattc tcttagtcac ttgttggtatt tcaaagcaa agttgacctc 180  
atcttcttct tcttcgaggt tttatacaag ttactccata aaccttcgag cttccagcaa 240  
ctttggcttc tctgttggtga attattgctt attatattct caacacgaaa tcaaatgcc 300  
aagaccaaga gtttcagagt tgtctcagag gcaagctcca aggctgaggt catcgctatc 360  
tacttctgat tccaatcatt ccaaccgtct gatcactacg gatcaaagtt ttaagcccgg 420  
tggtgaccgt aaatctcctc gaagcgggtg acctaacagt gatccgcttg gtcagaagaa 480  
acttggggga cgaatatcgg atctagagtc gcagtttagga caagcgcgaag aggaactgag 540  
attgctcaag gagcagttgg ctaatgctga agctgtgaag aaacaagctc aagatgagct 600  
tcataagaag tccaagaaac caaaccgct ggctcgagtg gaggaatctg caactgaggc 660  
tgagaggatt gatagagacg aaatccctgg tgatgtgcag aaagagactg atgtgtttga 720  
ggttcccgtt gaaaagattg cagtagaaga agaagaactg agaagcggca atgacgaagc 780  
tgagaaattg gttgcaaagg aagatgagat aaagatgctg aaagctagac tctatgacat 840  
ggagaaagag catgaatcac taggcaaaga aaacgagagc ttgaagaatc agttgagcga 900  
ttcagcttca gagatttcta atgtgaaagc taatgaagat gagatgggtt caaagggtgag 960  
taggattggg gaagagttag aagaaagcag agcaaagacg gctcacctga aggagaagct 1020  
tgagtccatg gaagaagcaa aagatgcttt agaggctgag atgaagaagc tcagggttca 1080  
aaccgagcag tggaggaagg cagcggatgc tgcagcagca gttcttttctg gagagtttga 1140  
gatgaatggt cgggatcgat ctgggtcaac tgagaagtat tatgcagggtg ggttctttga 1200  
cccgtcagct gggttcatgg atccaccggg aatggctgat gattatgatg atggactggg 1260  
aagtggcaag aggaagagtt ctgggatgaa gatgtttggt gagttgtgga ggaagaaagg 1320  
gcaaaagtga gttacagatt gtgtggagtgc tcattcaaga aatgggtgtgc tcaccgtttc 1380  
tctcttttat tttgctgtat ttacctgaa gtttttgtaa gtgggtccgc ttcacagaa 1440  
gctaactatc aatccaaatc aattgcaaaa acaatttcat g

(2) INFORMATION FOR SEQ ID NO:924:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 344 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..344  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1595679  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

Met Pro Arg Pro Arg Val Ser Glu Leu Ser Gln Arg Gln Ala Pro Arg  
1 5 10 15  
Leu Arg Ser Ser Ser Ser Thr Ser Asp Ser Asn His Ser Asn Arg Leu  
20 25 30  
Ile Thr Thr Asp Gln Ser Phe Lys Pro Gly Val Asp Arg Lys Ser Pro  
35 40 45  
Arg Ser Gly Gly Pro Asn Ser Asp Pro Leu Gly Gln Lys Lys Leu Gly  
50 55 60  
Gly Arg Ile Ser Asp Leu Glu Ser Gln Leu Gly Gln Ala Gln Glu Glu  
65 70 75 80  
Leu Arg Leu Leu Lys Glu Gln Leu Ala Asn Ala Glu Ala Val Lys Lys  
85 90 95  
Gln Ala Gln Asp Glu Leu His Lys Lys Ser Lys Lys Pro Asn Pro Leu  
100 105 110  
Ala Arg Val Glu Glu Ser Ala Thr Glu Ala Glu Arg Ile Asp Arg Asp  
115 120 125

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Glu Ile Pro Gly Asp Val Gln Lys Glu Thr Asp Val Phe Glu Val Pro  
130 135 140  
Val Glu Lys Ile Ala Val Glu Glu Glu Leu Arg Ser Gly Asn Asp  
145 150 155 160  
Glu Ala Glu Lys Leu Val Ala Lys Glu Asp Glu Ile Lys Met Leu Lys  
165 170 175  
Ala Arg Leu Tyr Asp Met Glu Lys Glu His Glu Ser Leu Gly Lys Glu  
180 185 190  
Asn Glu Ser Leu Lys Asn Gln Leu Ser Asp Ser Ala Ser Glu Ile Ser  
195 200 205  
Asn Val Lys Ala Asn Glu Asp Glu Met Val Ser Lys Val Ser Arg Ile  
210 215 220  
Gly Glu Glu Leu Glu Glu Ser Arg Ala Lys Thr Ala His Leu Lys Glu  
225 230 235 240  
Lys Leu Glu Ser Met Glu Glu Ala Lys Asp Ala Leu Glu Ala Glu Met  
245 250 255  
Lys Lys Leu Arg Val Gln Thr Glu Gln Trp Arg Lys Ala Ala Asp Ala  
260 265 270  
Ala Ala Ala Val Leu Ser Gly Glu Phe Glu Met Asn Gly Arg Asp Arg  
275 280 285  
Ser Gly Ser Thr Glu Lys Tyr Tyr Ala Gly Gly Phe Phe Asp Pro Ser  
290 295 300  
Ala Gly Phe Met Asp Pro Pro Gly Met Ala Asp Asp Tyr Asp Asp Gly  
305 310 315 320  
Leu Gly Ser Gly Lys Arg Lys Ser Ser Gly Met Lys Met Phe Gly Glu  
325 330 335  
Leu Trp Arg Lys Lys Gly Gln Lys  
340

(2) INFORMATION FOR SEQ ID NO:925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1068 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1068
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

|          |         |          |       |         |       |         |        |        |        |          |       |      |
|----------|---------|----------|-------|---------|-------|---------|--------|--------|--------|----------|-------|------|
| atttcata | gc      | aaaacac  | caa   | aacagag | ttc   | acagaa  | acat   | attcaa | agat   | ttttcaca | aaa   | 60   |
| tattacc  | att     | ttaaat   | ctat  | aaacaat | gac   | gaactc  | ggtg   | gctaag | ttgg   | cactact  | tagg  | 120  |
| gttttgc  | att     | ctgcaag  | tga   | cgagctt | act   | tgttcgc | caa    | gcaa   | atgcta | gggttt   | cct   | 180  |
| tgtgttt  | gga     | gattctc  | tctcg | ttgaca  | atgg  | taacaat | gac    | tttctt | gcta   | ccactg   | ctcg  | 240  |
| tgccgata | aat     | taccott  | atg   | gtatcg  | attt  | tccaact | cat    | cgtoct | acgg   | gccgtt   | tctc  | 300  |
| caatgg   | tcta    | aacatt   | ccag  | atctcgt | caa   | ttctct  | cttc   | ctgact | acgt   | tgtctt   | tgtc  | 360  |
| atttct   | gaat    | accgcaa  | agt   | cttacg  | gaaa  | atgtac  | gatt   | tgggtg | gctcg  | acgtgt   | ccct  | 420  |
| gtgact   | ggaa    | caggacca | at    | gggtt   | gcgtc | cggcgc  | gagc   | tggcgc | caacg  | tagccg   | caac  | 480  |
| ggcgagt  | gtg     | ctaccga  | act   | ccaacg  | agcc  | gcgtc   | actat  | tcaacc | caca   | actaat   | tcaa  | 540  |
| atgata   | acag    | acctcaa  | caa   | cgaagt  | tga   | tcttcg  | gcct   | tcattg | ccgc   | taatact  | caa   | 600  |
| caa      | atgcaca | tggact   | tcat  | tagcg   | accca | caagcat | atg    | gattc  | gtcac  | gtcga    | aggtg | 660  |
| gctt     | gtttgtg | gacaagg  | gcc   | gtaca   | atggg | atagg   | gctat  | gcact  | ccatt  | atcaa    | atcct | 720  |
| tgcc     | caaaca  | gagat    | ctctt | tgcct   | ttttg | gatc    | cttttc | acccat | caga   | aaaag    | caagt | 780  |
| aga      | atcatag | ctcaaca  | aat   | cctca   | atggc | tctc    | ctgaat | acatg  | catoc  | catga    | atcct | 840  |
| agc      | accatcc | tcaccg   | ttga  | ttccat  | gacc  | taag    | cttcta | ttcct  | catct  | atccca   | atc   | 900  |
| cact     | ttatgc  | tttgt    | ttttg | ttttg   | ccttt | ctcgt   | tttatt | atat   | attttt | acattg   | gtgc  | 960  |
| ttta     | aattagt | ttcctt   | gagt  | tatgt   | tgtga | gtttt   | gtgtt  | gttcat | caat   | aattag   | tcac  | 1020 |
| caatt    | gtgag   | ctgaga   | agta  | atatt   | caaca | atctt   | acgaa  | tgtt   | caact  |          |       |      |

(2) INFORMATION FOR SEQ ID NO:926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..112
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1595696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

Met Thr Asn Ser Val Ala Lys Leu Ala Leu Leu Gly Phe Cys Ile Leu  
1 5 10 15  
Gln Val Thr Ser Leu Leu Val Pro Gln Ala Asn Ala Arg Ala Phe Leu  
20 25 30  
Val Phe Gly Asp Ser Leu Val Asp Asn Gly Asn Asn Asp Phe Leu Ala  
35 40 45  
Thr Thr Ala Arg Ala Asp Asn Tyr Pro Tyr Gly Ile Asp Phe Pro Thr  
50 55 60  
His Arg Pro Thr Gly Arg Phe Ser Asn Gly Leu Asn Ile Pro Asp Leu  
65 70 75 80  
Val Asn Ser Leu Phe Leu Thr Thr Leu Ser Leu Ser Phe Leu Asn Thr  
85 90 95  
Ala Lys Ser Tyr Gly Lys Cys Thr Ile Trp Val Leu Asp Val Ser Leu  
100 105 110

(2) INFORMATION FOR SEQ ID NO:927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1595697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

Met Tyr Asp Leu Gly Ala Arg Arg Val Leu Val Thr Gly Thr Gly Pro  
1 5 10 15  
Met Gly Cys Val Pro Ala Glu Leu Ala Gln Arg Ser Arg Asn Gly Glu  
20 25 30  
Cys Ala Thr Glu Leu Gln Arg Ala Ala Ser Leu Phe Asn Pro Gln Leu  
35 40 45  
Ile Gln Met Ile Thr Asp Leu Asn Asn Glu Val Gly Ser Ser Ala Phe  
50 55 60  
Ile Ala Ala Asn Thr Gln Gln Met His Met Asp Phe Ile Ser Asp Pro  
65 70 75 80  
Gln Ala Tyr Gly Phe Val Thr Ser Lys Val Ala Cys Cys Gly Gln Gly  
85 90 95  
Pro Tyr Asn Gly Ile Gly Leu Cys Thr Pro Leu Ser Asn Leu Cys Pro  
100 105 110  
Asn Arg Asp Leu Phe Ala Phe Trp Asp Pro Phe His Pro Ser Glu Lys  
115 120 125  
Ala Ser Arg Ile Ile Ala Gln Gln Ile Leu Asn Gly Ser Pro Glu Tyr  
130 135 140  
Met His Pro Met Asn Leu Ser Thr Ile Leu Thr Val Asp Ser Met Thr  
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:928:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 144 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..144  
(D) OTHER INFORMATION: / Ceres Seq. ID 1595698  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

Met Gly Cys Val Pro Ala Glu Leu Ala Ser Arg Asn Gly Glu  
1 5 10 15  
Cys Ala Thr Glu Leu Gln Arg Ala Ala Ser Leu Phe Asn Pro Gln Leu  
20 25 30  
Ile Gln Met Ile Thr Asp Leu Asn Asn Glu Val Gly Ser Ser Ala Phe  
35 40 45  
Ile Ala Ala Asn Thr Gln Gln Met His Met Asp Phe Ile Ser Asp Pro  
50 55 60  
Gln Ala Tyr Gly Phe Val Thr Ser Lys Val Ala Cys Cys Gly Gln Gly  
65 70 75 80  
Pro Tyr Asn Gly Ile Gly Leu Cys Thr Pro Leu Ser Asn Leu Cys Pro  
85 90 95  
Asn Arg Asp Leu Phe Ala Phe Trp Asp Pro Phe His Pro Ser Glu Lys  
100 105 110  
Ala Ser Arg Ile Ile Ala Gln Gln Ile Leu Asn Gly Ser Pro Glu Tyr  
115 120 125  
Met His Pro Met Asn Leu Ser Thr Ile Leu Thr Val Asp Ser Met Thr  
130 135 140

(2) INFORMATION FOR SEQ ID NO:929:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2164 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..2164  
(D) OTHER INFORMATION: / Ceres Seq. ID 1595707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

atcaaaaaca cgaatatcga tagtacactt ctacgtgcaa tttttctcctt tctcttctgtg 60  
gacatctgtc tgtttattac attttcttgt aatctttctt ttggggattt gaaatatcta 120  
tcccctaaag tttcgaaaaa ttctgttttt ctgttctcat tcttcgtgat ctttttctact 180  
ttctttctaaa aaaacatgtg tggaataactt gccgtgttag gatgttccga tgattctcag 240  
gccaaagagag ttctgtgttct cgagctttct cgcagattga ggcacagagg acctgactgg 300  
agtggattat atcagaacgg agataattac ttggccatc aacgtcttgc cgtcacatgat 360  
cctgcttccg gtgatcaacc tcttttcaac gaggacaaga ccattgttgt cacggtgaac 420  
ggagagattt ataaccatga ggagctgaga aaacgtctga agaatacaca gtcccgactact 480  
ggtagtgatt gtgaagtcac tgctcacttg tacgaggagt atgggtgtgga ttttggtgat 540  
atgttggtat gaatcttctc ctttggtgtg ctgcacacac gagataactc ctcatgggtg 600  
gctcgtgatg cgattggtgt cacttcgctc tacattgggt ggggactaga cggatctgtg 660  
tgatatactt cagagatgaa aggcttaaac gatgattgtg agcatttcga aacgtttcct 720  
ccaggtcatt tttattcaag caagtttagga ggggttaagc aatgggtataa tcctccttg 780  
ttcaatgaat ctgttctctt aacgccttat gagcctcttg cgataagacg cgcctttgaa 840  
aacgctgtga ttaagcgggt gatgactgat gttccatttg gagttttgct ctctggtggt 900  
cttgattctt ccttgttgtc ctccatcact gcacgtcact tggccggtac taaggcggct 960  
aagcaatggg gtcctcagct ccattccttt tgcgttggtc ttgagggtc accggacttg 1020  
aaggcaggga aagaggtggc ggaatatttg gggacgggtg accacgagtt ccacttctcg 1080  
gtgcaggacg ggattgatgc gattgaggat gtgatttacc atgttgagac ctatgatgtg 1140

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acgactatca gagcgagcac accgatgttc ttgatgtccc ggaaaatcaa gtctctaggg 1200
gtcaagatgg ttctctccgg cgaaggtgcg gacgagatct ttggagggtta cctctatttc 1260
cacaaggcac ctaacaagaa agagttttcac caagaaactt gtcgcaagat caaggctctt 1320
cacaagtatg actgtctaaag agccaacaaa tctacctctg cctttggact agaggcacgt 1380
gttccttttc ttgacaaaga cttcatcaac acagctatgt ctctcgaccc tgaatccaag 1440
atgatcaagc cagaggaagg aaggatcgag aaatgggttc taaggagagc ctttgacgac 1500
gaagaacgtc cttatctacc aaaacacatt ctctacagac agaaagaaca gttcagtgat 1560
ggtgtttgct acagttggat cgatggcctg aaagatcvcg ctgctcaaaa tgtcaatgac 1620
aagatgatgt cgaacgcggg gcatatcttc cctcacaaca ctccaaacac taaagaagct 1680
tactactaca gaatgatctt tgaaagggttc ttcccgacaga actctgcgag actaacgggt 1740
cctggagggtg ccaccgtggc ttgttcgact gcaaaggcag tggagtggga tgcaagctgg 1800
tccaacaata tggatccatc aggaagagcc gctatcggag ttcacctttc ggcctacgat 1860
ggcaagaacg tggcattgac cataccacca cttagggcaa ttgacaacat gccgatgatg 1920
atgggtcaag gagttgtgat tcagtcataa cttcgaagga gaaatggatg aaatatgtgt 1980
tatatcttcc caatgggtga agtgttttgt atgattttta taataagaat gtgatccttt 2040
ttttttccta tgaagatctg aatgtattat ctatcttgta aaaatttggt tctttgtaag 2100
atttgaatgt accgctttta cgtagatcga tgtacatcaa tcttataagt ttcaattatg 2160
tatac

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(2) INFORMATION FOR SEQ ID NO:930:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 584 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..584

(D) OTHER INFORMATION: / Ceres Seq. ID 1595708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

```

Met Cys Gly Ile Leu Ala Val Leu Gly Cys Ser Asp Asp Ser Gln Ala
1 5 10 15
Lys Arg Val Arg Val Leu Glu Leu Ser Arg Arg Leu Arg His Arg Gly
20 25 30
Pro Asp Trp Ser Gly Leu Tyr Gln Asn Gly Asp Asn Tyr Leu Ala His
35 40 45
Gln Arg Leu Ala Val Ile Asp Pro Ala Ser Gly Asp Gln Pro Leu Phe
50 55 60
Asn Glu Asp Lys Thr Ile Val Val Thr Val Asn Gly Glu Ile Tyr Asn
65 70 75 80
His Glu Glu Leu Arg Lys Arg Leu Lys Asn His Lys Phe Arg Thr Gly
85 90 95
Ser Asp Cys Glu Val Ile Ala His Leu Tyr Glu Glu Tyr Gly Val Asp
100 105 110
Phe Val Asp Met Leu Asp Gly Ile Phe Ser Phe Val Leu Asp Thr
115 120 125
Arg Asp Asn Ser Phe Met Val Ala Arg Asp Ala Ile Gly Val Thr Ser
130 135 140
Leu Tyr Ile Gly Trp Gly Leu Asp Gly Ser Val Trp Ile Ser Ser Glu
145 150 155 160
Met Lys Gly Leu Asn Asp Asp Cys Glu His Phe Glu Thr Phe Pro Pro
165 170 175
Gly His Phe Tyr Ser Ser Lys Leu Gly Gly Phe Lys Gln Trp Tyr Asn
180 185 190
Pro Pro Trp Phe Asn Glu Ser Val Pro Ser Thr Pro Tyr Glu Pro Leu
195 200 205
Ala Ile Arg Arg Ala Phe Glu Asn Ala Val Ile Lys Arg Leu Met Thr
210 215 220
Asp Val Pro Phe Gly Val Leu Leu Ser Gly Gly Leu Asp Ser Ser Leu
225 230 235 240
Val Ala Ser Ile Thr Ala Arg His Leu Ala Gly Thr Lys Ala Ala Lys

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Leu Asn Asp Asp Cys Glu His Phe Glu Thr Phe Pro Pro Gly His Phe  
50 55 60  
Tyr Ser Ser Lys Leu Gly Gly Phe Lys Gln Trp Tyr Asn Pro Pro Trp  
65 70 75 80  
Phe Asn Glu Ser Val Pro Ser Thr Pro Tyr Glu Pro Leu Ala Ile Arg  
85 90 95  
Arg Ala Phe Glu Asn Ala Val Ile Lys Arg Leu Met Thr Asp Val Pro  
100 105 110  
Phe Gly Val Leu Leu Ser Gly Gly Leu Asp Ser Ser Leu Val Ala Ser  
115 120 125  
Ile Thr Ala Arg His Leu Ala Gly Thr Lys Ala Ala Lys Gln Trp Gly  
130 135 140  
Pro Gln Leu His Ser Phe Cys Val Gly Leu Glu Gly Ser Pro Asp Leu  
145 150 155 160  
Lys Ala Gly Lys Glu Val Ala Glu Tyr Leu Gly Thr Val His His Glu  
165 170 175  
Phe His Phe Ser Val Gln Asp Gly Ile Asp Ala Ile Glu Asp Val Ile  
180 185 190  
Tyr His Val Glu Thr Tyr Asp Val Thr Thr Ile Arg Ala Ser Thr Pro  
195 200 205  
Met Phe Leu Met Ser Arg Lys Ile Lys Ser Leu Gly Val Lys Met Val  
210 215 220  
Leu Ser Gly Glu Gly Ala Asp Glu Ile Phe Gly Gly Tyr Leu Tyr Phe  
225 230 235 240  
His Lys Ala Pro Asn Lys Lys Glu Phe His Gln Glu Thr Cys Arg Lys  
245 250 255  
Ile Lys Ala Leu His Lys Tyr Asp Cys Leu Arg Ala Asn Lys Ser Thr  
260 265 270  
Ser Ala Phe Gly Leu Glu Ala Arg Val Pro Phe Leu Asp Lys Asp Phe  
275 280 285  
Ile Asn Thr Ala Met Ser Leu Asp Pro Glu Ser Lys Met Ile Lys Pro  
290 295 300  
Glu Glu Gly Arg Ile Glu Lys Trp Val Leu Arg Arg Ala Phe Asp Asp  
305 310 315 320  
Glu Glu Arg Pro Tyr Leu Pro Lys His Ile Leu Tyr Arg Gln Lys Glu  
325 330 335  
Gln Phe Ser Asp Gly Val Gly Tyr Ser Trp Ile Asp Gly Leu Lys Asp  
340 345 350  
Xaa Ala Ala Gln Asn Val Asn Asp Lys Met Met Ser Asn Ala Gly His  
355 360 365  
Ile Phe Pro His Asn Thr Pro Asn Thr Lys Glu Ala Tyr Tyr Tyr Arg  
370 375 380  
Met Ile Phe Glu Arg Phe Phe Pro Gln Asn Ser Ala Arg Leu Thr Val  
385 390 395 400  
Pro Gly Gly Ala Thr Val Ala Cys Ser Thr Ala Lys Ala Val Glu Trp  
405 410 415  
Asp Ala Ser Trp Ser Asn Asn Met Asp Pro Ser Gly Arg Ala Ala Ile  
420 425 430  
Gly Val His Leu Ser Ala Tyr Asp Gly Lys Asn Val Ala Leu Thr Ile  
435 440 445  
Pro Pro Leu Lys Ala Ile Asp Asn Met Pro Met Met Met Gly Gln Gly  
450 455 460  
Val Val Ile Gln Ser  
465

(2) INFORMATION FOR SEQ ID NO:932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

00000000 00000000

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..451

(D) OTHER INFORMATION: / Ceres Seq. ID 1595710

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ala | Arg | Asp | Ala | Ile | Gly | Val | Thr | Ser | Leu | Tyr | Ile | Gly | Trp |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gly | Leu | Asp | Gly | Ser | Val | Trp | Ile | Ser | Ser | Glu | Met | Lys | Gly | Leu | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Asp | Cys | Glu | His | Phe | Glu | Thr | Phe | Pro | Pro | Gly | His | Phe | Tyr | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Lys | Leu | Gly | Gly | Phe | Lys | Gln | Trp | Tyr | Asn | Pro | Pro | Trp | Phe | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Ser | Val | Pro | Ser | Thr | Pro | Tyr | Glu | Pro | Leu | Ala | Ile | Arg | Arg | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Phe | Glu | Asn | Ala | Val | Ile | Lys | Arg | Leu | Met | Thr | Asp | Val | Pro | Phe | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Leu | Leu | Ser | Gly | Gly | Leu | Asp | Ser | Ser | Leu | Val | Ala | Ser | Ile | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Ala | Arg | His | Leu | Ala | Gly | Thr | Lys | Ala | Ala | Lys | Gln | Trp | Gly | Pro | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Leu | His | Ser | Phe | Cys | Val | Gly | Leu | Glu | Gly | Ser | Pro | Asp | Leu | Lys | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Gly | Lys | Glu | Val | Ala | Glu | Tyr | Leu | Gly | Thr | Val | His | His | Glu | Phe | His |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Phe | Ser | Val | Gln | Asp | Gly | Ile | Asp | Ala | Ile | Glu | Asp | Val | Ile | Tyr | His |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Glu | Thr | Tyr | Asp | Val | Thr | Thr | Ile | Arg | Ala | Ser | Thr | Pro | Met | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Met | Ser | Arg | Lys | Ile | Lys | Ser | Leu | Gly | Val | Lys | Met | Val | Leu | Ser |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Gly | Glu | Gly | Ala | Asp | Glu | Ile | Phe | Gly | Gly | Tyr | Leu | Tyr | Phe | His | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Pro | Asn | Lys | Lys | Glu | Phe | His | Gln | Glu | Thr | Cys | Arg | Lys | Ile | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Ala | Leu | His | Lys | Tyr | Asp | Cys | Leu | Arg | Ala | Asn | Lys | Ser | Thr | Ser | Ala |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Phe | Gly | Leu | Glu | Ala | Arg | Val | Pro | Phe | Leu | Asp | Lys | Asp | Phe | Ile | Asn |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Thr | Ala | Met | Ser | Leu | Asp | Pro | Glu | Ser | Lys | Met | Ile | Lys | Pro | Glu | Glu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Arg | Ile | Glu | Lys | Trp | Val | Leu | Arg | Arg | Ala | Phe | Asp | Asp | Glu | Glu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Arg | Pro | Tyr | Leu | Pro | Lys | His | Ile | Leu | Tyr | Arg | Gln | Lys | Glu | Gln | Phe |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Ser | Asp | Gly | Val | Gly | Tyr | Ser | Trp | Ile | Asp | Gly | Leu | Lys | Asp | Xaa | Ala |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ala | Gln | Asn | Val | Asn | Asp | Lys | Met | Met | Ser | Asn | Ala | Gly | His | Ile | Phe |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     |     | 350 |     |     |
| Pro | His | Asn | Thr | Pro | Asn | Thr | Lys | Glu | Ala | Tyr | Tyr | Tyr | Arg | Met | Ile |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Phe | Glu | Arg | Phe | Phe | Pro | Gln | Asn | Ser | Ala | Arg | Leu | Thr | Val | Pro | Gly |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Gly | Ala | Thr | Val | Ala | Cys | Ser | Thr | Ala | Lys | Ala | Val | Glu | Trp | Asp | Ala |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |     |
| Ser | Trp | Ser | Asn | Asn | Met | Asp | Pro | Ser | Gly | Arg | Ala | Ala | Ile | Gly | Val |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| His | Leu | Ser | Ala | Tyr | Asp | Gly | Lys | Asn | Val | Ala | Leu | Thr | Ile | Pro | Pro |
|     |     | 420 |     |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Leu | Lys | Ala | Ile | Asp | Asn | Met | Pro | Met | Met | Met | Gly | Gln | Gly | Val | Val |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     |     | 445 |     |     |

DOCKET "08663350"

Ile Gln Ser  
450

(2) INFORMATION FOR SEQ ID NO:933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2217

(D) OTHER INFORMATION: / Ceres Seq. ID 1595725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:

|            |            |             |             |             |            |      |
|------------|------------|-------------|-------------|-------------|------------|------|
| atagagattt | ggttttttga | ttcttccart  | ctcactctct  | ctgtctttct  | ctctccatca | 60   |
| aataccaaat | tatctggaag | ctgagtacat  | cttgttttct  | gctcattcct  | ctgtttcaac | 120  |
| aatggagagt | actattgtta | tgatgatgat  | gataacaaga  | tctttctttt  | gcttcttggg | 180  |
| atTTTTatgc | cttctctgct | cttctgttca  | cggattgctt  | tctcctaaag  | gtgttaactt | 240  |
| tgaagtgcaa | gctttgatgg | acataaaaagc | ttcattacat  | gacctcatg   | gtgttcttga | 300  |
| taactgggat | agagatgctg | ttgatccttg  | tagttggaca  | atggtcactt  | gttcttctga | 360  |
| aaactttgtc | attggcttag | gcacaccaag  | tcagaattta  | tctggtacac  | tatctccaag | 420  |
| cattaccaac | ttaacaaatc | ttcggattgt  | gctgttgcag  | aacaacaaca  | taacagggaa | 480  |
| aattcctgct | gagattggtc | ggcttacgag  | gcttgagact  | cttgatcttt  | ctgataattt | 540  |
| cttccacggt | gaaattcctt | tttcagtagg  | ctatctacaa  | agcctgcaat  | atctgaggct | 600  |
| taacaacaat | tctctctctg | gagtgtttcc  | tctgtcacta  | tctaatatga  | ctcaacttgc | 660  |
| ctttcttgat | ttatcatata | acaatcttag  | tggctcctgtt | ccaagatttg  | ctgcaaagac | 720  |
| gtttagcatc | gttgggaacc | cgctgatatg  | tccaacgggt  | accgaaccag  | actgcaatgg | 780  |
| aacaacattg | atacctatgt | ctatgaactt  | gaatcaaact  | ggagttcctt  | tatacgccgg | 840  |
| tggatcgagg | aatcacaaaa | tggcaatcgc  | gtgtggatcc  | agcgttgggg  | ctgtatcatt | 900  |
| aatcttcatt | gctgttggtt | tgtttctctg  | gtggagacaa  | agacataacc  | aaaacacatt | 960  |
| ctttgatgtt | aaagatggga | atcatcatga  | ggaagtttca  | cttggaacc   | tgaggagatt | 1020 |
| tggtttcagg | gagcttcaga | ttgcgaccaa  | taacttcagc  | agtaagaact  | tattggggaa | 1080 |
| aggtggctat | ggaaatgtat | acaaaggaat  | acttgagat   | agtacagtga  | ttgcagtga  | 1140 |
| aaggcttaaa | gatggaggag | cattgggagg  | agagattcag  | tttcagacag  | aagttgaaat | 1200 |
| gatcagttta | gctgttcac  | gaaatctctt  | aagactctac  | ggtttctgca  | tcacacaaac | 1260 |
| tgagaagcct | ctagtttatc | cttatatgtc  | taatggaagc  | gttgcatctc  | gaatgaaagc | 1320 |
| aaaacctgtt | cttgactgga | gcataaggaa  | gaggatagcc  | ataggagctg  | caagagggct | 1380 |
| tgtgtatctc | catgagcaat | gtgatccgaa  | gattatccac  | cgcgatgtca  | aagcagcgaa | 1440 |
| tatacttctt | gatgactact | gtgaagctgt  | ggttggcgat  | tttggtttag  | ctaaactctt | 1500 |
| ggatcatcaa | gattctcatg | tgacaaccgc  | ggttagaggc  | acgggtgggtc | acattgctcc | 1560 |
| agagtatctc | tcaactggtc | aatcctctga  | gaaaacagat  | gtttttggct  | tcgggattct | 1620 |
| tcttcttgag | cttgtaaccg | gacaaagagc  | ttttgagttt  | ggtaaagcgg  | ctaaccagaa | 1680 |
| aggtgtgatg | cttgattggg | ttaaaagat   | tcatcaagag  | aagaaacttg  | agctacttgt | 1740 |
| ggataaagag | ttgttgaaag | agaagagcta  | cgatgagatt  | gagttagacg  | aaatggtaag | 1800 |
| agtagctttg | ttgtgcacac | agtacctgcc  | aggacataga  | ccaaaaatgt  | ctgaagttgt | 1860 |
| tcgaatgctg | gaaggagatg | gacttgcaga  | gaaatgggaa  | gcttctcaaa  | gatacagacg | 1920 |
| tgtttcaaaa | tgtagcaaca | ggataaatga  | attgatgtca  | tcttcagaca  | gatactctga | 1980 |
| tcttaccgat | gactctagtt | tacttgtgca  | agcaatggag  | ctctctggtc  | ctagatgaaa | 2040 |
| tctatacatg | aatctgaaga | agaagaagaa  | catgcacatg  | tttcttgaat  | caagagggat | 2100 |
| tcttgttttt | ttgtataata | gagaggtttt  | ttggagggaa  | atgttgtgtc  | tctgtaactg | 2160 |
| tataggcttg | ttgtgtaaga | agttattact  | gcacttaggg  | ttaattcaaa  | gttctttt   |      |

(2) INFORMATION FOR SEQ ID NO:934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..638

036663950

(D) OTHER INFORMATION: / Ceres Seq. ID 1595726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ser | Thr | Ile | Val | Met | Met | Met | Met | Ile | Thr | Arg | Ser | Phe | Phe |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Cys | Phe | Leu | Gly | Phe | Leu | Cys | Leu | Leu | Cys | Ser | Ser | Val | His | Gly | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ser | Pro | Lys | Gly | Val | Asn | Phe | Glu | Val | Gln | Ala | Leu | Met | Asp | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Ala | Ser | Leu | His | Asp | Pro | His | Gly | Val | Leu | Asp | Asn | Trp | Asp | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Ala | Val | Asp | Pro | Cys | Ser | Trp | Thr | Met | Val | Thr | Cys | Ser | Ser | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asn | Phe | Val | Ile | Gly | Leu | Gly | Thr | Pro | Ser | Gln | Asn | Leu | Ser | Gly | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Ser | Pro | Ser | Ile | Thr | Asn | Leu | Thr | Asn | Leu | Arg | Ile | Val | Leu | Leu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Asn | Asn | Asn | Ile | Thr | Gly | Lys | Ile | Pro | Ala | Glu | Ile | Gly | Arg | Leu |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Thr | Arg | Leu | Glu | Thr | Leu | Asp | Leu | Ser | Asp | Asn | Phe | Phe | His | Gly | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Ile | Pro | Phe | Ser | Val | Gly | Tyr | Leu | Gln | Ser | Leu | Gln | Tyr | Leu | Arg | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asn | Asn | Asn | Ser | Leu | Ser | Gly | Val | Phe | Pro | Leu | Ser | Leu | Ser | Asn | Met |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Thr | Gln | Leu | Ala | Phe | Leu | Asp | Leu | Ser | Tyr | Asn | Asn | Leu | Ser | Gly | Pro |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Val | Pro | Arg | Phe | Ala | Ala | Lys | Thr | Phe | Ser | Ile | Val | Gly | Asn | Pro | Leu |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| Ile | Cys | Pro | Thr | Gly | Thr | Glu | Pro | Asp | Cys | Asn | Gly | Thr | Thr | Leu | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Pro | Met | Ser | Met | Asn | Leu | Asn | Gln | Thr | Gly | Val | Pro | Leu | Tyr | Ala | Gly |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Ser | Arg | Asn | His | Lys | Met | Ala | Ile | Ala | Val | Gly | Ser | Ser | Val | Gly |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Thr | Val | Ser | Leu | Ile | Phe | Ile | Ala | Val | Gly | Leu | Phe | Leu | Trp | Trp | Arg |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Gln | Arg | His | Asn | Gln | Asn | Thr | Phe | Phe | Asp | Val | Lys | Asp | Gly | Asn | His |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| His | Glu | Glu | Val | Ser | Leu | Gly | Asn | Leu | Arg | Arg | Phe | Gly | Phe | Arg | Glu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | Gln | Ile | Ala | Thr | Asn | Asn | Phe | Ser | Ser | Lys | Asn | Leu | Leu | Gly | Lys |
|     | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Gly | Gly | Tyr | Gly | Asn | Val | Tyr | Lys | Gly | Ile | Leu | Gly | Asp | Ser | Thr | Val |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Ile | Ala | Val | Lys | Arg | Leu | Lys | Asp | Gly | Gly | Ala | Leu | Gly | Gly | Glu | Ile |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     |     | 350 |     |     |
| Gln | Phe | Gln | Thr | Glu | Val | Glu | Met | Ile | Ser | Leu | Ala | Val | His | Arg | Asn |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     |     | 365 |     |     |
| Leu | Leu | Arg | Leu | Tyr | Gly | Phe | Cys | Ile | Thr | Gln | Thr | Glu | Lys | Leu | Leu |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Val | Tyr | Pro | Tyr | Met | Ser | Asn | Gly | Ser | Val | Ala | Ser | Arg | Met | Lys | Ala |
|     | 385 |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Lys | Pro | Val | Leu | Asp | Trp | Ser | Ile | Arg | Lys | Arg | Ile | Ala | Ile | Gly | Ala |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     |     | 415 |     |
| Ala | Arg | Gly | Leu | Val | Tyr | Leu | His | Glu | Gln | Cys | Asp | Pro | Lys | Ile | Ile |
|     |     | 420 |     |     |     |     | 425 |     |     |     |     |     | 430 |     |     |
| His | Arg | Asp | Val | Lys | Ala | Ala | Asn | Ile | Leu | Leu | Asp | Asp | Tyr | Cys | Glu |
|     | 435 |     |     |     |     | 440 |     |     |     |     |     | 445 |     |     |     |
| Ala | Val | Val | Gly | Asp | Phe | Gly | Leu | Ala | Lys | Leu | Leu | Asp | His | Gln | Asp |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Ser | His | Val | Thr | Thr | Ala | Val | Arg | Gly | Thr | Val | Gly | His | Ile | Ala | Pro |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Gln | Thr | Gly | Val | Pro | Leu | Tyr | Ala | Gly | Gly | Ser | Arg | Asn | His | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Met | Ala | Ile | Ala | Val | Gly | Ser | Ser | Val | Gly | Thr | Val | Ser | Leu | Ile | Phe |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |
| Ile | Ala | Val | Gly | Leu | Phe | Leu | Trp | Trp | Arg | Gln | Arg | His | Asn | Gln | Asn |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Thr | Phe | Phe | Asp | Val | Lys | Asp | Gly | Asn | His | His | Glu | Glu | Val | Ser | Leu |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Gly | Asn | Leu | Arg | Arg | Phe | Gly | Phe | Arg | Glu | Leu | Gln | Ile | Ala | Thr | Asn |
|     |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asn | Phe | Ser | Ser | Lys | Asn | Leu | Leu | Gly | Lys | Gly | Gly | Tyr | Gly | Asn | Val |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Tyr | Lys | Gly | Ile | Leu | Gly | Asp | Ser | Thr | Val | Ile | Ala | Val | Lys | Arg | Leu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Lys | Asp | Gly | Gly | Ala | Leu | Gly | Gly | Glu | Ile | Gln | Phe | Gln | Thr | Glu | Val |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Glu | Met | Ile | Ser | Leu | Ala | Val | His | Arg | Asn | Leu | Leu | Arg | Leu | Tyr | Gly |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Phe | Cys | Ile | Thr | Gln | Thr | Glu | Lys | Leu | Leu | Val | Tyr | Pro | Tyr | Met | Ser |
|     |     |     | 370 |     |     |     | 375 |     |     |     | 380 |     |     |     |     |
| Asn | Gly | Ser | Val | Ala | Ser | Arg | Met | Lys | Ala | Lys | Pro | Val | Leu | Asp | Trp |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Ser | Ile | Arg | Lys | Arg | Ile | Ala | Ile | Gly | Ala | Ala | Arg | Gly | Leu | Val | Tyr |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Leu | His | Glu | Gln | Cys | Asp | Pro | Lys | Ile | Ile | His | Arg | Asp | Val | Lys | Ala |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Ala | Asn | Ile | Leu | Leu | Asp | Asp | Tyr | Cys | Glu | Ala | Val | Val | Gly | Asp | Phe |
|     |     |     | 435 |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Gly | Leu | Ala | Lys | Leu | Leu | Asp | His | Gln | Asp | Ser | His | Val | Thr | Thr | Ala |
|     |     |     | 450 |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Val | Arg | Gly | Thr | Val | Gly | His | Ile | Ala | Pro | Glu | Tyr | Leu | Ser | Thr | Gly |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Gln | Ser | Ser | Glu | Lys | Thr | Asp | Val | Phe | Gly | Phe | Gly | Ile | Leu | Leu | Leu |
|     |     |     | 485 |     |     |     |     | 490 |     |     |     |     |     | 495 |     |
| Glu | Leu | Val | Thr | Gly | Gln | Arg | Ala | Phe | Glu | Phe | Gly | Lys | Ala | Ala | Asn |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Gln | Lys | Gly | Val | Met | Leu | Asp | Trp | Val | Lys | Lys | Ile | His | Gln | Glu | Lys |
|     |     |     | 515 |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Lys | Leu | Glu | Leu | Leu | Val | Asp | Lys | Glu | Leu | Leu | Lys | Lys | Lys | Ser | Tyr |
|     |     |     | 530 |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Asp | Glu | Ile | Glu | Leu | Asp | Glu | Met | Val | Arg | Val | Ala | Leu | Leu | Cys | Thr |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Gln | Tyr | Leu | Pro | Gly | His | Arg | Pro | Lys | Met | Ser | Glu | Val | Val | Arg | Met |
|     |     |     | 565 |     |     |     |     | 570 |     |     |     |     |     | 575 |     |
| Leu | Glu | Gly | Asp | Gly | Leu | Ala | Glu | Lys | Trp | Glu | Ala | Ser | Gln | Arg | Ser |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Asp | Ser | Val | Ser | Lys | Cys | Ser | Asn | Arg | Ile | Asn | Glu | Leu | Met | Ser | Ser |
|     |     |     | 595 |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Ser | Asp | Arg | Tyr | Ser | Asp | Leu | Thr | Asp | Asp | Ser | Ser | Leu | Leu | Val | Gln |
|     |     |     | 610 |     |     | 615 |     |     |     |     | 620 |     |     |     |     |
| Ala | Met | Glu | Leu | Ser | Gly | Pro | Arg |     |     |     |     |     |     |     |     |
| 625 |     |     |     |     | 630 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

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Arg Gly Thr Val Gly His Ile Ala Pro Glu Tyr Leu Ser Thr Gly Gln  
465 470 475 480  
Ser Ser Glu Lys Thr Asp Val Phe Gly Phe Gly Ile Leu Leu Leu Glu  
485 490 495  
Leu Val Thr Gly Gln Arg Ala Phe Glu Phe Gly Lys Ala Ala Asn Gln  
500 505 510  
Lys Gly Val Met Leu Asp Trp Val Lys Lys Ile His Gln Glu Lys Lys  
515 520 525  
Leu Glu Leu Leu Val Asp Lys Glu Leu Leu Lys Lys Lys Ser Tyr Asp  
530 535 540  
Glu Ile Glu Leu Asp Glu Met Val Arg Val Ala Leu Leu Cys Thr Gln  
545 550 555 560  
Tyr Leu Pro Gly His Arg Pro Lys Met Ser Glu Val Val Arg Met Leu  
565 570 575  
Glu Gly Asp Gly Leu Ala Glu Lys Trp Glu Ala Ser Gln Arg Ser Asp  
580 585 590  
Ser Val Ser Lys Cys Ser Asn Arg Ile Asn Glu Leu Met Ser Ser Ser  
595 600 605  
Asp Arg Tyr Ser Asp Leu Thr Asp Asp Ser Ser Leu Leu Val Gln Ala  
610 615 620  
Met Glu Leu Ser Gly Pro Arg  
625 630

(2) INFORMATION FOR SEQ ID NO:937:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1755
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:

|            |             |             |             |             |             |      |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| atctcacaca | ccgaaagtta  | ttttcgaatc  | cactaacgaa  | tcttccacag  | caaaaaaactt | 60   |
| tcgtgttcc  | ctgtaatttc  | tcagtatata  | tagataccaa  | atcgagcagt  | gaaaaaatgg  | 120  |
| ctatggcgag | tttatatcgg  | cgatctcttc  | cttctcctcc  | ggccattgac  | ttttcttccg  | 180  |
| ccgaaggcaa | gctaattcttc | aatgaagcgc  | ttcagaaagg  | aactatggaa  | ggatttttca  | 240  |
| ggttgatttc | gtatttttcag | acacaatccg  | aacctgcgta  | ttgtggtttg  | gctagtctct  | 300  |
| cagtgggtgt | gaatgctctt  | tctatcgatc  | ctggacgtaa  | atggaaaggg  | ccttggagggt | 360  |
| ggtttgatga | atcaatgttg  | gattgctgcg  | aacctctgga  | agtagtgaag  | gaaaaaggca  | 420  |
| tttcatattg | aaaagttgtc  | tgtttggttc  | attgttcagg  | agcaaaagtt  | gaggctttcc  | 480  |
| gtacaagtca | gagcaccatt  | gatgatttcc  | gcaaatttgt  | cgtgaaatgc  | acgagttctg  | 540  |
| agaattgcca | tatgatctca  | acatatcaca  | gagggtgtatt | taagcagact  | gggactggtc  | 600  |
| acttttccac | tattgggtgg  | tataatgctg  | agagagatat  | ggctttgatt  | cttgatgttg  | 660  |
| ctcgtttcaa | gtatccccct  | cactgggttc  | ctcttaaact  | tctttgggaa  | gcatggaca   | 720  |
| gtattgatca | gtcaacaggg  | aaacgtagag  | ggttcatgct  | catatctaga  | ccacacagag  | 780  |
| aaccgggatt | gctctatact  | ctgagctgca  | aggatgaaag  | ctggatcgaa  | atagccaagt  | 840  |
| atttgaagga | agatgttcc   | cgtcttgtaa  | gttcacagca  | tgtagattct  | gtggagaaaa  | 900  |
| tcatatcagt | tgtgttcaag  | tcacttccat  | caaatttcaa  | ccaattcatc  | agatgggtgg  | 960  |
| ctgagatccg | aattacagag  | gactcaaacc  | aaaatctcag  | cgcagaggag  | aagtctaggc  | 1020 |
| tgaactaaa  | gcaattggtg  | ctgaaggaag  | tgcacgaaac  | tgaactgttc  | aaacacatca  | 1080 |
| ataagttctt | atccacagtg  | ggttatgaag  | acagtctgac  | ttatgctgct  | gcaaaggctt  | 1140 |
| gttgccaagg | agctgaaatc  | ttatccggaa  | gctcatcaaa  | agagttttgt  | tgctcgggaaa | 1200 |
| cttgctgtaa | atgcatcaaa  | ggctcctgat  | actctgaagg  | cacagtgggtg | actggagttg  | 1260 |
| tggtgctgta | tgggaatgaa  | caaaaagggtg | atctgttagt  | gccatcgacg  | caaactgagt  | 1320 |
| gtgaattgtg | tcctgaagca  | acttatccag  | caggaaacga  | tgtgttcaact | gcacttctat  | 1380 |
| tggctttacc | tccacagaca  | tggtcagggga | tcaaagacca  | agctcttatg  | catgaaatga  | 1440 |
| agcagctcat | ttccatggct  | tccctcccaa  | ctttgcttca  | agaagaggta  | ttgcatcttc  | 1500 |
| gacggcaact | tcagctgcta  | aaacgatgcc  | aagagaacaa  | ggaagaggat  | gatctcgtcg  | 1560 |
| ctcctgccta | ttagttcatt  | gtcccaaact  | cactctcttc  | cccatttgaa  | tcccacgttc  | 1620 |

DOCKET # 08669960

tcaacacttg attgtagaa agtctcttta ttgtctgtac gattcaaact ctatttgcaa 1680  
tgagagatat ttgtaaacad attcattcta tgaattgtta atcacaataa gtaaagaatc 1740  
ttagaatcat atttc

(2) INFORMATION FOR SEQ ID NO:938:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..523
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Thr | His | Arg | Lys | Leu | Phe | Ser | Asn | Pro | Leu | Thr | Asn | Leu | Pro | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gln | Lys | Thr | Phe | Val | Phe | Leu | Cys | Asn | Phe | Ser | Val | Tyr | Ile | Asp | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Ser | Ser | Ser | Glu | Lys | Met | Ala | Met | Ala | Ser | Leu | Tyr | Arg | Arg | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Pro | Ser | Pro | Pro | Ala | Ile | Asp | Phe | Ser | Ser | Ala | Glu | Gly | Lys | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ile | Phe | Asn | Glu | Ala | Leu | Gln | Lys | Gly | Thr | Met | Glu | Gly | Phe | Phe | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Ile | Ser | Tyr | Phe | Gln | Thr | Gln | Ser | Glu | Pro | Ala | Tyr | Cys | Gly | Leu |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ala | Ser | Leu | Ser | Val | Val | Leu | Asn | Ala | Leu | Ser | Ile | Asp | Pro | Gly | Arg |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Lys | Trp | Lys | Gly | Pro | Trp | Arg | Trp | Phe | Asp | Glu | Ser | Met | Leu | Asp | Cys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Cys | Glu | Pro | Leu | Glu | Val | Val | Lys | Glu | Lys | Gly | Ile | Ser | Phe | Gly | Lys |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Val | Val | Cys | Leu | Ala | His | Cys | Ser | Gly | Ala | Lys | Val | Glu | Ala | Phe | Arg |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Thr | Ser | Gln | Ser | Thr | Ile | Asp | Asp | Phe | Arg | Lys | Phe | Val | Val | Lys | Cys |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Thr | Ser | Ser | Glu | Asn | Cys | His | Met | Ile | Ser | Thr | Tyr | His | Arg | Gly | Val |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Phe | Lys | Gln | Thr | Gly | Thr | Gly | His | Phe | Ser | Pro | Ile | Gly | Gly | Tyr | Asn |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Glu | Arg | Asp | Met | Ala | Leu | Ile | Leu | Asp | Val | Ala | Arg | Phe | Lys | Tyr |
|     |     |     | 210 |     |     | 215 |     |     |     | 220 |     |     |     |     |     |
| Pro | Pro | His | Trp | Val | Pro | Leu | Lys | Leu | Leu | Trp | Glu | Ala | Met | Asp | Ser |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Ile | Asp | Gln | Ser | Thr | Gly | Lys | Arg | Arg | Gly | Phe | Met | Leu | Ile | Ser | Arg |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Pro | His | Arg | Glu | Pro | Gly | Leu | Leu | Tyr | Thr | Leu | Ser | Cys | Lys | Asp | Glu |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Ser | Trp | Ile | Glu | Ile | Ala | Lys | Tyr | Leu | Lys | Glu | Asp | Val | Pro | Arg | Leu |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Val | Ser | Ser | Gln | His | Val | Asp | Ser | Val | Glu | Lys | Ile | Ile | Ser | Val | Val |
|     |     |     | 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Phe | Lys | Ser | Leu | Pro | Ser | Asn | Phe | Asn | Gln | Phe | Ile | Arg | Trp | Val | Ala |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |     |
| Glu | Ile | Arg | Ile | Thr | Glu | Asp | Ser | Asn | Gln | Asn | Leu | Ser | Ala | Glu | Glu |
|     |     |     |     | 325 |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Lys | Ser | Arg | Leu | Lys | Leu | Lys | Gln | Leu | Val | Leu | Lys | Glu | Val | His | Glu |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     |     | 350 |     |     |
| Thr | Glu | Leu | Phe | Lys | His | Ile | Asn | Lys | Phe | Leu | Ser | Thr | Val | Gly | Tyr |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |

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|                                                                 |     |     |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|-----|-----|
| 225                                                             |     | 230 |     | 235 |     | 240 |
| Lys Tyr Leu Lys Glu Asp Val Pro Arg Leu Val Ser Ser Gln His Val |     |     |     |     |     |     |
|                                                                 | 245 |     | 250 |     | 255 |     |
| Asp Ser Val Glu Lys Ile Ile Ser Val Val Phe Lys Ser Leu Pro Ser |     |     |     |     |     |     |
|                                                                 | 260 |     | 265 |     | 270 |     |
| Asn Phe Asn Gln Phe Ile Arg Trp Val Ala Glu Ile Arg Ile Thr Glu |     |     |     |     |     |     |
|                                                                 | 275 |     | 280 |     | 285 |     |
| Asp Ser Asn Gln Asn Leu Ser Ala Glu Glu Lys Ser Arg Leu Lys Leu |     |     |     |     |     |     |
|                                                                 | 290 |     | 295 |     | 300 |     |
| Lys Gln Leu Val Leu Lys Glu Val His Glu Thr Glu Leu Phe Lys His |     |     |     |     |     |     |
| 305                                                             |     | 310 |     | 315 |     | 320 |
| Ile Asn Lys Phe Leu Ser Thr Val Gly Tyr Glu Asp Ser Leu Thr Tyr |     |     |     |     |     |     |
|                                                                 | 325 |     | 330 |     | 335 |     |
| Ala Ala Ala Lys Ala Cys Cys Gln Gly Ala Glu Ile Leu Ser Gly Ser |     |     |     |     |     |     |
|                                                                 | 340 |     | 345 |     | 350 |     |
| Ser Ser Lys Glu Phe Cys Cys Arg Glu Thr Cys Val Lys Cys Ile Lys |     |     |     |     |     |     |
|                                                                 | 355 |     | 360 |     | 365 |     |
| Gly Pro Asp Asp Ser Glu Gly Thr Val Val Thr Gly Val Val Val Arg |     |     |     |     |     |     |
|                                                                 | 370 |     | 375 |     | 380 |     |
| Asp Gly Asn Glu Gln Lys Val Asp Leu Leu Val Pro Ser Thr Gln Thr |     |     |     |     |     |     |
| 385                                                             |     | 390 |     | 395 |     | 400 |
| Glu Cys Glu Cys Gly Pro Glu Ala Thr Tyr Pro Ala Gly Asn Asp Val |     |     |     |     |     |     |
|                                                                 | 405 |     | 410 |     | 415 |     |
| Phe Thr Ala Leu Leu Leu Ala Leu Pro Pro Gln Thr Trp Ser Gly Ile |     |     |     |     |     |     |
|                                                                 | 420 |     | 425 |     | 430 |     |
| Lys Asp Gln Ala Leu Met His Glu Met Lys Gln Leu Ile Ser Met Ala |     |     |     |     |     |     |
|                                                                 | 435 |     | 440 |     | 445 |     |
| Ser Leu Pro Thr Leu Leu Gln Glu Glu Val Leu His Leu Arg Arg Gln |     |     |     |     |     |     |
|                                                                 | 450 |     | 455 |     | 460 |     |
| Leu Gln Leu Leu Lys Arg Cys Gln Glu Asn Lys Glu Glu Asp Asp Leu |     |     |     |     |     |     |
| 465                                                             |     | 470 |     | 475 |     | 480 |
| Ala Ala Pro Ala Tyr                                             |     |     |     |     |     |     |
|                                                                 | 485 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..483

(D) OTHER INFORMATION: / Ceres Seq. ID 1595744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Ala Ser Leu Tyr Arg Arg Ser Leu Pro Ser Pro Pro Ala Ile Asp |     |     |
| 1                                                               | 5   | 10  |
| Phe Ser Ser Ala Glu Gly Lys Leu Ile Phe Asn Glu Ala Leu Gln Lys |     |     |
|                                                                 | 20  | 30  |
| Gly Thr Met Glu Gly Phe Phe Arg Leu Ile Ser Tyr Phe Gln Thr Gln |     |     |
|                                                                 | 35  | 45  |
| Ser Glu Pro Ala Tyr Cys Gly Leu Ala Ser Leu Ser Val Val Leu Asn |     |     |
|                                                                 | 50  | 60  |
| Ala Leu Ser Ile Asp Pro Gly Arg Lys Trp Lys Gly Pro Trp Arg Trp |     |     |
| 65                                                              | 70  | 80  |
| Phe Asp Glu Ser Met Leu Asp Cys Cys Glu Pro Leu Glu Val Val Lys |     |     |
|                                                                 | 85  | 95  |
| Glu Lys Gly Ile Ser Phe Gly Lys Val Val Cys Leu Ala His Cys Ser |     |     |
|                                                                 | 100 | 110 |
| Gly Ala Lys Val Glu Ala Phe Arg Thr Ser Gln Ser Thr Ile Asp Asp |     |     |
|                                                                 | 115 | 125 |

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atgggagactg tagctccggt gacatctccc ccaaagaaac gacggcagaa gaaacctaata 240  
aactatgact ccgacattga ggacatcaca ccaacttgca acgacagtgt tcctcctcct 300  
caagtcagta acatgtactc tgtacctaac aactctgtaa aagagagttt ttctaggata 360  
atgagagatc tgaatgtgga gaagaaatca ggtcccagct cctctagggt aacagatggg 420  
tctgagcaga acccatgtct gaaagagagg ttttttaggg ttagtgattt gggcgtggag 480  
aagaaatgtt cccctgagat tacagatttg gatgttggga tacCtggtcc gagattttTT 540  
ctaagttaaa ggatgtgtct gaacagaaga acacatgtct gatgcagaag agttctcctg 600  
agattgctga tttggatctt gtaatatcag ttccgagctc ttctgtgtta aaagatgtgt 660  
cagaagaaat cagatttttg aaggacaagt gttcccctga gattagaggt ttggtttttg 720  
aaaaatcagt ccttgacgaa atagagattc ttccagattc tgagtctgaa actgaagcta 780  
gaagaagagc ttcagccaag aagaagctat ttgaagaaag tagcagaatt gtagagtcta 840  
tcagtgatgg tgaagatagc tcaagtgaag ccgatgaaga ggaagaagaa aatcaagata 900  
gtgaagataa taacaccaaa gataatgtaa cggtggagtc tttgtcttct gaggatccat 960  
cttcatcatc atcatcgtcg ttttcatctt cctcttcctc ctcgagtgc gatgaatcat 1020  
atgtaaagga ggtagtggga gataatagag atgatgatga cttgagaaag gccagttcac 1080  
caatcaagag agtctcttta gtggaaagga aggccttggg aagggtataag aggtctggtt 1140  
ctagcttaac caagcctaga gaaagagaca acaagattca gaaactaaac caccg

(2) INFORMATION FOR SEQ ID NO:942:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1595749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

Met Glu Cys Ile Gly Lys Arg Val Lys Ser Arg Ser Trp Gln Arg Leu  
1 5 10 15  
Gln Ala Val Asn Lys Arg Lys Lys Met Glu Thr Val Ala Pro Val Thr  
20 25 30  
Ser Pro Pro Lys Lys Arg Arg Gln Lys Lys Pro Lys Asn Tyr Asp Ser  
35 40 45  
Asp Ile Glu Asp Ile Thr Pro Thr Cys Asn Asp Ser Val Pro Pro Pro  
50 55 60  
Gln Val Ser Asn Met Tyr Ser Val Pro Asn Asn Ser Val Lys Glu Ser  
65 70 75 80  
Phe Ser Arg Ile Met Arg Asp Leu Asn Val Glu Lys Lys Ser Gly Pro  
85 90 95  
Ser Ser Ser Arg Leu Thr Asp Gly Ser Glu Gln Asn Pro Cys Leu Lys  
100 105 110  
Glu Arg Ser Phe Arg Val Ser Asp Leu Gly Val Glu Lys Lys Cys Ser  
115 120 125  
Pro Glu Ile Thr Asp Leu Asp Val Gly Ile Pro Val Pro Arg Phe Phe  
130 135 140  
Leu Ser  
145

(2) INFORMATION FOR SEQ ID NO:943:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1595750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

0968980 "101300

Met Glu Thr Val Ala Pro Val Thr Ser Pro Pro Lys Lys Arg Arg Gln  
1 5 10 15  
Lys Lys Pro Lys Asn Tyr Asp Ser Asp Ile Glu Asp Ile Thr Pro Thr  
20 25 30  
Cys Asn Asp Ser Val Pro Pro Pro Gln Val Ser Asn Met Tyr Ser Val  
35 40 45  
Pro Asn Asn Ser Val Lys Glu Ser Phe Ser Arg Ile Met Arg Asp Leu  
50 55 60  
Asn Val Glu Lys Lys Ser Gly Pro Ser Ser Ser Arg Leu Thr Asp Gly  
65 70 75 80  
Ser Glu Gln Asn Pro Cys Leu Lys Glu Arg Ser Phe Arg Val Ser Asp  
85 90 95  
Leu Gly Val Glu Lys Lys Cys Ser Pro Glu Ile Thr Asp Leu Asp Val  
100 105 110  
Gly Ile Pro Val Pro Arg Phe Phe Leu Ser  
115 120

(2) INFORMATION FOR SEQ ID NO:944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1595751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

Met Gln Lys Ser Ser Pro Glu Ile Ala Asp Leu Val Ile Ser  
1 5 10 15  
Val Pro Ser Ser Ser Val Leu Lys Asp Val Ser Glu Glu Ile Arg Phe  
20 25 30  
Leu Lys Asp Lys Cys Ser Pro Glu Ile Arg Gly Leu Val Leu Glu Lys  
35 40 45  
Ser Val Pro Asp Glu Ile Glu Ile Leu Ser Asp Ser Glu Ser Glu Thr  
50 55 60  
Glu Ala Arg Arg Arg Ala Ser Ala Lys Lys Lys Leu Phe Glu Glu Ser  
65 70 75 80  
Ser Arg Ile Val Glu Ser Ile Ser Asp Gly Glu Asp Ser Ser Ser Glu  
85 90 95  
Thr Asp Glu Glu Glu Glu Glu Asn Gln Asp Ser Glu Asp Asn Asn Thr  
100 105 110  
Lys Asp Asn Val Thr Val Glu Ser Leu Ser Ser Glu Asp Pro Ser Ser  
115 120 125  
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Asp  
130 135 140  
Glu Ser Tyr Val Lys Glu Val Val Gly Asp Asn Arg Asp Asp Asp Asp  
145 150 155 160  
Leu Arg Lys Ala Ser Ser Pro Ile Lys Arg Val Ser Leu Val Glu Arg  
165 170 175  
Lys Ala Leu Val Arg Tyr Lys Arg Ser Gly Ser Ser Leu Thr Lys Pro  
180 185 190  
Arg Glu Arg Asp Asn Lys Ile Gln Lys Leu Asn His  
195 200

(2) INFORMATION FOR SEQ ID NO:945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1071 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

09699001 08663660









attgagagct atggcactac gatcagtaag caggaggctc gggagcagaa ttttgaatca 180  
acgttccttt gttgcttcgc ttcactctca tgccacaagt ttcgggtttc aagaagtaaa 240  
ggaagaagag aaaagcaaat tggttggtaa tgtattcacc aatgtagctt cgagttatga 300  
tattatgaat gatgtgatga gtggtggttt gcataggcta tggaaggaaa gactcgttgg 360  
gaagctaagt ccatttgacg ggatgaagca tcttgatgtg gccggaggaa caggtgatgt 420  
tgcccttagg atctatgatg ctgtttacag tgtcaaacga agagcattgc agaaagttga 480  
tgaggcttct cttgaggaaa ctcagatata cgtatgtgac attaatccta acatgttaaa 540  
cgttgggaaa caacgagctg ctgagagagg tctaagagat aacaagtcac tcgtatgggt 600  
cgaaggagat gcag

(2) INFORMATION FOR SEQ ID NO:950:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1595765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

Met Ala Leu Arg Ser Val Ser Arg Arg Leu Gly Ser Arg Ile Leu Asn  
1 5 10 15  
Gln Arg Ser Phe Val Ala Ser Leu His Ser His Ala Thr Ser Phe Gly  
20 25 30  
Phe Gln Glu Val Lys Glu Glu Glu Lys Ser Lys Leu Val Gly Asn Val  
35 40 45  
Phe Thr Asn Val Ala Ser Ser Tyr Asp Ile Met Asn Asp Val Met Ser  
50 55 60  
Gly Gly Leu His Arg Leu Trp Lys Glu Arg Leu Val Gly Lys Leu Ser  
65 70 75 80  
Pro Phe Ala Gly Met Lys His Leu Asp Val Ala Gly Gly Thr Gly Asp  
85 90 95  
Val Ala Phe Arg Ile Tyr Asp Ala Val Tyr Ser Val Lys Arg Arg Ala  
100 105 110  
Leu Gln Lys Val Asp Glu Ala Ser Leu Glu Glu Thr Gln Ile Tyr Val  
115 120 125  
Cys Asp Ile Asn Pro Asn Met Leu Asn Val Gly Lys Gln Arg Ala Ala  
130 135 140  
Glu Arg Gly Leu Arg Asp Asn Lys Ser Leu Val Trp Val Glu Gly Asp  
145 150 155 160  
Ala

(2) INFORMATION FOR SEQ ID NO:951:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1595766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

Met Asn Asp Val Met Ser Gly Gly Leu His Arg Leu Trp Lys Glu Arg  
1 5 10 15  
Leu Val Gly Lys Leu Ser Pro Phe Ala Gly Met Lys His Leu Asp Val  
20 25 30  
Ala Gly Gly Thr Gly Asp Val Ala Phe Arg Ile Tyr Asp Ala Val Tyr  
35 40 45

0966980 101300



- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 225 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..225  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1595784  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

Ile Glu Ile Glu Ser Ala Met Ala Ala Ser Ser Ser Val Phe Thr Val  
1                  5                  10                  15  
Ser Pro Ser Arg Asn Leu Ala Ala Ile Pro Leu His Gln Ser Leu Ser  
                  20                  25                  30  
Pro Pro Leu Leu Arg Ser Ser Ser Val Ala Phe Arg Pro Lys Arg Arg  
                  35                  40                  45  
Ser Ser Ser Leu Val Leu Cys Ser Thr Asp Glu Thr Lys Ser Thr Ala  
50                  55                  60  
Glu Lys Glu Ile Pro Ile Glu Leu Arg Tyr Glu Ala Phe Pro Thr Val  
65                  70                  75                  80  
Met Asp Ile Asn Lys Ile Gln Glu Ile Leu Pro His Arg Phe Pro Phe  
                  85                  90                  95  
Leu Leu Val Asp Arg Val Ile Glu Tyr Thr Ala Gly Val Ser Ala Val  
                  100                  105                  110  
Ala Ile Lys Asn Val Thr Ile Asn Asp Asn Phe Phe Pro Gly His Phe  
                  115                  120                  125  
Pro Glu Arg Pro Ile Met Pro Gly Val Leu Met Val Glu Ala Met Ala  
130                  135                  140  
Gln Val Gly Gly Ile Val Met Leu Gln Pro Glu Val Gly Gly Ser Arg  
145                  150                  155                  160  
Ser Asn Phe Phe Phe Ala Gly Ile Asp Lys Val Arg Phe Arg Lys Pro  
                  165                  170                  175  
Val Ile Ala Gly Asp Thr Leu Val Met Arg Met Thr Leu Val Lys Leu  
                  180                  185                  190  
Gln Lys Arg Phe Gly Ile Ala Lys Met Glu Gly Lys Ala Tyr Val Gly  
                  195                  200                  205  
Asn Ser Val Val Cys Glu Gly Glu Phe Leu Met Ala Met Gly Lys Glu  
210                  215                  220  
Glu  
225

(2) INFORMATION FOR SEQ ID NO:955:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 219 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..219  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1595785  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

Met Ala Ala Ser Ser Ser Val Phe Thr Val Ser Pro Ser Arg Asn Leu  
1                  5                  10                  15  
Ala Ala Ile Pro Leu His Gln Ser Leu Ser Pro Pro Leu Leu Arg Ser  
                  20                  25                  30  
Ser Ser Val Ala Phe Arg Pro Lys Arg Arg Ser Ser Ser Leu Val Leu  
                  35                  40                  45  
Cys Ser Thr Asp Glu Thr Lys Ser Thr Ala Glu Lys Glu Ile Pro Ile  
50                  55                  60

00583980 101300

Glu Leu Arg Tyr Glu Ala Phe Pro Thr Val Met Asp Ile Asn Lys Ile  
65 70 75 80  
Gln Glu Ile Leu Pro His Arg Phe Pro Phe Leu Leu Val Asp Arg Val  
85 90 95  
Ile Glu Tyr Thr Ala Gly Val Ser Ala Val Ala Ile Lys Asn Val Thr  
100 105 110  
Ile Asn Asp Asn Phe Phe Pro Gly His Phe Pro Glu Arg Pro Ile Met  
115 120 125  
Pro Gly Val Leu Met Val Glu Ala Met Ala Gln Val Gly Gly Ile Val  
130 135 140  
Met Leu Gln Pro Glu Val Gly Gly Ser Arg Ser Asn Phe Phe Phe Ala  
145 150 155 160  
Gly Ile Asp Lys Val Arg Phe Arg Lys Pro Val Ile Ala Gly Asp Thr  
165 170 175  
Leu Val Met Arg Met Thr Leu Val Lys Leu Gln Lys Arg Phe Gly Ile  
180 185 190  
Ala Lys Met Glu Gly Lys Ala Tyr Val Gly Asn Ser Val Val Cys Glu  
195 200 205  
Gly Glu Phe Leu Met Ala Met Gly Lys Glu Glu  
210 215

(2) INFORMATION FOR SEQ ID NO:956:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1595786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:

Met Asp Ile Asn Lys Ile Gln Glu Ile Leu Pro His Arg Phe Pro Phe  
1 5 10 15  
Leu Leu Val Asp Arg Val Ile Glu Tyr Thr Ala Gly Val Ser Ala Val  
20 25 30  
Ala Ile Lys Asn Val Thr Ile Asn Asp Asn Phe Phe Pro Gly His Phe  
35 40 45  
Pro Glu Arg Pro Ile Met Pro Gly Val Leu Met Val Glu Ala Met Ala  
50 55 60  
Gln Val Gly Gly Ile Val Met Leu Gln Pro Glu Val Gly Gly Ser Arg  
65 70 75 80  
Ser Asn Phe Phe Phe Ala Gly Ile Asp Lys Val Arg Phe Arg Lys Pro  
85 90 95  
Val Ile Ala Gly Asp Thr Leu Val Met Arg Met Thr Leu Val Lys Leu  
100 105 110  
Gln Lys Arg Phe Gly Ile Ala Lys Met Glu Gly Lys Ala Tyr Val Gly  
115 120 125  
Asn Ser Val Val Cys Glu Gly Glu Phe Leu Met Ala Met Gly Lys Glu  
130 135 140  
Glu  
145

(2) INFORMATION FOR SEQ ID NO:957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

09699900 08668960

(A) NAME/KEY: peptide

| Sociodemographic variables  |                |
|-----------------------------|----------------|
| Age (mean $\pm$ SD)         | 24.6 $\pm$ 3.6 |
| Gender                      |                |
| Male                        | 100            |
| Female                      | 100            |
| Marital status              |                |
| Married                     | 100            |
| Single                      | 100            |
| Education level             |                |
| High school                 | 100            |
| University                  | 100            |
| Occupation                  |                |
| Student                     | 100            |
| Unemployed                  | 100            |
| Employed                    | 100            |
| Family size (mean $\pm$ SD) | 3.2 $\pm$ 1.2  |
| Family income (TL/month)    |                |
| Less than 1000              | 100            |
| 1000-2000                   | 100            |
| 2000-3000                   | 100            |
| 3000-4000                   | 100            |
| 4000-5000                   | 100            |
| 5000-6000                   | 100            |
| 6000-7000                   | 100            |
| 7000-8000                   | 100            |
| 8000-9000                   | 100            |
| 9000-10000                  | 100            |
| 10000-11000                 | 100            |
| 11000-12000                 | 100            |
| 12000-13000                 | 100            |
| 13000-14000                 | 100            |
| 14000-15000                 | 100            |
| 15000-16000                 | 100            |
| 16000-17000                 | 100            |
| 17000-18000                 | 100            |
| 18000-19000                 | 100            |
| 19000-20000                 | 100            |
| 20000-21000                 | 100            |
| 21000-22000                 | 100            |
| 22000-23000                 | 100            |
| 23000-24000                 | 100            |
| 24000-25000                 | 100            |
| 25000-26000                 | 100            |
| 26000-27000                 | 100            |
| 27000-28000                 | 100            |
| 28000-29000                 | 100            |
| 29000-30000                 | 100            |
| 30000-31000                 | 100            |
| 31000-32000                 | 100            |
| 32000-33000                 | 100            |
| 33000-34000                 | 100            |
| 34000-35000                 | 100            |
| 35000-36000                 | 100            |
| 36000-37000                 | 100            |
| 37000-38000                 | 100            |
| 38000-39000                 | 100            |
| 39000-40000                 | 100            |
| 40000-41000                 | 100            |
| 41000-42000                 | 100            |
| 42000-43000                 | 100            |
| 43000-44000                 | 100            |
| 44000-45000                 | 100            |
| 45000-46000                 | 100            |
| 46000-47000                 | 100            |
| 47000-48000                 | 100            |
| 48000-49000                 | 100            |
| 49000-50000                 | 100            |
| 50000-51000                 | 100            |
| 51000-52000                 | 100            |
| 52000-53000                 | 100            |
| 53000-54000                 | 100            |
| 54000-55000                 | 100            |
| 55000-56000                 | 100            |
| 56000-57000                 | 100            |
| 57000-58000                 | 100            |
| 58000-59000                 | 100            |
| 59000-60000                 | 100            |
| 60000-61000                 | 100            |
| 61000-62000                 | 100            |
| 62000-63000                 | 100            |
| 63000-64000                 | 100            |
| 64000-65000                 | 100            |
| 65000-66000                 | 100            |
| 66000-67000                 | 100            |
| 67000-68000                 | 100            |
| 68000-69000                 | 100            |
| 69000-70000                 | 100            |
| 70000-71000                 | 100            |
| 71000-72000                 | 100            |
| 72000-73000                 | 100            |
| 73000-74000                 | 100            |
| 74000-75000                 | 100            |
| 75000-76000                 | 100            |
| 76000-77000                 | 100            |
| 77000-78000                 | 100            |
| 78000-79000                 | 100            |
| 79000-80000                 | 100            |
| 80000-81000                 | 100            |
| 81000-82000                 | 100            |
| 82000-83000                 | 100            |
| 83000-84000                 | 100            |
| 84000-85000                 | 100            |
| 85000-86000                 | 100            |
| 86000-87000                 | 100            |
| 87000-88000                 | 100            |
| 88000-89000                 | 100            |
| 89000-90000                 | 100            |
| 90000-91000                 | 100            |
| 91000-92000                 | 100            |
| 92000-93000                 | 100            |
| 93000-94000                 | 100            |
| 94000-95000                 | 100            |
| 95000-96000                 | 100            |
| 96000-97000                 | 100            |
| 97000-98000                 | 100            |
| 98000-99000                 | 100            |
| 99000-100000                | 100            |
| 100000-101000               | 100            |
| 101000-102000               | 100            |
| 102000-103000               | 100            |
| 103000-104000               | 100            |
| 104000-105000               | 100            |
| 105000-106000               | 100            |
| 106000-107000               | 100            |
| 107000-108000               | 100            |
| 108000-109000               | 100            |
| 109000-110000               | 100            |
| 110000-111000               | 1              |

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1595789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Glu | Gly | Asp | Ala | Val | Val | Ile | Pro | Lys | Glu | Ser | Ser | Trp | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Tyr | Tyr | Pro | Asp | Gly | Ala | Ser | Ser | Pro | Leu | Leu | Ser | Pro | Gln | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Lys | Leu | Tyr | Thr | Glu | Asp | Trp | Ile | Gly | Leu | Lys | Thr | Leu | Asp | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Arg | Lys | Val | Lys | Phe | Val | Ser | Val | Pro | Gly | Glu | His | Leu | Arg | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Gln | Asp | Asp | Val | Val | Lys | His | Val | Val | Pro | Tyr | Leu | Lys | Asn | Gln |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Ala | Ser | Met | Ser | Glu | Asp | Leu | Glu | Ile | Leu | His | Leu |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:960:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1219 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1219

(D) OTHER INFORMATION: / Ceres Seq. ID 1595790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| aaatggcgat  | ggagatcgga  | gaagatgaat  | ggaaggtttg | ctgtggaagc  | tccgaattcg  | 60   |
| cgaaGcagat  | gtctacgtct  | ggaccgttaa  | cttctcaaga | agcaatatat  | actgcaagag  | 120  |
| acatctgggt  | caaccaagtt  | aatgtgacag  | attggcttga | agctttctct  | gtcatcctc   | 180  |
| agattgggaa  | tactccttca  | ccttctatca  | actccgattt | tgctcgtcgg  | agcgtatcag  | 240  |
| aacagtcaac  | cgccctttgcc | acaacttctg  | cttctgcttt | acaggagctt  | gccgaatgga  | 300  |
| atgtacttta  | caaaaagaag  | tttggcttta  | tcttcattat | ttgcgcttct  | ggcaggactc  | 360  |
| acgctgagat  | gctccatgcg  | ttaaagggtca | acttttgcac | ttccaaatca  | gtttttgttg  | 420  |
| agtgtgagtg  | aatgagaaag  | ttacatatct  | atcaaatcgt | ctctttttca  | ggaaagggtat | 480  |
| aaaaataggc  | caatagtggg  | gcttgagatt  | gctgctatgg | aacaaatgaa  | aataacagag  | 540  |
| ctacgaatgg  | caaagctgtt  | ctccgataag  | gctaaagtta | tatcagaaac  | tgacagctct  | 600  |
| agctctcctg  | tttcaacaaa  | acctcaagat  | cgtcagagaa | tcattggagg  | gcatttgaat  | 660  |
| gttgacagctg | aagcaaaaagc | tcccaagaga  | agtaggccac | cgatcacgac  | tcattgthtta | 720  |
| gacgtctcac  | gtggtgctcc  | agctgcagggt | gttgaagtgc | acttagaagt  | gtggagtggg  | 780  |
| actaccgggtc | cttccctttgt | tcattggagg  | gggtgggtct | gggtccagtgt | gggcacatca  | 840  |
| gctactgata  | gagatgggag  | cagtgggcca  | ctgatggatt | tggttgacgc  | tttgaatcca  | 900  |
| gggacatata  | ggattagctt  | cgacactgca  | aagtattccc | caggctgctt  | ctttccctat  | 960  |
| gtttccattg  | tatttcagggt | tacagaatca  | cagaaatggg | agcattttcca | tgtcccactg  | 1020 |
| ttgcttgacac | ctttttcttt  | ctccacatac  | cgtgggagct | agagctatgc  | tactgctgtc  | 1080 |
| tgcggcacca  | actttccaac  | acattttgtt  | ttggttgtag | cactacggga  | acatgtatca  | 1140 |
| aaattgctat  | gaaatgaagt  | ctttattcga  | catgtataaa | aattgctatg  | aaataatgtc  | 1200 |
| tattcgagta  | tttatttgg   |             |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:961:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..181

(D) OTHER INFORMATION: / Ceres Seq. ID 1595791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

Met Glu Gln Met Lys Ile Thr Glu Leu Arg Met Ala Lys Leu Phe Ser

00569300 00569300



1 5 10 15  
Asp Lys Ala Lys Val Ile Ser Glu Thr Asp Ser Ser Ser Ser Pro Val  
20 25 30  
Ser Thr Lys Pro Gln Asp Arg Gln Arg Ile Ile Gly Gly His Leu Asn  
35 40 45  
Val Ala Ala Glu Ala Lys Ala Pro Lys Arg Ser Arg Pro Pro Ile Thr  
50 55 60  
Thr His Xaa Leu Asp Val Ser Arg Gly Ala Pro Ala Ala Gly Val Glu  
65 70 75 80  
Val His Leu Glu Val Trp Ser Gly Thr Thr Gly Pro Ser Phe Val His  
85 90 95  
Gly Gly Gly Gly Val Trp Ser Ser Val Gly Thr Ser Ala Thr Asp Arg  
100 105 110  
Asp Gly Arg Ser Gly Pro Leu Met Asp Leu Val Asp Ala Leu Asn Pro  
115 120 125  
Gly Thr Tyr Arg Ile Ser Phe Asp Thr Ala Lys Tyr Ser Pro Gly Cys  
130 135 140  
Phe Phe Pro Tyr Val Ser Ile Val Phe Gln Val Thr Glu Ser Gln Lys  
145 150 155 160  
Trp Glu His Phe His Val Pro Leu Leu Leu Ala Pro Phe Ser Phe Ser  
165 170 175  
Thr Tyr Arg Gly Ser  
180

(2) INFORMATION FOR SEQ ID NO:962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

Met Lys Ile Thr Glu Leu Arg Met Ala Lys Leu Phe Ser Asp Lys Ala  
1 5 10 15  
Lys Val Ile Ser Glu Thr Asp Ser Ser Ser Ser Pro Val Ser Thr Lys  
20 25 30  
Pro Gln Asp Arg Gln Arg Ile Ile Gly Gly His Leu Asn Val Ala Ala  
35 40 45  
Glu Ala Lys Ala Pro Lys Arg Ser Arg Pro Pro Ile Thr Thr His Xaa  
50 55 60  
Leu Asp Val Ser Arg Gly Ala Pro Ala Ala Gly Val Glu Val His Leu  
65 70 75 80  
Glu Val Trp Ser Gly Thr Thr Gly Pro Ser Phe Val His Gly Gly Gly  
85 90 95  
Gly Val Trp Ser Ser Val Gly Thr Ser Ala Thr Asp Arg Asp Gly Arg  
100 105 110  
Ser Gly Pro Leu Met Asp Leu Val Asp Ala Leu Asn Pro Gly Thr Tyr  
115 120 125  
Arg Ile Ser Phe Asp Thr Ala Lys Tyr Ser Pro Gly Cys Phe Phe Pro  
130 135 140  
Tyr Val Ser Ile Val Phe Gln Val Thr Glu Ser Gln Lys Trp Glu His  
145 150 155 160  
Phe His Val Pro Leu Leu Ala Pro Phe Ser Phe Ser Thr Tyr Arg  
165 170 175  
Gly Ser

(2) INFORMATION FOR SEQ ID NO:963:

(i) SEQUENCE CHARACTERISTICS:

0965960 101300

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide  
(B) LOCATION: 1..146  
(D) OTHER INFORMATION: / Ceres Seq. ID 1595795

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

```
(A) NAME/KEY: peptide
(B) LOCATION: 1..143
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

| (A17) SEQUENCE DESCRIPTION: SEQ ID NO: 1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met                                      | Ala | Thr | Gly | Lys | Thr | Val | Lys | Asp | Val | Ser | Pro | His | Asp | Phe | Val |  |
| 1                                        |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys                                      | Ala | Tyr | Ala | Ser | His | Leu | Lys | Arg | Ser | Gly | Lys | Ile | Glu | Leu | Pro |  |
|                                          |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu                                      | Trp | Thr | Asp | Ile | Val | Lys | Thr | Gly | Arg | Leu | Lys | Glu | Leu | Ala | Pro |  |
|                                          |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Tyr                                      | Asp | Pro | Asp | Trp | Tyr | Tyr | Ile | Arg | Ala | Ala | Ser | Met | Ala | Arg | Lys |  |
|                                          | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ile                                      | Tyr | Leu | Arg | Gly | Gly | Leu | Gly | Val | Gly | Ala | Phe | Arg | Arg | Ile | Tyr |  |
| 65                                       |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Gly                                      | Gly | Ser | Lys | Arg | Asn | Gly | Ser | Arg | Pro | Pro | His | Phe | Cys | Lys | Ser |  |
|                                          |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ser                                      | Gly | Gly | Ile | Ala | Arg | His | Ile | Leu | Gln | Gln | Leu | Glu | Thr | Met | Ser |  |
|                                          |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ile                                      | Val | Glu | Leu | Asp | Thr | Lys | Gly | Gly | Arg | Arg | Ile | Thr | Ser | Ser | Gly |  |
|                                          |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Gln                                      | Arg | Asp | Leu | Asp | Gln | Val | Ala | Gly | Arg | Ile | Ala | Ala | Glu | Ser |     |  |
|                                          | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

| Socioeconomic characteristics        |             |
|--------------------------------------|-------------|
| Age (years)                          | Mean (SD)   |
| Male                                 | 50.2 (10.5) |
| Female                               | 49.8 (10.3) |
| Marital status                       |             |
| Married                              | 65.2%       |
| Single                               | 34.8%       |
| Education (years)                    | Mean (SD)   |
| Male                                 | 12.5 (2.1)  |
| Female                               | 12.3 (2.0)  |
| Occupation                           |             |
| Professional                         | 25.1%       |
| Managerial                           | 18.7%       |
| Technical                            | 15.3%       |
| Skilled                              | 12.9%       |
| Unskilled                            | 28.0%       |
| Income (€ per month)                 | Mean (SD)   |
| Male                                 | 1,250 (350) |
| Female                               | 1,180 (320) |
| Health insurance                     |             |
| Public                               | 78.5%       |
| Private                              | 21.5%       |
| Smoking status                       |             |
| Smoker                               | 32.1%       |
| Non-smoker                           | 67.9%       |
| Alcohol consumption (times per week) | Mean (SD)   |
| Male                                 | 2.5 (1.5)   |
| Female                               | 2.2 (1.4)   |
| Physical activity (times per week)   | Mean (SD)   |
| Male                                 | 3.0 (1.8)   |
| Female                               | 2.8 (1.7)   |
| Chronic diseases                     |             |
| Hypertension                         | 28.5%       |
| Diabetes                             | 12.3%       |
| Heart disease                        | 15.7%       |
| Arthritis                            | 22.1%       |
| Depression                           | 18.9%       |
| Medication use (times per day)       | Mean (SD)   |
| Male                                 | 1.5 (0.8)   |
| Female                               | 1.4 (0.7)   |
| Health status (self-rated)           |             |
| Good                                 | 62.3%       |
| Fair                                 | 37.7%       |

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..83  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1595797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

Met Ala Arg Lys Ile Tyr Leu Arg Gly Gly Leu Gly Val Gly Ala Phe  
1                    5                    10                    15  
Arg Arg Ile Tyr Gly Gly Ser Lys Arg Asn Gly Ser Arg Pro Pro His  
                    20                    25                    30  
Phe Cys Lys Ser Ser Gly Gly Ile Ala Arg His Ile Leu Gln Gln Leu  
                    35                    40                    45  
Glu Thr Met Ser Ile Val Glu Leu Asp Thr Lys Gly Gly Arg Arg Ile  
                    50                    55                    60  
Thr Ser Ser Gly Gln Arg Asp Leu Asp Gln Val Ala Gly Arg Ile Ala  
65                    70                    75                    80  
Ala Glu Ser

(2) INFORMATION FOR SEQ ID NO:968:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 571 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..571  
(D) OTHER INFORMATION: / Ceres Seq. ID 1595802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

atcgtcaaag caaccaaaca cataaaagag agattttaata caaaagaaag agaaaaaaga 60  
aagatatggc aggactcatc aacaagatcg gagacgcact ccacattgga ggaggcaaca 120  
aggaaggtga gcacaagaag gaagaggaac acaagaaaca cggtgacgag cacaagagtg 180  
gtgagcacia agaaggtatt gttgacaaga tcaaagacaa gatccacggt ggtgaaggta 240  
aaagccacga cggagaaggc aaaagccacg acggtgagaa gaaaaagaat aaggacaaga 300  
aggagaagaa acatcatgat gatggtcacc acagcagcag cagtgcacgc gacaGcgaGt 360  
taaggtgagg aagtgaggag gatcgcttga ataaaacaga tctggttctg gctattatta 420  
attaatggtg ctgtatgttc ttatcatctt agagagaggt taaagacagg agaaccgtgc 480  
atctatcttt gtttggttatg tttctgtttt cttgtcatga aaattatgct catgtatott 540  
atctaaatca aaaataataa tttgatgaat c

(2) INFORMATION FOR SEQ ID NO:969:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 120 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..120  
(D) OTHER INFORMATION: / Ceres Seq. ID 1595803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

Ile Val Lys Ala Thr Lys His Ile Lys Glu Arg Phe Asn Thr Lys Glu  
1                    5                    10                    15  
Arg Glu Lys Arg Lys Ile Trp Gln Asp Ser Ser Thr Arg Ser Glu Thr  
                    20                    25                    30  
His Ser Thr Leu Glu Glu Ala Thr Arg Lys Val Ser Thr Arg Arg Lys  
                    35                    40                    45  
Arg Asn Thr Arg Asn Thr Leu Thr Ser Thr Arg Val Val Ser Thr Lys  
50                    55                    60  
Lys Val Leu Leu Thr Arg Ser Lys Thr Arg Ser Thr Val Val Lys Val

09589960 10100

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ttttttttt  | tccttcctcc | tagatccacc | acttcacct  | ctctctctc  | ctctctttt  | 60  |
| cgccctttt  | cctctctcc  | gtccatgtct | tccgccgcg  | ctgccgcgt  | ggaatccgtc | 120 |
| gtctccga   | agactcttt  | ctcgaatcct | ctcttgca   | acttcgatt  | ccctccgtt  | 180 |
| gattccgtt  | atgccagtca | tgttcgtcct | gggattcgt  | ctctattgca | gcattctgaa | 240 |
| gtcgaattg  | aggagctaga | gaaatctgtg | gagccaacat | ggccaaaact | ggtggaacca | 300 |
| ttagagaaaa | tcgttgatct | gttaactgtt | gtttgggaa  | tgatcaatca | ccctaaggct | 360 |
| gtcaaggaca | cacctgagct | acgtgctgcc | atcgaagacg | ttagccaga  | gaaagtgaag | 420 |
| ttccagctca | ggttggggca | aagcaagcct | attacaatg  | cctttaaaag | tattcgtgaa | 480 |
| tctcctgatt | ggtcacgcct | cagtgaagct | cgtcaacgct | tagtagaagc | tcaaaAtaaa | 540 |
| ggaggcggtt | ctcattggta | ttgctcttga | tgatgaaaag | agagaagagt | ttaataaaat | 600 |
| tgaacaggaa | ctcgaaaaac | tttcccataa | gttttctgag | aatgttttgg | atgcaacaaa | 660 |
| gaaatttgaa | aagttgataa | cagacaagaa | agagatcgag | ggattgcctc | catctgctct | 720 |
| tgggctattc | gcacaagcag | ctgtctccaa | gggccatgaa | aatgcaactg | ctgagattgg | 780 |
| accatggatc | attacactgg | atgctctcag | ttatcttctc | tgcatgcaac | atgctaaaaa | 840 |
| ccgtgctctg | cgtgaggaag | tctaccgtgc | ttacctatct | cgtgcctctt | ctggcgattt | 900 |
| ggataatacg | gcaattattg | accagatttt | gaagcttcgc | ttggaaaaag | ctaagcttct | 960 |

(2) INFORMATION FOR SEQ ID NO:972:

(A) LENGTH: 189 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(D) OTHER INFORMATION: / Ceres Seq. ID 1595806

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Phe | Phe | Leu | Pro | Pro | Pro | Arg | Ser | Thr | Thr | Ser | Thr | Ser | Leu | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ser | Ser | Phe | Arg | Pro | Phe | Ser | Ser | Pro | Pro | Ser | Met | Ser | Ser | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ala | Ala | Ala | Val | Glu | Ser | Val | Val | Ser | Asp | Glu | Thr | Leu | Ser | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Pro | Leu | Leu | Gln | Asp | Phe | Asp | Phe | Pro | Pro | Phe | Asp | Ser | Val | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Ser | His | Val | Arg | Pro | Gly | Ile | Arg | Ala | Leu | Leu | Gln | His | Leu | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Glu | Leu | Glu | Glu | Leu | Glu | Lys | Ser | Val | Glu | Pro | Thr | Trp | Pro | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Val | Glu | Pro | Leu | Glu | Lys | Ile | Val | Asp | Arg | Leu | Thr | Val | Val | Trp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Met | Ile | Asn | His | Leu | Lys | Ala | Val | Lys | Asp | Thr | Pro | Glu | Leu | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Ala | Ile | Glu | Asp | Val | Gln | Pro | Glu | Lys | Val | Lys | Phe | Gln | Leu | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Gly | Gln | Ser | Lys | Pro | Ile | Tyr | Asn | Ala | Phe | Lys | Ala | Ile | Arg | Glu |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Pro | Asp | Trp | Ser | Ser | Leu | Ser | Glu | Ala | Arg | Gln | Arg | Leu | Val | Glu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Gln | Asn | Lys | Gly | Gly | Gly | Ser | His | Trp | Tyr | Cys | Ser |     |     |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     |     |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ser | Ala | Ala | Ala | Ala | Val | Glu | Ser | Val | Val | Ser | Asp | Glu |     |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Thr | Leu | Ser | Ser | Asn | Pro | Leu | Leu | Gln | Asp | Phe | Asp | Phe | Pro | Pro | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Ser | Val | Asp | Ala | Ser | His | Val | Arg | Pro | Gly | Ile | Arg | Ala | Leu | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | His | Leu | Glu | Ala | Glu | Leu | Glu | Glu | Leu | Glu | Lys | Ser | Val | Glu | Pro |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Trp | Pro | Lys | Leu | Val | Glu | Pro | Leu | Glu | Lys | Ile | Val | Asp | Arg | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

Thr Val Val Trp Gly Met Ile Asn His Leu Lys Ala Val Lys Asp Thr  
85 90 95  
Pro Glu Leu Arg Ala Ala Ile Glu Asp Val Gln Pro Glu Lys Val Lys  
100 105 110  
Phe Gln Leu Arg Leu Gly Gln Ser Lys Pro Ile Tyr Asn Ala Phe Lys  
115 120 125  
Ala Ile Arg Glu Ser Pro Asp Trp Ser Ser Leu Ser Glu Ala Arg Gln  
130 135 140  
Arg Leu Val Glu Ala Gln Asn Lys Gly Gly Gly Ser His Trp Tyr Cys  
145 150 155 160  
Ser

(2) INFORMATION FOR SEQ ID NO:974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..648
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

aaagggtttgg aaacgtgaga tcagaggggaa gcgtacggcg cactctttgg tccaaacttt 60  
gctaaagcaa gaatcagcgg tcacggcttt ggtcacgagc cacatggcag tgtatagtgg 120  
ttcaagcgac ggagctgtga atttttggga gatgggagag aagaaaatct tgaagcattg 180  
tgaagttttc aagaagcata gacttgctgt cctttgtatc gcggctgccg gaaaattggt 240  
gttttagcggg ggggoggata agaagatatg cgtgtggagg agggaaggga aggtacacac 300  
gtgtgtctct gtgttaaccg gtcataccgg accagttaag tgtttggcgg tggtaggagcc 360  
atcgggaggt gaagaagaag acggaggaga tgggaggttg gttttgtata gtggaagtct 420  
tgacaaatcg gtcaaagtgt ggagggtacc acgtcattaa atgtaggatt ttattcgggtg 480  
tcttaagaga tttgggatgt atgtaggtaa gtaagaacaa aaaccctaagt caaatgatga 540  
attatgaggt tctgaatata tgatatttat tagtaattta atatatcttt gatacatgta 600  
taattgaact aggggttatcg ttacgggtga atatcaaata tcaatatt

(2) INFORMATION FOR SEQ ID NO:975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

Lys Val Trp Lys Arg Glu Ile Arg Gly Lys Arg Thr Ala His Ser Leu  
1 5 10 15  
Val Gln Thr Leu Leu Lys Gln Glu Ser Ala Val Thr Ala Leu Val Thr  
20 25 30  
Ser His Met Ala Val Tyr Ser Gly Ser Ser Asp Gly Ala Val Asn Phe  
35 40 45  
Trp Glu Met Gly Glu Lys Lys Ile Leu Lys His Cys Glu Val Phe Lys  
50 55 60  
Lys His Arg Leu Ala Val Leu Cys Ile Ala Ala Ala Gly Lys Leu Leu  
65 70 75 80  
Phe Ser Gly Gly Ala Asp Lys Lys Ile Cys Val Trp Arg Arg Glu Gly  
85 90 95  
Lys Val His Thr Cys Val Ser Val Leu Thr Gly His Thr Gly Pro Val  
100 105 110

095898010130

(2) INFORMATION FOR SEQ ID NO:976:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1595814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

(2) INFORMATION FOR SEQ ID NO:977:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1595815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

(2) INFORMATION FOR SEQ ID NO:978:



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:

(2) INFORMATION FOR SEQ ID NO:979:

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1595821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

(2) INFORMATION FOR SEQ ID NO:980:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1595822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Leu | Pro | Ser | Ser | Ser | Ile | Leu | Lys | Lys | Lys | Arg | Arg | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Val | Arg | Val | Ser | Ser | Val | Ser | Ile | Glu | Asp | Val | Arg | Asp | Val | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Leu | Gln | Ala | Val | Asp | Glu | Phe | Arg | Gln | Ala | Leu | Val | Met | Glu | Glu |

35 40 45  
Leu Leu Pro His Lys His Asp Tyr His Met Met Leu Arg Phe Leu  
50 55 60  
Lys Ala Arg Lys Phe Asp Ile Glu Lys Ala  
65 70

(2) INFORMATION FOR SEQ ID NO:981:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..782
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

aaaagaaaag atgttggtgta gaatgggtgg ggtgactggc cggaaaaaga aaccgggttc 60  
ggttccgggtt tatctgaatg tatacgaatc cacacccatc aatgggtacg cttactgggt 120  
aggacttggg atctatcact ctgggtgttg agttcatgga gttgaatatg gtttcggagc 180  
tcacgatcat tcgactaccg ggatattcga ggtaaccgaa gcaatgtccg ggtttcacat 240  
ttagggaagtc tatattgatt ggaagaactg atttagatcc tgaaaacgtt cgtgtcttta 300  
tgagaaaact tgcggaagaa tatagtggaa acagttatca tttgattact aagaattgca 360  
atcacttttg caatgatgtt tgtgtgcaac tgactcgaag atcgatccct agttgggtta 420  
accgtcttgc tcgctttggg ttgttttgca actgtgttct gccggcggag ttgaatgaga 480  
ctaagggtgag gcaggtgaga tcaaaggaag agaagattcc ggaagtagag aagaagaaac 540  
ttcggagtag atcaagtagg tttccacctg gtccttcgct ttcttcgtcg ggttctttaa 600  
accgaagcag aagaggagaa aggagaagac aatgtcttcc tccatcacca actgtgagtg 660  
tttagctcta gtcctagtaa aattatacct ttttgtttcg caatttgatt ctgtagtaat 720  
gtttaagcta caagatatgg attgaacaaa cattttcttg atagtaatgg tataagattt 780  
tc

(2) INFORMATION FOR SEQ ID NO:982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

Lys Glu Lys Met Leu Cys Arg Met Val Val Val Thr Gly Arg Lys Lys  
1 5 10 15  
Lys Pro Gly Ser Val Pro Val Tyr Leu Asn Val Tyr Asp Leu Thr Pro  
20 25 30  
Ile Asn Gly Tyr Ala Tyr Trp Leu Gly Leu Gly Ile Tyr His Ser Gly  
35 40 45  
Val Glu Val His Gly Val Glu Tyr Gly Phe Gly Ala His Asp His Ser  
50 55 60  
Thr Thr Gly Ile Phe Glu Val Thr Glu Ala Met Ser Gly Phe His Ile  
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

095830-10100

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1595831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

Met Leu Cys Arg Met Val Val Val Thr Gly Arg Lys Lys Lys Pro Gly  
1 5 10 15  
Ser Val Pro Val Tyr Leu Asn Val Tyr Asp Leu Thr Pro Ile Asn Gly  
20 25 30  
Tyr Ala Tyr Trp Leu Gly Leu Gly Ile Tyr His Ser Gly Val Glu Val  
35 40 45  
His Gly Val Glu Tyr Gly Phe Gly Ala His Asp His Ser Thr Thr Gly  
50 55 60  
Ile Phe Glu Val Thr Glu Ala Met Ser Gly Phe His Ile  
65 70 75

(2) INFORMATION FOR SEQ ID NO:984:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1595832

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

Met Glu Lys Leu Ala Glu Glu Tyr Ser Gly Asn Ser Tyr His Leu Ile  
1 5 10 15  
Thr Lys Asn Cys Asn His Phe Cys Asn Asp Val Cys Val Gln Leu Thr  
20 25 30  
Arg Arg Ser Ile Pro Ser Trp Val Asn Arg Leu Ala Arg Phe Gly Leu  
35 40 45  
Phe Cys Asn Cys Val Leu Pro Ala Glu Leu Asn Glu Thr Lys Val Arg  
50 55 60  
Gln Val Arg Ser Lys Glu Glu Lys Ile Pro Glu Val Glu Lys Lys Lys  
65 70 75 80  
Leu Arg Ser Arg Ser Ser Arg Phe Pro Pro Gly Pro Ser Leu Ser Ser  
85 90 95  
Ser Gly Ser Leu Asn Arg Ser Arg Arg Gly Glu Arg Arg Arg Gln Cys  
100 105 110  
Leu Pro Pro Ser Pro Thr Val Ser Val  
115 120

(2) INFORMATION FOR SEQ ID NO:985:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1579 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1579

(D) OTHER INFORMATION: / Ceres Seq. ID 1595837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

agctctgttg tggaacatcg gaaatcagaa ctgaaacaga aacagaaacc atggagaaga 60  
gagaagacga acaacaaaag cgcgacgatt ctagattcaa tcaaacactc aagaacgtcc 120  
aagggtttct taaaggtaga agtattcctg gtaagggtatt gttgactagg agatcagatc 180  
ctcctccata cccaatctct ccaacatatc aacggagctt atctgagaat gacgccggaa 240  
gaaatgagct attcgaaaagt cctgttgagg tggaggatca caattcaagc aagaaacatg 300

0968980-101300

ataatacata tgctggttaag ctacgatcaa actctagtgc tgaaaggagt gtgaaagaag 360  
ttcaaaactt gaagataggt gttcgcataa gtgactctgc tagagttatg aagttcaaca 420  
aagtgccttc agaaacaact gtcataattag agaaactgog cgagctagca tggaaatggtg 480  
taccacacta tatgcggcct gatgtctggc ggcttctctt gggatatgca ccacctaatt 540  
cagatagaag ggaggctggt ctgagaagaa aacgtcttga atatctggaa tctgttggtcc 600  
aatttttatga ccttccagat tccgaacggt ctgatgatga gatcaatatg cttcgccaga 660  
ttgctgttga ctgtccgagg actgtaccag atgtcagttt ctttcagcaa gaacaggtgc 720  
agaaatcact ggagcgtatt ctttacacgt gggccattag acatccagca agcggatatg 780  
ttcagggaat aaatgacctg gtcacgcctt tcttagtgat tttcttgtaa gaatatctag 840  
atggcgggtg agacagttgg tcaatggatg atctatctgc tgaaaaagtc tcagatgtag 900  
aagcggattg ctactggtgc ttaacaaagc tccttgacgg tatgcaagat cattacacgt 960  
ttgctcaacc tggatccag agacttgtgt ttaagctgaa ggaactggtc aggcgtatcg 1020  
atgaacctgt ttcaagacac atggaagagc atgggctaga gtttcttcaa tttgctttcc 1080  
ggtggtataa ttgtcttctg attcgtgaga tccattcaa tctcatcaat cgactatggg 1140  
acacttatct tgctgaagga gatgcgttgc cagacttcct ggkgtatata tgctagcttt 1200  
ctcttgacgt ggtctgatga gctgaagaag ctagattttc aagaaatggt aatgttcctg 1260  
caacaccttc cgacacataa ctggtcagac caagagctcg aaatggtttt gtcaagagct 1320  
tacatgtggc atagtatggt caataattcc ccaaaccatt tggttagctg aaatgacttt 1380  
tcttccatgg tgcttgctgc tgtttttccc tttgttatat tatcttcttc tcttgttgt 1440  
ctaaatcagc tttcgttttg ttttggtta tggtaaatgc taacattctt gtcttgtaa 1500  
ttgttattag tttatgtatg gtttcacttg ttgaatctgt caccagtttg tgtgtttgta 1560  
atattttag ctttcactg

(2) INFORMATION FOR SEQ ID NO:986:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..275

(D) OTHER INFORMATION: / Ceres Seq. ID 1595838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Cys | Cys | Gly | Thr | Ser | Glu | Ile | Arg | Thr | Glu | Thr | Glu | Thr | Glu | Thr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Met | Glu | Lys | Arg | Glu | Asp | Glu | Gln | Gln | Lys | Arg | Asp | Asp | Ser | Arg | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Gln | Thr | Leu | Lys | Asn | Val | Gln | Gly | Phe | Leu | Lys | Gly | Arg | Ser | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Gly | Lys | Val | Leu | Leu | Thr | Arg | Arg | Ser | Asp | Pro | Pro | Pro | Tyr | Pro |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ile | Ser | Pro | Thr | Tyr | Gln | Arg | Ser | Leu | Ser | Glu | Asn | Asp | Ala | Gly | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asn | Glu | Leu | Phe | Glu | Ser | Pro | Val | Glu | Val | Glu | Asp | His | Asn | Ser | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Lys | His | Asp | Asn | Thr | Tyr | Ala | Gly | Lys | Leu | Arg | Ser | Asn | Ser | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Glu | Arg | Ser | Val | Lys | Glu | Val | Gln | Asn | Leu | Lys | Ile | Gly | Val | Arg |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Ser | Asp | Ser | Ala | Arg | Val | Met | Lys | Phe | Asn | Lys | Val | Leu | Ser | Glu |
|     |     |     | 130 |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Thr | Thr | Val | Ile | Leu | Glu | Lys | Leu | Arg | Glu | Leu | Ala | Trp | Asn | Gly | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Pro | His | Tyr | Met | Arg | Pro | Asp | Val | Trp | Arg | Leu | Leu | Leu | Gly | Tyr | Ala |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Pro | Pro | Asn | Ser | Asp | Arg | Arg | Glu | Ala | Val | Leu | Arg | Arg | Lys | Arg | Leu |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Glu | Tyr | Leu | Glu | Ser | Val | Gly | Gln | Phe | Tyr | Asp | Leu | Pro | Asp | Ser | Glu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Ser | Asp | Asp | Glu | Ile | Asn | Met | Leu | Arg | Gln | Ile | Ala | Val | Asp | Cys |

210 215 220  
Pro Arg Thr Val Pro Asp Val Ser Phe Phe Gln Gln Glu Val Gln  
225 230 235 240  
Lys Ser Leu Glu Arg Ile Leu Tyr Thr Trp Ala Ile Arg His Pro Ala  
245 250 255  
Ser Gly Tyr Val Gln Gly Ile Asn Asp Leu Val Thr Pro Phe Leu Val  
260 265 270  
Ile Phe Leu  
275

(2) INFORMATION FOR SEQ ID NO:987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..259

(D) OTHER INFORMATION: / Ceres Seq. ID 1595839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

Met Glu Lys Arg Glu Asp Glu Gln Gln Lys Arg Asp Asp Ser Arg Phe  
1 5 10 15  
Asn Gln Thr Leu Lys Asn Val Gln Gly Phe Leu Lys Gly Arg Ser Ile  
20 25 30  
Pro Gly Lys Val Leu Leu Thr Arg Arg Ser Asp Pro Pro Tyr Pro  
35 40 45  
Ile Ser Pro Thr Tyr Gln Arg Ser Leu Ser Glu Asn Asp Ala Gly Arg  
50 55 60  
Asn Glu Leu Phe Glu Ser Pro Val Glu Val Glu Asp His Asn Ser Ser  
65 70 75 80  
Lys Lys His Asp Asn Thr Tyr Ala Gly Lys Leu Arg Ser Asn Ser Ser  
85 90 95  
Ala Glu Arg Ser Val Lys Glu Val Gln Asn Leu Lys Ile Gly Val Arg  
100 105 110  
Ser Ser Asp Ser Ala Arg Val Met Lys Phe Asn Lys Val Leu Ser Glu  
115 120 125  
Thr Thr Val Ile Leu Glu Lys Leu Arg Glu Leu Ala Trp Asn Gly Val  
130 135 140  
Pro His Tyr Met Arg Pro Asp Val Trp Arg Leu Leu Leu Gly Tyr Ala  
145 150 155 160  
Pro Pro Asn Ser Asp Arg Arg Glu Ala Val Leu Arg Arg Lys Arg Leu  
165 170 175  
Glu Tyr Leu Glu Ser Val Gly Gln Phe Tyr Asp Leu Pro Asp Ser Glu  
180 185 190  
Arg Ser Asp Asp Glu Ile Asn Met Leu Arg Gln Ile Ala Val Asp Cys  
195 200 205  
Pro Arg Thr Val Pro Asp Val Ser Phe Phe Gln Gln Glu Gln Val Gln  
210 215 220  
Lys Ser Leu Glu Arg Ile Leu Tyr Thr Trp Ala Ile Arg His Pro Ala  
225 230 235 240  
Ser Gly Tyr Val Gln Gly Ile Asn Asp Leu Val Thr Pro Phe Leu Val  
245 250 255  
Ile Phe Leu

(2) INFORMATION FOR SEQ ID NO:988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

00658390-101300

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1595840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

```
Met Lys Phe Asn Lys Val Leu Ser Glu Thr Thr Val Ile Leu Glu Lys
1 5 10 15
Leu Arg Glu Leu Ala Trp Asn Gly Val Pro His Tyr Met Arg Pro Asp
20 25 30
Val Trp Arg Leu Leu Leu Gly Tyr Ala Pro Pro Asn Ser Asp Arg Arg
35 40 45
Glu Ala Val Leu Arg Arg Lys Arg Leu Glu Tyr Leu Glu Ser Val Gly
50 55 60
Gln Phe Tyr Asp Leu Pro Asp Ser Glu Arg Ser Asp Asp Glu Ile Asn
65 70 75 80
Met Leu Arg Gln Ile Ala Val Asp Cys Pro Arg Thr Val Pro Asp Val
85 90 95
Ser Phe Phe Gln Gln Glu Gln Val Gln Lys Ser Leu Glu Arg Ile Leu
100 105 110
Tyr Thr Trp Ala Ile Arg His Pro Ala Ser Gly Tyr Val Gln Gly Ile
115 120 125
Asn Asp Leu Val Thr Pro Phe Leu Val Ile Phe Leu
130 135 140
```

(2) INFORMATION FOR SEQ ID NO:989:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 764 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..764

(D) OTHER INFORMATION: / Ceres Seq. ID 1595841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

```
acacggaaca agtaataaga acgaataact tttttttttt tgtttgacta gcaatgttac 60
aatagagaat attattttctt gagagaactt tgggaagatt acagagaaaa attgatggca 120
acttcgaagc ttcaagctct ttggaatcat ccagctggac ctaagacaat tcatttttgg 180
gcgccgacgt tcaagtgggg tataagcatt gccaatatcg cagactttca aaaacctcca 240
gagacacttt cataccctca acaaattgtg atcacaggta ctggacttgt ttggtcacgt 300
tacagcactg taattactcc gaaaaactgg aatctcttta gcgtgagtct tggtatggct 360
gtgtctctgg aatattttatt ggaagaccag tggtttttgc actagctgct gaaggagaag 420
ccggagtcaa aaaggtgctt caaatgttgc gtgatgagtt cgagctaacc atggcactaa 480
gtgggtgccg gtcaactcagt gaaatcacc gtaaccacat tgtcacggaa tgggacactc 540
cacgccattt gccaggtta tagagaagaa aaaaaaacag agaacagaaa caacacggca 600
ccaaaacgta ttcataattct gattgatcac tttgcttcta ctctgctata tttatatctc 660
gaaaaacttg tttctcccta tatcgatca caaaaacgtg cgtagagatt ctctgtaatg 720
ctatttggtc acattttacc tttccgttta ttcttattgc ttgt
```

(2) INFORMATION FOR SEQ ID NO:990:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1595842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

00669900 "08559950

Met Ala Thr Ser Lys Leu Gln Ala Leu Trp Asn His Pro Ala Gly Pro  
1 5 10 15  
Lys Thr Ile His Phe Trp Ala Pro Thr Phe Lys Trp Gly Ile Ser Ile  
20 25 30  
Ala Asn Ile Ala Asp Phe Gln Lys Pro Pro Glu Thr Leu Ser Tyr Pro  
35 40 45  
Gln Gln Ile Val Ile Thr Gly Thr Gly Leu Val Trp Ser Arg Tyr Ser  
50 55 60  
Thr Val Ile Thr Pro Lys Asn Trp Asn Leu Phe Ser Val Ser Leu Gly  
65 70 75 80  
Met Ala Val Ser Leu Glu Tyr Leu Leu Glu Asp Gln Trp Phe Leu His  
85 90 95

(2) INFORMATION FOR SEQ ID NO:991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..741
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

acatcaacac gccctaaaac cgctctcgag agacgaatcg ctctcagctt cttctagaac 60  
cttctccttc tccttcgaag catcgctgcc ttcaagatca cactacctcg cacaacaatg 120  
gagttctggg gtgttgaagt taagaatggc aaaccacttc acctagatcc tgggctagac 180  
aggctcgatg acatctctca ggttgctttg ggagagagta agaacaatgt aaccgaacca 240  
atccagcttt acgtgactgt tggatcggt aagcttctca ttggaacgct atctcatgag 300  
aagtttcctc agctgtctac ggagattgtc ttggaaagga actttgcgct gtctcatact 360  
tggaagaatg ggagcgtttt cttctctggt tacaagttg atgcatctga tcccagacct 420  
gaggatttga ttgatgatca acttgaggct gctggtttca aagctgctcc gaaatctgct 480  
gcgaaacagg tgaactttca gttgccaaat gaagatgtca aagccaagca agatgatgac 540  
gctgacggtg gtgaagaaga ttcttcagat gatgatgata gtgaaaactc tggagacgag 600  
gaggaagaga aggttactgc tgaatctgac agtgaggaag atgactcatc agacgacgaa 660  
gaagatgact cctcagaaga ggaaccccca aagaagcctg aagaacccaa gaagagggtc 720  
gcagaaccca actcctccaa g

(2) INFORMATION FOR SEQ ID NO:992:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..208
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

Met Glu Phe Trp Gly Val Glu Val Lys Asn Gly Lys Pro Leu His Leu  
1 5 10 15  
Asp Pro Gly Leu Asp Arg Leu Val His Ile Ser Gln Val Ala Leu Gly  
20 25 30  
Glu Ser Lys Asn Asn Val Thr Glu Pro Ile Gln Leu Tyr Val Thr Val  
35 40 45  
Gly Ser Asp Lys Leu Leu Ile Gly Thr Leu Ser His Glu Lys Phe Pro  
50 55 60  
Gln Leu Ser Thr Glu Ile Val Leu Glu Arg Asn Phe Ala Leu Ser His  
65 70 75 80

00689980 101300

(2) INFORMATION FOR SEQ ID NO:993:

(A) LENGTH: 1128 base pairs

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1128

(D) OTHER INFORMATION: / Ceres Seq. ID 1595853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:999. |            |            |            |            |            |      |
|-------------------------------------------|------------|------------|------------|------------|------------|------|
| gattggatcg                                | gggaatttgg | gaaaagtatg | gagaagaaga | cgaaagtgtc | aattgtggga | 60   |
| ggtactggat                                | acttgggtca | gcactcttct | caagctttcg | ccggcaacta | agcggtgaat | 120  |
| gtgagctata                                | cgacgtcgct | ttcactcacc | attcttctcc | acttcccgct | cgtttgctcg | 180  |
| acgctttccc                                | tcattccccc | gcgtttcctg | tcgatcttaa | atccgggtct | gggctcaatt | 240  |
| ccatatccca                                | ggactttcgt | cagcctgatg | tggtcgtgaa | ttgtgctgct | ctgtctgtcc | 300  |
| cacgagcttg                                | cgagcaagat | ccagattccg | ccatgtccat | caacgtacct | acttctcttg | 360  |
| taaactgggt                                | atcaagtttt | gagactaaca | aaaccttggt | gattcatctc | tctactgata | 420  |
| aagtttatca                                | aggtgtcaag | tctttctaca | aggaagaaga | tgagactggt | gcagtcaacg | 480  |
| tttatgggaa                                | atcaaaagtt | gcagcagagc | ttctcatcaa | ggataagtgt | caaagctttg | 540  |
| caatattgag                                | aagtagtata | atctttggtc | ctcaaactgt | atcacctctc | cccaagactc | 600  |
| tcccaattca                                | gtggattgat | agctccttaa | agaaagggga | cacggtagac | ttcttccatg | 660  |
| acgagtttcg                                | ttgccccatt | taogttaagg | atcttgtgaa | tatcactttc | aaattaatag | 720  |
| acagatgggt                                | ctctgatgat | aaacagatgc | ggctagtctt | gaatgctgtg | ggacccgaga | 780  |
| ggctatctcg                                | tgttcaaagt | gctcaaatgg | ttgcagaagt | cagaggatac | gacctgtcct | 840  |
| tgattaaaca                                | tgtgtctgca | tcatcgattg | atcggtgcgt | agtgacacca | gcagatatat | 900  |
| ctatggacat                                | aactaaactg | attcatatac | ttgagctctc | tccaacttct | ttcaaggaag | 960  |
| tggttgaggt                                | aacgcttgac | tctgaatctc | attctcatat | gctcccatga | tagtattccc | 1020 |
| ttatgtgctc                                | ttctttacca | ctctgcttct | ttctatggag | aaaaatctcg | gtttgagaaa | 1080 |
| accaatgtaa                                | aacggttgat | atggtttcgg | aattaaggtt | tggttttc   |            |      |

(2) INFORMATION FOR SEQ ID NO:994:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 335 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..335

(D) OTHER INFORMATION: / Ceres Seq. ID 1595854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:



Leu Asp Arg Gly Ile Trp Glu Lys Tyr Gly Glu Glu Asp Glu Ser Ala  
1 5 10 15  
Asn Cys Gly Arg Tyr Trp Ile Leu Gly Ser Ala Ser Ser Ser Ser Phe  
20 25 30  
Arg Arg Gln Leu Ser Gly Glu Cys Glu Leu Tyr Asp Val Ala Phe Thr  
35 40 45  
His His Ser Ser Pro Leu Pro Ala Arg Leu Leu Asp Ala Phe Pro His  
50 55 60  
Ser Pro Ala Phe Pro Val Asp Leu Lys Ser Gly Leu Gly Leu Asn Ser  
65 70 75 80  
Ile Ser Gln Asp Phe Arg Gln Pro Asp Val Val Val Asn Cys Ala Ala  
85 90 95  
Leu Ser Val Pro Arg Ala Cys Glu Gln Asp Pro Asp Ser Ala Met Ser  
100 105 110  
Ile Asn Val Pro Thr Ser Leu Val Asn Trp Leu Ser Ser Phe Glu Thr  
115 120 125  
Asn Lys Thr Leu Leu Ile His Leu Ser Thr Asp Gln Val Tyr Gln Gly  
130 135 140  
Val Lys Ser Phe Tyr Lys Glu Glu Asp Glu Thr Val Ala Val Asn Val  
145 150 155 160  
Tyr Gly Lys Ser Lys Val Ala Ala Glu Leu Leu Ile Lys Asp Lys Cys  
165 170 175  
Gln Ser Phe Ala Ile Leu Arg Ser Ser Ile Ile Phe Gly Pro Gln Thr  
180 185 190  
Val Ser Pro Leu Pro Lys Thr Leu Pro Ile Gln Trp Ile Asp Ser Ser  
195 200 205  
Leu Lys Lys Gly Asp Thr Val Asp Phe Phe His Asp Glu Phe Arg Cys  
210 215 220  
Pro Ile Tyr Val Lys Asp Leu Val Asn Ile Thr Phe Lys Leu Ile Asp  
225 230 235 240  
Arg Trp Val Ser Asp Asp Lys Gln Met Arg Leu Val Leu Asn Ala Gly  
245 250 255  
Gly Pro Glu Arg Leu Ser Arg Val Gln Met Ala Gln Met Val Ala Glu  
260 265 270  
Val Arg Gly Tyr Asp Leu Ser Leu Ile Lys His Val Ser Ala Ser Ser  
275 280 285  
Ile Asp Arg Gly Val Val Ser Pro Ala Asp Ile Ser Met Asp Ile Thr  
290 295 300  
Lys Leu Ile His Thr Leu Glu Leu Ser Pro Thr Ser Phe Lys Glu Gly  
305 310 315 320  
Val Arg Leu Thr Leu Asp Ser Glu Ser His Ser His Met Leu Pro  
325 330 335

(2) INFORMATION FOR SEQ ID NO:995:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..225
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

Met Ser Ile Asn Val Pro Thr Ser Leu Val Asn Trp Leu Ser Ser Phe  
1 5 10 15  
Glu Thr Asn Lys Thr Leu Leu Ile His Leu Ser Thr Asp Gln Val Tyr  
20 25 30  
Gln Gly Val Lys Ser Phe Tyr Lys Glu Glu Asp Glu Thr Val Ala Val  
35 40 45  
Asn Val Tyr Gly Lys Ser Lys Val Ala Ala Glu Leu Leu Ile Lys Asp

00669900 101300

Cys Leu Leu Leu Ile Ser His Gln Leu Pro Pro Asn Pro Thr Lys Val

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ser | Val | Ser | Thr | Ala | Glu | Lys | Ala | Ser | Glu | Ile | Val | Leu | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ile | Arg | Glu | Ile | Ser | Gly | Leu | Ile | Lys | Leu | Pro | Gly | Ser | Lys | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ser | Asn | Arg | Ile | Leu | Leu | Leu | Ala | Ala | Leu | Ser | Glu | Gly | Thr | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Val | Asp | Asn | Leu | Leu | Asn | Ser | Asp | Asp | Ile | Asn | Tyr | Met | Leu | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ala | Leu | Lys | Arg | Leu | Gly | Leu | Asn | Val | Glu | Thr | Asp | Ser | Glu | Asn | Asn |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Ala | Xaa | Val | Glu | Gly | Cys | Gly | Gly | Ile | Phe | Pro | Ala | Ser | Ile | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Lys | Ser | Asp | Ile | Glu | Leu | Tyr | Leu | Gly | Asn | Ala | Gly | Thr | Ala | Met |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

[illegible]

(2) INFORMATION FOR SEO ID NO:1000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..985

(D) OTHER INFORMATION: / Ceres Seq. ID 1595906

|             |             |            |            |             |             |     |
|-------------|-------------|------------|------------|-------------|-------------|-----|
| tctaataattc | aatagttaca  | agacacttga | tgggagagga | gctaattgttc | acattgtttg  | 60  |
| tgggtggtgc  | atcactcttc  | aatatgtctc | caatatcatc | attcacaaca  | tccatatcca  | 120 |
| ccattgttac  | caatccggga  | atactaacgt | gcggtcaagt | ccaacgcact  | atgggttcag  | 180 |
| aacgaaatcg  | gacggtgatg  | gtatctctat | attcggatca | aaggacattt  | ggatcgacca  | 240 |
| ttgtttctcta | tcgagatgca  | aggacggtct | gatagatgcg | gtaatgggtt  | ccacaggaat  | 300 |
| aactatatgg  | aacaactctt  | tctctcacca | taatgaagtc | atgcttcttg  | gtcacagcga  | 360 |
| ccactatgaa  | ccagacagtg  | gcatgcaggt | aacaatttcg | tttaatacct  | ttggagagaa  | 420 |
| attgatacaa  | aggatgccga  | ggtgtcgacg | tggataatct | catgtggtta  | ataacgattt  | 480 |
| tactcaatgg  | gaaatgtatg  | ccattggcgg | tagcggtaac | ccgactatta  | acagtcaggg  | 540 |
| taaccgctac  | accgccccaa  | ccaaccggtt | tgccaaggag | gtgacaaaga  | gagtggaaac  | 600 |
| accggatggg  | gatttgaaag  | ggtggaattg | gagatcggag | ggggacattt  | tgggtgaatgg | 660 |
| agccttcttc  | gtggcatccg  | gggaaggtgc | ggaaatgagg | tatgagaagg  | catatagcgt  | 720 |
| cgagcctaaa  | tccgcctcat  | tcatcaccca | aatcacattt | cactctgggtg | ttcttggcgt  | 780 |
| tgggtggcagg | aataacaatc  | tggggatgtg | gactactact | ggatcggaag  | gtactagcgg  | 840 |
| tttagattct  | tataattgact | ataccgatga | aatgtctggc | gctggttcaa  | ccaaccggtt  | 900 |
| atcttttttc  | gttcttgttt  | tcttgctaag | ttcgatatca | tatttggctcg | tgttcacttc  | 960 |
| ttcaacccaa  | atgttttatgt | tgttaa     |            |             |             |     |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..327

(D) OTHER INFORMATION: / Ceres Seq. ID 1595907

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Phe | Asn | Ser | Tyr | Lys | Thr | Leu | Asp | Gly | Arg | Gly | Ala | Asn | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Ile | Val | Gly | Gly | Gly | Cys | Ile | Thr | Leu | Gln | Tyr | Val | Ser | Asn | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ile | His | Asn | Ile | His | Ile | His | His | Cys | Tyr | Gln | Ser | Gly | Asn | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Val | Arg | Ser | Ser | Pro | Thr | His | Tyr | Gly | Phe | Arg | Thr | Lys | Ser | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Asp | Gly | Ile | Ser | Ile | Phe | Gly | Ser | Lys | Asp | Ile | Trp | Ile | Asp | His |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Cys | Ser | Leu | Ser | Arg | Cys | Lys | Asp | Gly | Leu | Ile | Asp | Ala | Val | Met | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Thr | Gly | Ile | Thr | Ile | Ser | Asn | Asn | Phe | Phe | Ser | His | His | Asn | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Met | Leu | Leu | Gly | His | Ser | Asp | His | Tyr | Glu | Pro | Asp | Ser | Gly | Met |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Val | Thr | Ile | Ala | Phe | Asn | His | Phe | Gly | Glu | Lys | Leu | Ile | Gln | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ser | Thr | Gly | Ile | Thr | Ile | Ser | Asn | Asn | Phe | Phe | Ser | His | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Glu | Val | Met | Leu | Leu | Gly | His | Ser | Asp | His | Tyr | Glu | Pro | Asp | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Met | Gln | Val | Thr | Ile | Ala | Phe | Asn | His | Phe | Gly | Glu | Lys | Leu | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Arg | Met | Pro | Arg | Cys | Arg | Arg | Gly | Tyr | Ile | His | Val | Val | Asn | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Phe | Thr | Gln | Trp | Glu | Met | Tyr | Ala | Ile | Gly | Gly | Ser | Gly | Asn | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Ile | Asn | Ser | Gln | Gly | Asn | Arg | Tyr | Thr | Ala | Pro | Thr | Asn | Pro | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Lys | Glu | Val | Thr | Lys | Arg | Val | Glu | Thr | Pro | Asp | Gly | Asp | Trp | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Trp | Asn | Trp | Arg | Ser | Glu | Gly | Asp | Ile | Leu | Val | Asn | Gly | Ala | Phe |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Val | Ala | Ser | Gly | Glu | Gly | Ala | Glu | Met | Arg | Tyr | Glu | Lys | Ala | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Val | Glu | Pro | Lys | Ser | Ala | Ser | Phe | Ile | Thr | Gln | Ile | Thr | Phe | His |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Gly | Val | Leu | Gly | Val | Gly | Gly | Arg | Asn | Asn | Asn | Leu | Gly | Met | Trp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Thr | Thr | Thr | Gly | Ser | Glu | Gly | Thr | Ser | Gly | Leu | Asp | Ser | Tyr | Asn | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Tyr | Thr | Asp | Glu | Met | Ser | Gly | Ala | Gly | Ser | Thr | Asn | Arg | Leu | Ser | Phe |

[illegible]

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| atggctgaca | aatgttggtg  | gtacctcaga | cctatgttga | aatccggggc | tcatggaaga | 60  |
| aacatagtct | accgaccgga  | tgtcctgaaa | gatgcaaata | ttttcagcat | gtgcgacgat | 120 |
| cccgatgact | tctacgcggc  | tggccacgat | ccaaatgaca | tcaactctga | atgtcgctat | 180 |
| agacccttct | tcaaacgggtg | cttagaggct | gagcgaattg | tccttaggta | cgccgctgca | 240 |

(2) INFORMATION FOR SEO ID NO:1005:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..186

(D) OTHER INFORMATION: / Ceres Seq. ID 1595932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

|            |            |            |            |            |           |            |            |            |            |           |            |           |            |            |     |
|------------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|-----------|------------|------------|-----|
| Met<br>1   | Ala        | Asp        | Lys        | Cys<br>5   | Trp       | Trp        | Tyr        | Leu        | Arg<br>10  | Pro       | Met        | Leu       | Lys        | Ser<br>15  | Gly |
| Pro        | His        | Gly        | Arg        | Asn<br>20  | Ile       | Val        | Tyr        | Arg<br>25  | Pro        | Asp       | Val        | Leu       | Lys<br>30  | Asp        | Ala |
| Asn        | Ile        | Phe<br>35  | Ser        | Met        | Cys       | Asp        | Asp<br>40  | Pro        | Asp        | Asp       | Phe        | Tyr<br>45 | Ala        | Ala        | Gly |
| His        | Asp<br>50  | Pro        | Asn        | Asp        | Ile       | Asn<br>55  | Ser        | Glu        | Cys        | Arg       | Tyr<br>60  | Arg       | Pro        | Phe        | Phe |
| Lys<br>65  | Arg        | Cys        | Leu        | Glu        | Ala<br>70 | Glu        | Arg        | Ile        | Val        | Pro<br>75 | Arg        | Tyr       | Ala        | Ala        | Ala |
| Thr        | Leu        | Ala        | Cys        | Ala<br>85  | Ile       | Leu        | Tyr        | Ile        | Cys<br>90  | Val       | Val        | Asn       | Ala        | His<br>95  | Met |
| Gly        | Gly        | Val        | Tyr<br>100 | Phe        | Arg       | Leu        | Phe        | Gly<br>105 | Ser        | Asn       | His        | Tyr       | Ala<br>110 | Leu        | Glu |
| Ser        | Glu        | Asp<br>115 | Thr        | Arg        | Asp       | Ile        | Cys<br>120 | Glu        | Glu        | Val       | Leu        | Glu       | Glu        | Ile        | Lys |
| Lys        | Tyr<br>130 | Gly        | Asn        | Thr        | Leu       | Lys<br>135 | Tyr        | Thr        | Tyr        | Ala       | Lys<br>140 | Ser       | Phe        | Ser        | Tyr |
| Pro<br>145 | Glu        | Cys        | Gly        | Asp<br>150 | Ile       | Arg        | Thr        | Leu        | Asp<br>155 | Cys       | Ala        | Met       | Met        | Cys        | Tyr |
| Met        | Arg        | Ser        | Gly        | Leu<br>165 | Phe       | Asn        | Asn        | Leu        | Cys<br>170 | Asn       | Glu        | Cys       | Tyr        | Ile<br>175 | Trp |
| Trp        | Cys        | Ala        | Lys<br>180 | Arg        | Ile       | Ser        | Gln        | Ile<br>185 | Leu        |           |            |           |            |            |     |

(2) INFORMATION FOR SEO ID NO:1006:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1595934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Lys | Ser | Gly | Pro | His | Gly | Arg | Asn | Ile | Val | Tyr | Arg | Pro | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Leu | Lys | Asp | Ala | Asn | Ile | Phe | Ser | Met | Cys | Asp | Asp | Pro | Asp | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Tyr | Ala | Ala | Gly | His | Asp | Pro | Asn | Asp | Ile | Asn | Ser | Glu | Cys | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Arg | Pro | Phe | Phe | Lys | Arg | Cys | Leu | Glu | Ala | Glu | Arg | Ile | Val | Pro |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 50                                                              | 55  | 60  |
| Arg Tyr Ala Ala Ala Thr Leu Ala Cys Ala Ile Leu Tyr Ile Cys Val |     |     |
| 65                                                              | 70  | 75  |
| Val Asn Ala His Met Gly Gly Val Tyr Phe Arg Leu Phe Gly Ser Asn |     | 80  |
|                                                                 | 85  | 90  |
| His Tyr Ala Leu Glu Ser Glu Asp Thr Arg Asp Ile Cys Glu Glu Val |     | 95  |
|                                                                 | 100 | 105 |
| Leu Glu Glu Ile Lys Lys Tyr Gly Asn Thr Leu Lys Tyr Thr Tyr Ala |     | 110 |
|                                                                 | 115 | 120 |
| Lys Ser Phe Ser Tyr Pro Glu Cys Gly Asp Ile Arg Thr Leu Asp Cys |     | 125 |
|                                                                 | 130 | 135 |
| Ala Met Met Cys Tyr Met Arg Ser Gly Leu Phe Asn Asn Leu Cys Asn |     | 140 |
| 145                                                             | 150 | 155 |
| Glu Cys Tyr Ile Trp Trp Cys Ala Lys Arg Ile Ser Gln Ile Leu     |     | 160 |
|                                                                 | 165 | 170 |
|                                                                 |     | 175 |

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1305
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

|             |             |            |             |             |            |      |
|-------------|-------------|------------|-------------|-------------|------------|------|
| atggcggaagc | cttcaacatc  | tcagaagaaa | tctcatagtg  | aagatgataa  | aaagcaaaga | 60   |
| gtatccaaca  | tttacaatga  | ggccaagaaa | catctgtctg  | agatgttaaa  | caatggagat | 120  |
| cttgattcga  | agtcaacgag  | cagacaggtt | caaagaagcc  | tagggagaat  | tctctccttt | 180  |
| cctgagtact  | tgtctcctct  | aaacagccca | ggaagaagat  | gggaaaagag  | ctcaatagct | 240  |
| cacaagaagt  | ctgcttcagc  | ggatttcata | aatcttgtga  | acatcaagaa  | agaaactcat | 300  |
| gcgagccaac  | cagaggaaaa  | tgctgatatt | caggtctgca  | atctaagcaa  | agaacctgat | 360  |
| gattctatcc  | aaccaatcgc  | aagtgaacct | actgagaaaa  | gtgttgacat  | tgaagatgaa | 420  |
| actgctaacg  | aagataaaat  | gtcttctgca | ggttctgcag  | atgatgtgat  | gattcccaat | 480  |
| gagctagatg  | aaacctctct  | tgaagagagc | caaccaccac  | tgtcctcctc  | tgtggcctca | 540  |
| ccatcccaact | ggttngctca  | aactgaggag | tgcaaatcag  | ctattactga  | tttcccggag | 600  |
| tggtcaagcc  | caatatcagt  | tcttgagcca | ctcttcggtg  | aagatgatat  | aagcccagca | 660  |
| aaaaatgcgat | ctcagtcctg  | tgaagcagag | gtgcaaccgt  | ggtgtatcca  | cttcgatgaa | 720  |
| aaagatcctg  | cacctacata  | ccgagagaat | tctgtgacaa  | gtgacaaaaga | attgggtgtt | 780  |
| aagtatgtaa  | aagctgtctt  | ggacgcagta | gactcagaca  | tcgaagagct  | ctatctaaag | 840  |
| gcgcaattct  | ctgaccagct  | tcttgaacca | gcacttatca  | gcaatatacc  | attctgtcca | 900  |
| aaccagcttt  | gtcctgacca  | tgagctcctc | tttgactgca  | tcaatgaagc  | tctcatggag | 960  |
| ttatgtctgt  | gcccaccttg  | ggcttcggtt | gttacaccaa  | gaaccagagt  | cttctctacc | 1020 |
| gtcaaaagcg  | tcattccatga | ggttcaagaa | gcgggtttact | ggcatctctt  | gccattgcca | 1080 |
| ctccctcaag  | ccttgggatca | gatagttaga | aaagatatgg  | ctagagctgg  | aaactggtta | 1140 |
| gacatcagat  | gtgacattga  | ctgcattggc | ttcgaaacta  | gtgaactgat  | tctcaacgag | 1200 |
| ttactcgaag  | agctcactct  | caactctctc | aacaacactg  | agcactctct  | ggtttcacct | 1260 |
| gagttgaaga  | cggatgggag  | catccttatt | ctagaaaggt  | cttga       |            |      |

(2) INFORMATION FOR SEQ ID NO:1008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..434
- (D) OTHER INFORMATION: / Ceres Seq. ID 1595944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

09595943 1007



(2) INFORMATION FOR SEQ ID NO:1009:  
 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 400 amino acids  
     (B) TYPE: amino acid  
     (C) STRANDEDNESS:

[illegible]

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..400  
(D) OTHER INFORMATION: / Ceres Seq. ID 1595946  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Asn | Asn | Gly | Asp | Leu | Asp | Ser | Lys | Ser | Thr | Ser | Arg | Gln | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Arg | Ser | Leu | Gly | Arg | Ile | Leu | Ser | Phe | Pro | Glu | Tyr | Leu | Ser | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Asn | Ser | Pro | Gly | Arg | Arg | Trp | Glu | Lys | Ser | Ser | Ile | Ala | His | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Ser | Ala | Ser | Ala | Asp | Phe | Ile | Asn | Leu | Val | Asn | Ile | Lys | Lys | Glu |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Thr | His | Ala | Ser | Gln | Pro | Glu | Glu | Asn | Ala | Asp | Ile | Gln | Val | Cys | Asn |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Ser | Lys | Glu | Pro | Asp | Asp | Ser | Ile | Gln | Pro | Ile | Ala | Ser | Glu | Pro |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Glu | Lys | Ser | Val | Asp | Ile | Glu | Asp | Glu | Thr | Ala | Asn | Glu | Asp | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Met | Ser | Ser | Ala | Gly | Ser | Ala | Asp | Asp | Val | Met | Ile | Pro | Asn | Glu | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Asp | Glu | Thr | Ser | Leu | Glu | Glu | Ser | Gln | Pro | Pro | Leu | Ser | Ser | Ser | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Ser | Pro | Ser | His | Trp | Xaa | Ala | Gln | Thr | Glu | Glu | Cys | Lys | Ser | Ala |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Thr | Asp | Phe | Pro | Glu | Trp | Ser | Ser | Pro | Ile | Ser | Val | Leu | Glu | Pro |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Phe | Val | Glu | Asp | Asp | Ile | Ser | Pro | Ala | Lys | Met | Arg | Ser | Gln | Ser |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Glu | Ala | Glu | Val | Gln | Pro | Trp | Cys | Ile | His | Phe | Asp | Glu | Lys | Asp |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Pro | Ala | Pro | Thr | Tyr | Arg | Glu | Asn | Ser | Val | Thr | Ser | Asp | Lys | Glu | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Val | Phe | Lys | Tyr | Val | Lys | Ala | Val | Leu | Asp | Ala | Val | Asp | Ser | Asp | Ile |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Glu | Leu | Tyr | Leu | Lys | Ala | Gln | Phe | Ser | Asp | Gln | Leu | Leu | Glu | Pro |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Leu | Ile | Ser | Asn | Ile | Pro | Phe | Cys | Pro | Asn | Gln | Leu | Cys | Pro | Asp |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| His | Glu | Leu | Leu | Phe | Asp | Cys | Ile | Asn | Glu | Ala | Leu | Met | Glu | Leu | Cys |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Cys | Cys | Pro | Pro | Trp | Ala | Ser | Phe | Val | Thr | Pro | Arg | Thr | Arg | Val | Phe |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ser | Thr | Val | Lys | Ser | Val | Ile | His | Glu | Val | Gln | Glu | Ala | Val | Tyr | Trp |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| His | Leu | Leu | Pro | Leu | Pro | Leu | Pro | His | Ala | Leu | Asp | Gln | Ile | Val | Arg |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Lys | Asp | Met | Ala | Arg | Ala | Gly | Asn | Trp | Leu | Asp | Ile | Arg | Cys | Asp | Ile |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Asp | Cys | Ile | Gly | Phe | Glu | Thr | Ser | Glu | Leu | Ile | Leu | Asn | Glu | Leu | Leu |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Glu | Glu | Leu | Thr | Leu | Asn | Ser | Leu | Asn | Asn | Thr | Glu | His | Ser | Leu | Val |
|     | 370 |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |     |
| Ser | Pro | Glu | Leu | Lys | Thr | Asp | Gly | Ser | Ile | Leu | Ile | Leu | Glu | Arg | Ser |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |

(2) INFORMATION FOR SEQ ID NO:1010:  
(i) SEQUENCE CHARACTERISTICS:

0960990010300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

(2) INFORMATION FOR SEQ ID NO:1011:

(A) LENGTH: 148 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

```
(A) NAME/KEY: peptide
(B) LOCATION: 1..148
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

(2) INFORMATION FOR SEQ ID NO:1012:

(A) LENGTH: 136 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

```
(A) NAME/KEY: peptide
(B) LOCATION: 1..136
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1595994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:

Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu  
1 5 10 15  
Leu Asn Ser Ser Glu Tyr Thr Gly Ala Ile Asp Ile Trp Ser Val Gly  
20 25 30  
Cys Ile Phe Met Glu Ile Leu Arg Arg Glu Thr Leu Phe Pro Gly Lys  
35 40 45  
Asp Tyr Val Gln Gln Leu Lys Leu Ile Thr Glu Leu Gly Ser Pro  
50 55 60  
Asp Asp Ser Asp Leu Asp Phe Leu Arg Ser Asp Asn Ala Arg Lys Tyr  
65 70 75 80  
Val Lys Gln Leu Pro His Val Gln Lys Gln Ser Phe Arg Glu Lys Phe  
85 90 95  
Pro Asn Ile Ser Pro Met Ala Leu Asp Leu Ala Glu Lys Met Leu Val  
100 105 110  
Phe Asp Pro Ser Lys Arg Ile Thr Gly Ala Tyr His Val Val Leu Leu  
115 120 125  
Leu Cys Tyr Ala Ile Asn Gly Met  
130 135

(2) INFORMATION FOR SEQ ID NO:1013:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1595995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

Met Glu Ile Leu Arg Arg Glu Thr Leu Phe Pro Gly Lys Asp Tyr Val  
1 5 10 15  
Gln Gln Leu Lys Leu Ile Thr Glu Leu Leu Gly Ser Pro Asp Asp Ser  
20 25 30  
Asp Leu Asp Phe Leu Arg Ser Asp Asn Ala Arg Lys Tyr Val Lys Gln  
35 40 45  
Leu Pro His Val Gln Lys Gln Ser Phe Arg Glu Lys Phe Pro Asn Ile  
50 55 60  
Ser Pro Met Ala Leu Asp Leu Ala Glu Lys Met Leu Val Phe Asp Pro  
65 70 75 80  
Ser Lys Arg Ile Thr Gly Ala Tyr His Val Val Leu Leu Leu Cys Tyr  
85 90 95  
Ala Ile Asn Gly Met  
100

(2) INFORMATION FOR SEQ ID NO:1014:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..699

(D) OTHER INFORMATION: / Ceres Seq. ID 1596012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| tctccgacgg aagctctttt ccttctcaac ggcaaatgga tctctgccta cacatcggtc | 60  |
| gtgaatttgt tcccgttgct atcacgagga atcgtagcgt taataaaagt cgatgagatc | 120 |
| tctcaaacca ttgattcaga taacttcacc gtccagaact ctgttcgttt cgctggtcct | 180 |
| ttaggtacaa actcgattag caccaacgct aaattcgaaa tccgaagccc taaacgcgtc | 240 |

00969980 00668960

cagattaagt ttgagcaagg cgtaattggg acgcctcagc taacggattc tattgagata 300  
ccggaatatg tagaggttct tgggtcaaaag attgatctta acccgatcag aggggttactt 360  
acctcggtgc aagacacagc ctcgtctgtg gctagaacca tatcaagcca accaccgttg 420  
aaattctctt tgccggcgga caatgcgcag tcttggtac tcacgactta tctagacaaa 480  
gacattcgga tctctagagg agacggtgga agtttactgt acttgatgta ctcagtcatt 540  
ggaaatggtt ctattagcat gagacaatca gccaatcagt ttgttagagg gtttgatgca 600  
gagagcatga aagcatttga agagcttaga atcagagcca aaactgaaag tggaggagac 660  
gataataatg ataacaatga agaagaatct gtaaactga

(2) INFORMATION FOR SEQ ID NO:1015:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..232
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

Ser Pro Thr Glu Ala Leu Phe Leu Leu Asn Gly Lys Trp Ile Leu Ala  
1 5 10 15  
Tyr Thr Ser Phe Val Asn Leu Phe Pro Leu Leu Ser Arg Gly Ile Val  
20 25 30  
Pro Leu Ile Lys Val Asp Glu Ile Ser Gln Thr Ile Asp Ser Asp Asn  
35 40 45  
Phe Thr Val Gln Asn Ser Val Arg Phe Ala Gly Pro Leu Gly Thr Asn  
50 55 60  
Ser Ile Ser Thr Asn Ala Lys Phe Glu Ile Arg Ser Pro Lys Arg Val  
65 70 75 80  
Gln Ile Lys Phe Glu Gln Gly Val Ile Gly Thr Pro Gln Leu Thr Asp  
85 90 95  
Ser Ile Glu Ile Pro Glu Tyr Val Glu Val Leu Gly Gln Lys Ile Asp  
100 105 110  
Leu Asn Pro Ile Arg Gly Leu Leu Thr Ser Val Gln Asp Thr Ala Ser  
115 120 125  
Ser Val Ala Arg Thr Ile Ser Ser Gln Pro Pro Leu Lys Phe Ser Leu  
130 135 140  
Pro Ala Asp Asn Ala Gln Ser Trp Leu Leu Thr Thr Tyr Leu Asp Lys  
145 150 155 160  
Asp Ile Arg Ile Ser Arg Gly Asp Gly Gly Ser Leu Leu Tyr Leu Met  
165 170 175  
Tyr Ser Val Ile Gly Asn Gly Ser Ile Ser Met Arg Gln Ser Ala Asn  
180 185 190  
Gln Phe Val Arg Gly Phe Asp Ala Glu Ser Met Lys Ala Phe Glu Glu  
195 200 205  
Leu Arg Ile Arg Ala Lys Thr Glu Ser Gly Gly Asp Asp Asn Asn Asp  
210 215 220  
Asn Asn Glu Glu Glu Ser Val Asn  
225 230

(2) INFORMATION FOR SEQ ID NO:1016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1969
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596022

09689980-101300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

|            |            |             |            |            |             |      |
|------------|------------|-------------|------------|------------|-------------|------|
| tctaaagatc | gaggaggctc | gggaatccac  | aaaaccaatc | cctgatccgg | taatatctat  | 60   |
| ctgccttgac | gacaaaaaac | ccgagcgatg  | cgtggaaatc | ggcagagatc | taggagaaga  | 120  |
| attaacagct | gaactcacca | cattcctcag  | agaaaaagtc | aatatattcg | cctgggtcccc | 180  |
| agaagatctg | cccggagtaa | gtgttgacat  | cgtatcacac | gagctcaaca | tcgacccgac  | 240  |
| ttttaaatct | gttaagcaga | agaggaggaa  | attgggtcga | gagcgagcag | aagccgtgaa  | 300  |
| agccgaagta | gaaaaattac | taaggatcga  | ctccatcacc | gaggcaaaat | atcttgattg  | 360  |
| gctcgcgaa  | ccaatcgtag | taaaaaagaa  | aaacggcaaa | tggaaagtct | gcgtagattt  | 420  |
| caccgaccat | aacaaagcct | gcccgaagaa  | cagtttccca | ttaccgcaca | tcgatcgcc   | 480  |
| cgtagaatca | actttctgaa | acaagttgtt  | gtcattcatg | gacgctttcg | ctgggttaca  | 540  |
| ccagatcatg | atgaaccccg | acgatcaaga  | aaaaaatgca | ttcgacacag | aacaaggcat  | 600  |
| cttctgttac | cgagtgtatg | cattcggaat  | caaaaacgct | ggggcgactt | atcaacgctt  | 660  |
| cgtcaacaaa | atcttcacat | tacagatcag  | gaagacaatg | gaagtttaca | tcgaagacat  | 720  |
| gttagtgaaa | tccatggcag | aggaagaaca  | catatcccat | ttgcgcgaat | gtttccaaca  | 780  |
| gcttaacctc | tacaacgtca | aactcaatcc  | agctaagtgc | cgcttcgggg | taagatccgg  | 840  |
| agagttcctc | gggtatctag | tcacgcacca  | cggcatcgag | gtgaatccga | agcaaatcga  | 900  |
| cgcattgttg | ggaatgacat | cacctcagaa  | caagcgagaa | gtgcagcgcc | taacaggaag  | 960  |
| agttacggcc | cttaactgtt | tcattctctg  | ctcaaccgac | aaatgcttga | ccttttacga  | 1020 |
| tgtgcttcgg | gaaacaaga  | agttcgaatg  | gacgatccgg | tgcgaagaag | cttttcagga  | 1080 |
| actcaagaaa | tatctggcaa | caccacccat  | cctcgcaaaa | cccataatcg | aagaaccact  | 1140 |
| atacttgtag | gttgtcatat | gggatactgc  | agtcagtggg | gtgttagttc | gagaagacaa  | 1200 |
| aggtgaacag | aaaccgattt | tttacgtatc  | gcagactttc | accagtgcgg | aatcttgcta  | 1260 |
| cccgcgaatg | gagaaactcg | ctttggcagc  | cataatgtcg | gctcggaaac | tgcgacccta  | 1320 |
| ctttcaatcc | aatttcacat | tagtaatggg  | atccatgccg | ctccgcgcta | tcttacacag  | 1380 |
| tccaagcgaa | tcaggatgcc | tagctaaatg  | ggcgatcgag | ctcagcgaat | atgacatcaa  | 1440 |
| gtatcggaac | aaaacatacg | gctcgctcat  | aaaacaaggc | tggggtgtag | gcacccgcct  | 1500 |
| cacttcgcc  | acagcagagg | tcctcgagca  | atcatttaga | ttaaacttca | aggctaccaa  | 1560 |
| caatgtggcc | gaatacgaag | cgctcgtagc  | aggacttaat | ctggatcggg | ggctaaagat  | 1620 |
| agagaaaatc | cgagctttta | gcgaccccca  | acttgctgca | aatcagttca | acagagaata  | 1680 |
| catagctcgg | gacgaaagaa | tggaaagccta | tctaactcat | gtacaaaatc | tgacgaagaa  | 1740 |
| tttcgacgag | ttcgagttaa | caaggatccc  | tcgaggagaa | aatacatcgg | ctgacgccct  | 1800 |
| agctgctcta | gcctcgacat | ctgacccgcg  | cctgagaaga | gtcatcccag | tagagttcat  | 1860 |
| cgaaaagcca | aattattgag | tcaacgaaga  | agaacatgtc | ctccccatac | aaatcggcac  | 1920 |
| ggatcacaa  | gacgctcgg  | acgacagccc  | ggacgaattc | aactcatag  |             |      |

(2) INFORMATION FOR SEQ ID NO:1017:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 655 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..655

(D) OTHER INFORMATION: / Ceres Seq. ID 1596023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Lys | Ile | Glu | Ala | Arg | Glu | Ser | Thr | Lys | Pro | Ile | Pro | Asp | Pro |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ile | Ser | Ile | Cys | Leu | Asp | Asp | Lys | Lys | Pro | Glu | Arg | Cys | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Ile | Gly | Arg | Asp | Leu | Gly | Glu | Glu | Leu | Thr | Ala | Glu | Leu | Thr | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Leu | Arg | Glu | Asn | Val | Asn | Ile | Phe | Ala | Trp | Ser | Pro | Glu | Asp | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Gly | Val | Ser | Val | Asp | Ile | Val | Ser | His | Glu | Leu | Asn | Ile | Asp | Pro |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     | 80  |     |
| Phe | Lys | Ser | Val | Lys | Gln | Lys | Arg | Arg | Lys | Leu | Gly | Arg | Glu | Arg |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |
| Glu | Ala | Val | Lys | Ala | Glu | Val | Glu | Lys | Leu | Leu | Arg | Ile | Asp | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Thr | Glu | Ala | Lys | Tyr | Leu | Asp | Trp | Leu | Ala | Asn | Pro | Ile | Val | Val |

|            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|            | Lys | Lys | Asn | Gly | Lys | Trp | Lys | Val | Cys | Val | Asp | Phe | Thr | Asp | His | Asn |
|            |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys<br>145 | Ala | Cys | Pro | Lys | Asp | Ser | Phe | Pro | Leu | Pro | His | Ile | Asp | Arg | Leu |     |
| Val        | Glu | Ser | Thr | Ser | Glu | Asn | Lys | Leu | Leu | Ser | Phe | Met | Asp | Ala | Phe |     |
|            |     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala        | Gly | Tyr | Asn | Gln | Ile | Met | Met | Asn | Pro | Asp | Asp | Gln | Glu | Lys | Asn |     |
|            |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Ala        | Phe | Asp | Thr | Glu | Gln | Gly | Ile | Phe | Cys | Tyr | Arg | Val | Met | Pro | Phe |     |
|            |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Gly        | Leu | Lys | Asn | Ala | Gly | Ala | Thr | Tyr | Gln | Arg | Phe | Val | Asn | Lys | Ile |     |
|            | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Phe        | Thr | Leu | Gln | Ile | Arg | Lys | Thr | Met | Glu | Val | Tyr | Ile | Glu | Asp | Met |     |
| 225        |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Leu        | Val | Lys | Ser | Met | Ala | Glu | Glu | Glu | His | Ile | Ser | His | Leu | Arg | Glu |     |
|            |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Cys        | Phe | Gln | Gln | Leu | Asn | Leu | Tyr | Asn | Val | Lys | Leu | Asn | Pro | Ala | Lys |     |
|            |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Cys        | Arg | Phe | Gly | Val | Arg | Ser | Gly | Glu | Phe | Leu | Gly | Tyr | Leu | Val | Thr |     |
|            |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| His        | His | Gly | Ile | Glu | Val | Asn | Pro | Lys | Gln | Ile | Asp | Ala | Leu | Leu | Gly |     |
|            |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
| Met        | Thr | Ser | Pro | Gln | Asn | Lys | Arg | Glu | Val | Gln | Arg | Leu | Thr | Gly | Arg |     |
| 305        |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |
| Val        | Thr | Ala | Leu | Asn | Cys | Phe | Ile | Ser | Arg | Ser | Thr | Asp | Lys | Cys | Leu |     |
|            |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Thr        | Phe | Tyr | Asp | Val | Leu | Arg | Gly | Asn | Lys | Lys | Phe | Glu | Trp | Thr | Ile |     |
|            |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Arg        | Cys | Glu | Glu | Ala | Phe | Gln | Glu | Leu | Lys | Lys | Tyr | Leu | Ala | Thr | Pro |     |
|            |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |     |
| Pro        | Ile | Leu | Ala | Lys | Pro | Ile | Ile | Glu | Glu | Pro | Leu | Tyr | Leu | Tyr | Val |     |
|            |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |     |
| Val        | Ile | Trp | Asp | Thr | Ala | Val | Ser | Gly | Val | Leu | Val | Arg | Glu | Asp | Lys |     |
| 385        |     |     |     |     | 390 |     |     |     | 395 |     |     |     |     | 400 |     |     |
| Gly        | Glu | Gln | Lys | Pro | Ile | Phe | Tyr | Val | Ser | Gln | Thr | Phe | Thr | Ser | Ala |     |
|            |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |     |
| Glu        | Ser | Cys | Tyr | Pro | Gln | Met | Glu | Lys | Leu | Ala | Leu | Ala | Ala | Ile | Met |     |
|            |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |     |
| Ser        | Ala | Arg | Lys | Leu | Arg | Pro | Tyr | Phe | Gln | Ser | Asn | Phe | Ile | Ile | Val |     |
|            |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |     |
| Met        | Gly | Ser | Met | Pro | Leu | Arg | Ala | Ile | Leu | His | Ser | Pro | Ser | Glu | Ser |     |
|            |     | 450 |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |     |
| Gly        | Cys | Leu | Ala | Lys | Trp | Ala | Ile | Glu | Leu | Ser | Glu | Tyr | Asp | Ile | Lys |     |
| 465        |     |     | </  |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1018:

(A) LENGTH: 483 amino acids

(C) STRANDEDNESS:

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: pep

(ix) FEATURE:

(A) NAM

(A) NAME/KEY: peptide

(B) LOCATION: 1..483

(D) OTHER INFORMATION: / Ceres Seq. ID 1596024

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

[illegible]



```
(2) INFORMATION FOR SEQ ID NO:1019:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 473 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..473
 (D) OTHER INFORMATION: / Ceres Seq. ID 1596025
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:
```

|                                       |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |
|---------------------------------------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|
| SEQUENCE DESCRIPTION: SEQ ID NO:10151 |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |
| Met 1                                 | Met 5   | Asn 10  | Pro 15  | Asp 20  | Asp 25  | Gln 30  | Glu 35  | Lys 40  | Asn 45  | Ala 50  | Phe 55  | Asp 60  | Thr 65  | Glu 70  | Gln 75  |
| Gly 1                                 | Ile 5   | Phe 10  | Cys 15  | Tyr 20  | Arg 25  | Val 30  | Met 35  | Pro 40  | Phe 45  | Gly 50  | Leu 55  | Lys 60  | Asn 65  | Ala 70  | Gly 75  |
| Ala 1                                 | Thr 5   | Tyr 10  | Gln 15  | Arg 20  | Phe 25  | Val 30  | Asn 35  | Lys 40  | Ile 45  | Phe 50  | Thr 55  | Leu 60  | Gln 65  | Ile 70  | Arg 75  |
| Lys 1                                 | Thr 5   | Met 10  | Glu 15  | Val 20  | Tyr 25  | Ile 30  | Glu 35  | Asp 40  | Met 45  | Leu 50  | Val 55  | Lys 60  | Ser 65  | Met 70  | Ala 75  |
| Glu 65                                | Glu 70  | Glu 75  | His 80  | Ile 85  | Ser 90  | His 95  | Leu 100 | Arg 105 | Glu 110 | Cys 115 | Phe 120 | Gln 125 | Gln 130 | Leu 135 | Asn 140 |
| Leu 1                                 | Tyr 5   | Asn 10  | Val 15  | Lys 20  | Leu 25  | Asn 30  | Pro 35  | Ala 40  | Lys 45  | Cys 50  | Arg 55  | Phe 60  | Gly 65  | Val 70  | Arg 75  |
| Ser 1                                 | Gly 5   | Glu 10  | Phe 15  | Leu 20  | Gly 25  | Tyr 30  | Leu 35  | Val 40  | Thr 45  | His 50  | His 55  | Gly 60  | Ile 65  | Glu 70  | Val 75  |
| Asn 1                                 | Pro 5   | Lys 10  | Gln 15  | Ile 20  | Asp 25  | Ala 30  | Leu 35  | Leu 40  | Gly 45  | Met 50  | Thr 55  | Ser 60  | Pro 65  | Gln 70  | Asn 75  |
| Lys 1                                 | Arg 5   | Glu 10  | Val 15  | Gln 20  | Arg 25  | Leu 30  | Thr 35  | Gly 40  | Arg 45  | Val 50  | Thr 55  | Ala 60  | Leu 65  | Asn 70  | Cys 75  |
| Phe 145                               | Ile 150 | Ser 155 | Arg 160 | Ser 165 | Thr 170 | Asp 175 | Lys 180 | Cys 185 | Leu 190 | Thr 195 | Phe 200 | Tyr 205 | Asp 210 | Val 215 | Leu 220 |
| Arg 1                                 | Gly 5   | Asn 10  | Lys 15  | Phe 20  | Glu 25  | Trp 30  | Thr 35  | Ile 40  | Arg 45  | Cys 50  | Glu 55  | Glu 60  | Ala 65  | Phe 70  |         |
| Gln 1                                 | Glu 5   | Leu 10  | Lys 15  | Lys 20  | Tyr 25  | Leu 30  | Ala 35  | Thr 40  | Pro 45  | Pro 50  | Ile 55  | Leu 60  | Ala 65  | Lys 70  | Pro 75  |
| Ile 1                                 | Ile 5   | Glu 10  | Glu 15  | Pro 20  | Leu 25  | Tyr 30  | Leu 35  | Tyr 40  | Val 45  | Val 50  | Ile 55  | Trp 60  | Asp 65  | Thr 70  | Ala 75  |
| Val 1                                 | Ser 5   | Gly 10  | Val 15  | Leu 20  | Val 25  | Arg 30  | Glu 35  | Asp 40  | Lys 45  | Gly 50  | Glu 55  | Gln 60  | Lys 65  | Pro 70  | Ile 75  |
| Phe 225                               | Tyr 230 | Val 235 | Ser 240 | Gln 245 | Thr 250 | Phe 255 | Thr 260 | Ser 265 | Ala 270 | Glu 275 | Ser 280 | Cys 285 | Tyr 290 | Pro 295 | Gln 300 |

[illegible]

Met Glu Lys Leu Ala Leu Ala Ala Ile Met Ser Ala Arg Lys Leu Arg  
245 250 255  
Pro Tyr Phe Gln Ser Asn Phe Ile Ile Val Met Gly Ser Met Pro Leu  
260 265 270  
Arg Ala Ile Leu His Ser Pro Ser Glu Ser Gly Cys Leu Ala Lys Trp  
275 280 285  
Ala Ile Glu Leu Ser Glu Tyr Asp Ile Lys Tyr Arg Asn Lys Thr Tyr  
290 295 300  
Gly Ser Ser Ser Lys Gln Gly Ser Gly Val Gly Ile Arg Leu Thr Ser  
305 310 315 320  
Pro Thr Ala Glu Val Leu Glu Gln Ser Phe Arg Leu Asn Phe Lys Ala  
325 330 335  
Thr Asn Asn Val Ala Glu Tyr Glu Ala Leu Val Ala Gly Leu Asn Leu  
340 345 350  
Asp Arg Gly Leu Lys Ile Glu Lys Ile Arg Ala Phe Ser Asp Pro Gln  
355 360 365  
Leu Val Ala Asn Gln Phe Asn Arg Glu Tyr Ile Ala Arg Asp Glu Arg  
370 375 380  
Met Glu Ala Tyr Leu Thr His Val Gln Asn Leu Thr Lys Asn Phe Asp  
385 390 395 400  
Glu Phe Glu Leu Thr Arg Ile Pro Arg Gly Glu Asn Thr Ser Ala Asp  
405 410 415  
Ala Leu Ala Ala Leu Ala Ser Thr Ser Asp Pro Arg Leu Arg Arg Val  
420 425 430  
Ile Pro Val Glu Phe Ile Glu Lys Pro Asn Ile Glu Leu Asn Glu Glu  
435 440 445  
Glu His Val Leu Pro Ile Gln Ile Gly Thr Asp His Asn Asp Ala Pro  
450 455 460  
Asp Asp Ser Pro Asp Glu Phe Asn Ser  
465 470

(2) INFORMATION FOR SEQ ID NO:1020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..969
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:

|             |             |             |             |              |             |     |
|-------------|-------------|-------------|-------------|--------------|-------------|-----|
| tcttcacttt  | cttcatacaca | acaataacttc | tgcgctcctg  | caacgcacatcc | gcaaaggcca  | 60  |
| aaacgcaacc  | ngctgttccc  | agcgattcta  | atctttgggtg | attcaacagt   | cgacacagggc | 120 |
| aacaataact  | acccttcaca  | aacaatcttc  | agagctaaac  | atgttcttac   | gtttgttcct  | 180 |
| cccttccttac | aaccaaatct  | caccgaccaa  | gaaattgtaa  | ccggagtctg   | ttttgcatca  | 240 |
| gcaggtgccg  | gttacgatga  | ccaaaccagt  | ctcacgacac  | aagcgattcg   | tgtctcggaa  | 300 |
| caaccaaata  | tgttcaagag  | ttacattgct  | cgtcttaaga  | gtatcgtagg   | agacaagaaa  | 360 |
| gccatgaaga  | tcataaacia  | tgctttgggtg | gttgtgagtg  | cagggccctaa  | tgatttcac   | 420 |
| ttgaattatt  | acgaggttcc  | cacatggcgt  | cgcacgtatc  | ctagcatttc   | tgattaccaa  | 480 |
| gattttgttc  | ttaataagct  | taacaatttc  | gtgatggagc  | tttacagcct   | agggttgcgg  | 540 |
| aaaatttttg  | tcggagggtt  | accgccaatg  | ggatgtttac  | cgattcaaat   | gactgctcaa  | 600 |
| ttccgcaacg  | tcctaagggt  | ttgcttgga   | caagagaaca  | gagactctgt   | ttatacaat   | 660 |
| cagaaacttc  | agaagctctt  | acctcagaca  | caagcatctc  | ttacaggaag   | caagatcctt  | 720 |
| tactctgatg  | tctatgaccc  | tatgatggag  | atgctccaaa  | accctagcaa   | atacgggttt  | 780 |
| aaagagacga  | cgagaggatg  | ttgtggaaca  | gggttcttgg  | agacgagctt   | catgtgtaat  | 840 |
| gcttattctt  | ccatgtgtga  | gaatcgctcg  | gagtttctgt  | tctttgactc   | gattcatcca  | 900 |
| tctgaagcta  | cctacaatta  | cattggtaat  | gttctggata  | ctaagattcg   | tgggtggctt  | 960 |
| aaggcttaa   |             |             |             |              |             |     |

(2) INFORMATION FOR SEQ ID NO:1021:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..322
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1596039
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

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Ser Ser Leu Ser Ser Ser Gln Gln Tyr Phe Ser Arg Pro Ala Thr His
1 5 10 15
Pro Gln Arg Pro Lys Arg Asn Xaa Leu Phe Pro Ala Ile Leu Ile Phe
 20 25 30
Gly Asp Ser Thr Val Asp Thr Gly Asn Asn Asn Tyr Pro Ser Gln Thr
 35 40 45
Ile Phe Arg Ala Lys His Val Leu Thr Phe Val Pro Pro Phe Leu Gln
 50 55 60
Pro Asn Leu Thr Asp Gln Glu Ile Val Thr Gly Val Cys Phe Ala Ser
65 70 75 80
Ala Gly Ala Gly Tyr Asp Asp Gln Thr Ser Leu Thr Thr Gln Ala Ile
 85 90 95
Arg Val Ser Glu Gln Pro Asn Met Phe Lys Ser Tyr Ile Ala Arg Leu
 100 105 110
Lys Ser Ile Val Gly Asp Lys Lys Ala Met Lys Ile Ile Asn Asn Ala
 115 120 125
Leu Val Val Val Ser Ala Gly Pro Asn Asp Phe Ile Leu Asn Tyr Tyr
 130 135 140
Glu Val Pro Thr Trp Arg Arg Met Tyr Pro Ser Ile Ser Asp Tyr Gln
145 150 155 160
Asp Phe Val Leu Asn Lys Leu Asn Asn Phe Val Met Glu Leu Tyr Ser
 165 170 175
Leu Gly Cys Arg Lys Ile Leu Val Gly Gly Leu Pro Pro Met Gly Cys
 180 185 190
Leu Pro Ile Gln Met Thr Ala Gln Phe Arg Asn Val Leu Arg Phe Cys
 195 200 205
Leu Glu Gln Glu Asn Arg Asp Ser Val Leu Tyr Asn Gln Lys Leu Gln
 210 215 220
Lys Leu Leu Pro Gln Thr Gln Ala Ser Leu Thr Gly Ser Lys Ile Leu
225 230 235 240
Tyr Ser Asp Val Tyr Asp Pro Met Met Glu Met Leu Gln Asn Pro Ser
 245 250 255
Lys Tyr Gly Phe Lys Glu Thr Thr Arg Gly Cys Cys Gly Thr Gly Phe
 260 265 270
Leu Glu Thr Ser Phe Met Cys Asn Ala Tyr Ser Ser Met Cys Glu Asn
 275 280 285
Arg Ser Glu Phe Leu Phe Phe Asp Ser Ile His Pro Ser Glu Ala Thr
 290 295 300
Tyr Asn Tyr Ile Gly Asn Val Leu Asp Thr Lys Ile Arg Gly Trp Leu
305 310 315 320
Lys Ala

```

- (2) INFORMATION FOR SEQ ID NO:1022:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 219 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide

0966980, 101300

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1596040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

Met Phe Lys Ser Tyr Ile Ala Arg Leu Lys Ser Ile Val Gly Asp Lys  
1 5 10 15  
Lys Ala Met Lys Ile Ile Asn Asn Ala Leu Val Val Val Ser Ala Gly  
20 25 30  
Pro Asn Asp Phe Ile Leu Asn Tyr Tyr Glu Val Pro Thr Trp Arg Arg  
35 40 45  
Met Tyr Pro Ser Ile Ser Asp Tyr Gln Asp Phe Val Leu Asn Lys Leu  
50 55 60  
Asn Asn Phe Val Met Glu Leu Tyr Ser Leu Gly Cys Arg Lys Ile Leu  
65 70 75 80  
Val Gly Gly Leu Pro Pro Met Gly Cys Leu Pro Ile Gln Met Thr Ala  
85 90 95  
Gln Phe Arg Asn Val Leu Arg Phe Cys Leu Glu Gln Glu Asn Arg Asp  
100 105 110  
Ser Val Leu Tyr Asn Gln Lys Leu Gln Lys Leu Leu Pro Gln Thr Gln  
115 120 125  
Ala Ser Leu Thr Gly Ser Lys Ile Leu Tyr Ser Asp Val Tyr Asp Pro  
130 135 140  
Met Met Glu Met Leu Gln Asn Pro Ser Lys Tyr Gly Phe Lys Glu Thr  
145 150 155 160  
Thr Arg Gly Cys Cys Gly Thr Gly Phe Leu Glu Thr Ser Phe Met Cys  
165 170 175  
Asn Ala Tyr Ser Ser Met Cys Glu Asn Arg Ser Glu Phe Leu Phe Phe  
180 185 190  
Asp Ser Ile His Pro Ser Glu Ala Thr Tyr Asn Tyr Ile Gly Asn Val  
195 200 205  
Leu Asp Thr Lys Ile Arg Gly Trp Leu Lys Ala  
210 215

(2) INFORMATION FOR SEQ ID NO:1023:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..201

(D) OTHER INFORMATION: / Ceres Seq. ID 1596041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

Met Lys Ile Ile Asn Asn Ala Leu Val Val Val Ser Ala Gly Pro Asn  
1 5 10 15  
Asp Phe Ile Leu Asn Tyr Tyr Glu Val Pro Thr Trp Arg Arg Met Tyr  
20 25 30  
Pro Ser Ile Ser Asp Tyr Gln Asp Phe Val Leu Asn Lys Leu Asn Asn  
35 40 45  
Phe Val Met Glu Leu Tyr Ser Leu Gly Cys Arg Lys Ile Leu Val Gly  
50 55 60  
Gly Leu Pro Pro Met Gly Cys Leu Pro Ile Gln Met Thr Ala Gln Phe  
65 70 75 80  
Arg Asn Val Leu Arg Phe Cys Leu Glu Gln Glu Asn Arg Asp Ser Val  
85 90 95  
Leu Tyr Asn Gln Lys Leu Gln Lys Leu Leu Pro Gln Thr Gln Ala Ser  
100 105 110  
Leu Thr Gly Ser Lys Ile Leu Tyr Ser Asp Val Tyr Asp Pro Met Met  
115 120 125  
Glu Met Leu Gln Asn Pro Ser Lys Tyr Gly Phe Lys Glu Thr Thr Arg  
130 135 140

00669900-101300





[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Leu | Asp | Arg | Val | Ile | Gln | Gln | Val | Gly | Ser | Met | Lys | Ile | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Gly | Gly | Leu | Ile | Ser | Glu | Ala | Met | Lys | Arg | Ala | Glu | Ala | Met | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Glu | Thr | Asn | Asp | Asp | Ser | Glu | Lys | Phe | Gly | Val | Gly | Leu | Glu | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Gly | Lys | Val | Lys | Val | Lys | Lys | Met | Met | Phe | Glu | Ser | Gln | Gly | Gly | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Gly | Ile | Ser | Gly | Met | Gly | Gly | Val | Gly | Lys | Thr | Thr | Leu | Ala | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |





565 570 575  
Ser Lys Leu Gln Ala Leu Glu Ile Leu Arg Leu Tyr Ala Cys Pro Glu  
580 585 590  
Leu Lys Thr Leu Pro Gly Glu Ile Cys Glu Leu Pro Gly Leu Lys Tyr  
595 600 605  
Leu Asp Ile Ser Gln Cys Val Ser Leu Ser Cys Leu Pro Glu Glu Ile  
610 615 620  
Gly Lys Leu Lys Lys Leu Glu Lys Ile Asp Met Arg Glu Cys Cys Phe  
625 630 635 640  
Ser Asp Arg Pro Ser Ser Ala Val Ser Leu Lys Ser Leu Arg His Val  
645 650 655  
Ile Cys Asp Thr Asp Val Ala Phe Met Trp Glu Glu Val Glu Lys Ala  
660 665 670  
Val Pro Gly Leu Lys Ile Glu Ala Ala Glu Lys Cys Phe Ser Leu Asp  
675 680 685  
Trp Leu Asp Glu  
690

(2) INFORMATION FOR SEQ ID NO:1027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..411
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| ggatctaaga tacagattac cattagaaag cattatatattg gcaagtttaa catgtcacta | 60  |
| aagggtatttc tttaacaatgg cagacatatt aggtcaagtg aaaaagtatt tagtgcttta | 120 |
| aaaagtgtaa agcatgacga gaagacagtg gttctgatat gctatgctaa aatcaataat   | 180 |
| tttaaagctt tacacattgc aagcaattct gttttccata aaagaacgaa gcatattgag   | 240 |
| cgtgattgtc acaaggtttag ggaatgtatt gaagctggga ttctcaaaac catgtttgtt  | 300 |
| cgttctgata atcagcttgc ggatatgcta actaaacctc tttatccggc gctctttcga   | 360 |
| gctaacaaca ccaagcttgg agttctcaac atatatgaag ctcaagcttg a            |     |

(2) INFORMATION FOR SEQ ID NO:1028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596070

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Gly Ser Lys Ile Gln Ile Thr Ile Arg Lys His Tyr Ile Gly Lys Phe |  |
| 1 5 10 15                                                       |  |
| Asn Met Ser Leu Lys Gly Ile Leu Tyr Asn Gly Arg His Ile Arg Ser |  |
| 20 25 30                                                        |  |
| Ser Glu Lys Val Phe Ser Ala Leu Lys Ser Val Lys His Asp Glu Lys |  |
| 35 40 45                                                        |  |
| Thr Val Val Leu Ile Cys Tyr Ala Lys Ile Asn Asn Phe Lys Ala Leu |  |
| 50 55 60                                                        |  |
| His Ile Ala Ser Asn Ser Val Phe His Lys Arg Thr Lys His Ile Glu |  |
| 65 70 75 80                                                     |  |
| Arg Asp Cys His Lys Val Arg Glu Cys Ile Glu Ala Gly Ile Leu Lys |  |
| 85 90 95                                                        |  |
| Thr Met Phe Val Arg Ser Asp Asn Gln Leu Ala Asp Met Leu Thr Lys |  |

DOCKET# 08668960

100 105 110  
Pro Leu Tyr Pro Ala Leu Phe Arg Ala Asn Asn Thr Lys Leu Gly Val  
115 120 125  
Leu Asn Ile Tyr Glu Ala Gln Ala  
130 135

(2) INFORMATION FOR SEQ ID NO:1029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1596071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:

Met Ser Leu Lys Gly Ile Leu Tyr Asn Gly Arg His Ile Arg Ser Ser  
1 5 10 15  
Glu Lys Val Phe Ser Ala Leu Lys Ser Val Lys His Asp Glu Lys Thr  
20 25 30  
Val Val Leu Ile Cys Tyr Ala Lys Ile Asn Asn Phe Lys Ala Leu His  
35 40 45  
Ile Ala Ser Asn Ser Val Phe His Lys Arg Thr Lys His Ile Glu Arg  
50 55 60  
Asp Cys His Lys Val Arg Glu Cys Ile Glu Ala Gly Ile Leu Lys Thr  
65 70 75 80  
Met Phe Val Arg Ser Asp Asn Gln Leu Ala Asp Met Leu Thr Lys Pro  
85 90 95  
Leu Tyr Pro Ala Leu Phe Arg Ala Asn Asn Thr Lys Leu Gly Val Leu  
100 105 110  
Asn Ile Tyr Glu Ala Gln Ala  
115

(2) INFORMATION FOR SEQ ID NO:1030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..1224

(D) OTHER INFORMATION: / Ceres Seq. ID 1596072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

|             |             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| atgtctcaaa  | acgggaagat  | aatcccaaat  | ctggaccaa   | acagtacgag  | gctcctcaat  | 60  |
| ctcacagttc  | tccagcggat  | cgatccatac  | atcgaggaaa  | tcctcatcac  | agccgctcat  | 120 |
| gtcactttct  | atgaattcaa  | cattgagctc  | agccaatgga  | gtcgtaagga  | cgttgaagga  | 180 |
| tctttgtttg  | ttgtcaaaaag | aagtacacaa  | cctcgatttc  | agttttattgt | gatgaatcgt  | 240 |
| cgtaatacag  | ataatctggt  | ggagaatctc  | ctgggagatt  | ttgagtatga  | agtacaaggt  | 300 |
| ccatattttac | tttaccgtaa  | tgcattctcaa | gaagtaaattg | gcattttggtt | ctacaataaaa | 360 |
| cgtgaatgcg  | aggaggtagc  | aactcttttc  | aacagaatac  | tcagtgcata  | ttccaaggtt  | 420 |
| aaccagaagc  | caaaggcctc  | atcttcaaaag | agtgagtttg  | aggaattgga  | agctaagcct  | 480 |
| acaatggcag  | ttatggatgg  | tcctcttgaa  | ccatcatcaa  | ctgctaggga  | tgccctgat   | 540 |
| gacctgctt   | ttgtcaactt  | ctttagctca  | acgatgaatc  | ttgggaacac  | tgcgagtggg  | 600 |
| tcagcaagtg  | gaccttacca  | atcatcagcg  | attcctcacc  | aacctcacca  | gcctcaccaa  | 660 |
| cctcaccaac  | ccaccattgc  | tcctcctgta  | gcggcagcag  | cacctccaca  | gatacnatca  | 720 |
| ccaccgcctn  | tacnatectc  | ctctcctctg  | atgactctct  | ttgacaacaa  | ccctgaagtt  | 780 |
| atcagcagca  | actccaacat  | tcacacagat  | ttggtgacgc  | cgtctttctt  | tggcccccca  | 840 |
| cgaatgatgg  | cacagccaca  | cctcattcct  | ggtgtatcta  | tgcccagtg   | tcctcctctc  | 900 |
| aatcctaata  | atgcgagtca  | ccagcagcgg  | tcatatggta  | ctccggtgct  | ccagcctttc  | 960 |

```
ccacccccaa ctccaccacc atcaactcgct cctgcaccca ctgggtccggt tatcagcaga 1020
gacaaagtga aggaagccct tttatccctg ttgcagctgg aggagtcggg aagtgagcga 1080
gctcagttcc gatgctatcg aagaagagac ccgtcagggt cttcccattt atcgcntgga 1140
atgctcgacg gagctagcca tccgatcagc ccaaataccta ccacgttcaa atctctctc 1200
aaccagttcc tctcaaagct ttaa
```

(2) INFORMATION FOR SEQ ID NO:1031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..407

(D) OTHER INFORMATION: / Ceres Seq. ID 1596073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Gln | Asn | Gly | Lys | Ile | Ile | Pro | Asn | Leu | Asp | Gln | Asn | Ser | Thr |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Arg | Leu | Leu | Asn | Leu | Thr | Val | Leu | Gln | Arg | Ile | Asp | Pro | Tyr | Ile | Glu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu | Ile | Leu | Ile | Thr | Ala | Ala | His | Val | Thr | Phe | Tyr | Glu | Phe | Asn | Ile |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Glu | Leu | Ser | Gln | Trp | Ser | Arg | Lys | Asp | Val | Glu | Gly | Ser | Leu | Phe | Val |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Val | Lys | Arg | Ser | Thr | Gln | Pro | Arg | Phe | Gln | Phe | Ile | Val | Met | Asn | Arg |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Arg | Asn | Thr | Asp | Asn | Leu | Val | Glu | Asn | Leu | Leu | Gly | Asp | Phe | Glu | Tyr |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Glu | Val | Gln | Gly | Pro | Tyr | Leu | Leu | Tyr | Arg | Asn | Ala | Ser | Gln | Glu | Val |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Asn | Gly | Ile | Trp | Phe | Tyr | Asn | Lys | Arg | Glu | Cys | Glu | Glu | Val | Ala | Thr |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Leu | Phe | Asn | Arg | Ile | Leu | Ser | Ala | Tyr | Ser | Lys | Val | Asn | Gln | Lys | Pro |  |
|     |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |  |
| Lys | Ala | Ser | Ser | Ser | Lys | Ser | Glu | Phe | Glu | Glu | Leu | Glu | Ala | Lys | Pro |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Thr | Met | Ala | Val | Met | Asp | Gly | Pro | Leu | Glu | Pro | Ser | Ser | Thr | Ala | Arg |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Asp | Ala | Pro | Asp | Asp | Pro | Ala | Phe | Val | Asn | Phe | Phe | Ser | Ser | Thr | Met |  |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Asn | Leu | Gly | Asn | Thr | Ala | Ser | Gly | Ser | Ala | Ser | Gly | Pro | Tyr | Gln | Ser |  |
|     |     |     |     | 195 |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Ser | Ala | Ile | Pro | His | Gln | Pro | His | Gln | Pro | His | Gln | Pro | His | Gln | Pro |  |
|     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |  |
| Thr | Ile | Ala | Pro | Pro | Val | Ala | Ala | Ala | Pro | Pro | Gln | Ile | Xaa | Ser |     |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |  |
| Pro | Pro | Pro | Xaa | Xaa | Ser | Ser | Ser | Pro | Leu | Met | Thr | Leu | Phe | Asp | Asn |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Asn | Pro | Glu | Val | Ile | Ser | Ser | Asn | Ser | Asn | Ile | His | Thr | Asp | Leu | Val |  |
|     |     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Thr | Pro | Ser | Phe | Phe | Gly | Pro | Pro | Arg | Met | Met | Ala | Gln | Pro | His | Leu |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Ile | Pro | Gly | Val | Ser | Met | Pro | Ser | Ala | Pro | Pro | Leu | Asn | Pro | Asn | Asn |  |
|     |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Ala | Ser | His | Gln | Gln | Arg | Ser | Tyr | Gly | Thr | Pro | Val | Leu | Gln | Pro | Phe |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Pro | Pro | Pro | Thr | Pro | Pro | Pro | Ser | Leu | Ala | Pro | Ala | Pro | Thr | Gly | Pro |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Val | Ile | Ser | Arg | Asp | Lys | Val | Lys | Glu | Ala | Leu | Leu | Ser | Leu | Leu | Gln |  |
|     |     |     |     | 340 |     |     |     | 345 |     |     |     |     | 350 |     |     |  |

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Leu Glu Glu Ser Gly Ser Glu Arg Ala Gln Phe Arg Cys Tyr Arg Arg  
355 360 365  
Arg Asp Pro Ser Gly Ser Ser His Leu Ser Xaa Gly Met Leu Asp Gly  
370 375 380  
Ala Ser His Pro Ile Ser Pro Asn Pro Thr Thr Phe Lys Ser Leu Leu  
385 390 395 400  
Asn Gln Phe Leu Ser Lys Leu  
405

(2) INFORMATION FOR SEQ ID NO:1032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..330

(D) OTHER INFORMATION: / Ceres Seq. ID 1596075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:

Met Asn Arg Arg Asn Thr Asp Asn Leu Val Glu Asn Leu Leu Gly Asp  
1 5 10 15  
Phe Glu Tyr Glu Val Gln Gly Pro Tyr Leu Leu Tyr Arg Asn Ala Ser  
20 25 30  
Gln Glu Val Asn Gly Ile Trp Phe Tyr Asn Lys Arg Glu Cys Glu Glu  
35 40 45  
Val Ala Thr Leu Phe Asn Arg Ile Leu Ser Ala Tyr Ser Lys Val Asn  
50 55 60  
Gln Lys Pro Lys Ala Ser Ser Ser Lys Ser Glu Phe Glu Glu Leu Glu  
65 70 75 80  
Ala Lys Pro Thr Met Ala Val Met Asp Gly Pro Leu Glu Pro Ser Ser  
85 90 95  
Thr Ala Arg Asp Ala Pro Asp Asp Pro Ala Phe Val Asn Phe Phe Ser  
100 105 110  
Ser Thr Met Asn Leu Gly Asn Thr Ala Ser Gly Ser Ala Ser Gly Pro  
115 120 125  
Tyr Gln Ser Ser Ala Ile Pro His Gln Pro His Gln Pro His Gln Pro  
130 135 140  
His Gln Pro Thr Ile Ala Pro Pro Val Ala Ala Ala Ala Pro Pro Gln  
145 150 155 160  
Ile Xaa Ser Pro Pro Pro Xaa Xaa Ser Ser Ser Pro Leu Met Thr Leu  
165 170 175  
Phe Asp Asn Asn Pro Glu Val Ile Ser Ser Asn Ser Asn Ile His Thr  
180 185 190  
Asp Leu Val Thr Pro Ser Phe Phe Gly Pro Pro Arg Met Met Ala Gln  
195 200 205  
Pro His Leu Ile Pro Gly Val Ser Met Pro Ser Ala Pro Pro Leu Asn  
210 215 220  
Pro Asn Asn Ala Ser His Gln Gln Arg Ser Tyr Gly Thr Pro Val Leu  
225 230 235 240  
Gln Pro Phe Pro Pro Pro Thr Pro Pro Ser Leu Ala Pro Ala Pro  
245 250 255  
Thr Gly Pro Val Ile Ser Arg Asp Lys Val Lys Glu Ala Leu Leu Ser  
260 265 270  
Leu Leu Gln Leu Glu Glu Ser Gly Ser Glu Arg Ala Gln Phe Arg Cys  
275 280 285  
Tyr Arg Arg Arg Asp Pro Ser Gly Ser Ser His Leu Ser Xaa Gly Met  
290 295 300  
Leu Asp Gly Ala Ser His Pro Ile Ser Pro Asn Pro Thr Thr Phe Lys  
305 310 315 320  
Ser Leu Leu Asn Gln Phe Leu Ser Lys Leu

09583930-1032

325

330

(2) INFORMATION FOR SEQ ID NO:1033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..636
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| atgagtaagc | ttcagagtga | ggccgttcgt | gaagccatca | ctactatcac  | agggaaatcc | 60  |
| gaggcaaaga | aacgtaactt | tgctgagact | attgagctcc | agatcgggtct | gaagaactat | 120 |
| gaccctcaaa | aggacaagcg | tttcagtggg | tctgtcaagt | taccacatat  | cccccgctct | 180 |
| aaaatgaaga | tctgcatgct | cggagatgcc | cagcatgttg | aagagggtga  | gaagatgggg | 240 |
| ttggaaaaca | tggatgttga | gtctctaaaa | aagcttaaca | agaacaagaa  | actcgtcaag | 300 |
| aagcttgcaa | agaaatacca | tgtcttcttg | gcctctgagt | ctgtcattaa  | gcagattcct | 360 |
| cgtcttcttg | gtcctggaaa | attcccaact | cttgtgagcc | accaggaatc  | cttgaggtca | 420 |
| aaggtgaatg | aaacaaaggc | aacagtgaag | ttccagctga | agaaggttct  | gtgcatggga | 480 |
| gttgcaattg | gtaacctttc | aatggaagag | aagcagatct | ttcagaatgt  | gcagatgagc | 540 |
| gtcaacttcc | tcgtctcgct | attgaagaag | aactggcaaa | atgtcaggtg  | tttgtacctc | 600 |
| aagagcacia | tgggaccacc | acaaagaatc | ttctga     |             |            |     |

(2) INFORMATION FOR SEQ ID NO:1034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..211
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Lys | Leu | Gln | Ser | Glu | Ala | Val | Arg | Glu | Ala | Ile | Thr | Thr | Ile |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Gly | Lys | Ser | Glu | Ala | Lys | Lys | Arg | Asn | Phe | Val | Glu | Thr | Ile | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Gln | Ile | Gly | Leu | Lys | Asn | Tyr | Asp | Pro | Gln | Lys | Asp | Lys | Arg | Phe |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Gly | Ser | Val | Lys | Leu | Pro | His | Ile | Pro | Arg | Pro | Lys | Met | Lys | Ile |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Cys | Met | Leu | Gly | Asp | Ala | Gln | His | Val | Glu | Glu | Ala | Glu | Lys | Met | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Glu | Asn | Met | Asp | Val | Glu | Ser | Leu | Lys | Lys | Leu | Asn | Lys | Asn | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Leu | Val | Lys | Lys | Leu | Ala | Lys | Lys | Tyr | His | Ala | Phe | Leu | Ala | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Ser | Val | Ile | Lys | Gln | Ile | Pro | Arg | Leu | Leu | Gly | Pro | Gly | Lys | Phe |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Thr | Leu | Val | Ser | His | Gln | Glu | Ser | Leu | Glu | Ser | Lys | Val | Asn | Glu |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Thr | Lys | Ala | Thr | Val | Lys | Phe | Gln | Leu | Lys | Lys | Val | Leu | Cys | Met | Gly |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Val | Ala | Val | Gly | Asn | Leu | Ser | Met | Glu | Glu | Lys | Gln | Ile | Phe | Gln | Asn |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Val | Gln | Met | Ser | Val | Asn | Phe | Leu | Val | Ser | Leu | Leu | Lys | Lys | Asn | Trp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gln | Asn | Val | Arg | Cys | Leu | Tyr | Leu | Lys | Ser | Thr | Met | Gly | Pro | Pro | Gln |

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atcaataaca aaatatctga tagcgagaag cttgatagga ttttgacaat ccttgaagat 900
cttaacaaga gagtgcgagct gattgagagg attttggaca ttagaatgga ggaaaagaat 960
aatcagagat ctgaggaaga tgaagaaaga aaacaagaag atgaaggagt agaaagacaa 1020
ccagaggctg aagaagaagg aggactagaa agaaaagcag agaatgacaa tgaatcattt 1080
gaagattcaa tccgagagcc aaacacacag tatgggagct atccgggtga tgatgaaaac 1140
acccaacgtg atgttggtga tgaattagtt gaagaatcat caaaagataa gtctcctact 1200
ccacgatcct ctacaccaa tttcaatatt ttgtctgaag aaagtctgga tgttcaaaag 1260
gataagaaga gagttagcag aggaagaaat gagaacaaga gagttaaacc aaatgtttat 1320
gctgaggata atcttaaaac aagaaaacag gtgccgagaa agaggcataa acaagttgat 1380
attgctgatg ttcattgttcc aacaaggaaa gaggcacaga gtaagaaaag gaaaaatatt 1440
ggcaatgatg gtgataacgc tgataatgat ggagacaatg atgattttca gcccgctccg 1500
caaagaaaga gtaagcgggg tacggctcct tccattcata cccaagcacc tttcacagct 1560
gagaagaaga agcatccaat tttgcatcca tttgcgaaag ttgatgccac aagacttgag 1620
aaattggctg tatggaagaa gtcaaggaaa aacaagccac tatcaatcgc gggaaataat 1680
gtagatacaa agtggtttac aaccctagag acgccaggga aagcaatcac agcaacgcat 1740
gttgatgcag ctttggagtt gatgaaaacg aggaaggaaa gcaatccaga attattcaaa 1800
aacaatcag ttgtatttgt tggatcgtct ttcttaaagt tgattgatga gtcatacatg 1860
gagtttttgg ataacaaaga gggatttcag tttcagtcctg aagaaatcag taagctgata 1920
atagaggaag aaaccaagtg catattggct cctttctgta tcaaaggaaa atgttgggtt 1980
gccttgctca tccacttgga acagaagaca gtttgatat gggaatgtgc agcttcttat 2040
ttaacagaag aagtcaagaa aaaatatgtt gctgcctact ctatagctat gccatacatt 2100
gttcggaaca tcctcaaaaa agaagacatg gatgtctctc catttagcat caaagtcctg 2160
accacttttc ctcaggctcc tagaaatgaa gagtctggta tctatatgct gaagtttatg 2220
gaatgctact caatgtatac cagccattca aacyttgaag ggaacataat tcaaaacggt 2280
aggaataaat tggctgctga catcttcacc gaattagggg gctttgattt gaatggaaaa 2340
ggacttta

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(2) INFORMATION FOR SEQ ID NO:1037:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 782 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..782

(D) OTHER INFORMATION: / Ceres Seq. ID 1596088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:

```

Met Lys Ala Lys Lys Gly Ile Arg Phe Ser Gly Lys Ile Phe His Tyr
1 5 10 15
Leu Met Gln Gln Arg Val Lys Thr Lys Gly Ser Thr Leu Trp Phe Arg
20 25 30
Val Asp Ser Gln Pro Ile Arg Phe Ser Leu Arg Glu Phe Tyr Leu Thr
35 40 45
Thr Gly Ile Gln Cys Glu Pro Val His Arg Glu Leu Arg Arg Lys Gly
50 55 60
Lys Asp Pro Val Lys Glu Pro Tyr Phe Trp Ala Ser Lys Gly Ser Tyr
65 70 75 80
Thr Leu Gly Asp Leu Glu Asp Arg Leu Phe Leu Lys Pro Lys Glu Gly
85 90 95
Glu Pro Ala Val Glu Asp Glu Glu Lys Leu Cys Leu Ala Ala Val Val
100 105 110
Leu Ile Glu Gly Ile Leu Leu Thr Pro Tyr Gly Lys Glu Lys Ile Pro
115 120 125
Leu Pro Arg Leu Gln His Ala Ser Asp Phe Glu Met Tyr Thr Ala Gln
130 135 140
Pro Met Asp Glu Lys Thr Trp Ala Lys Glu Lys Tyr Asp Leu Arg Gly
145 150 155 160
Phe Gly Leu Ala Leu Thr Ile Trp Val Leu Ser Ala Val Leu Ala Phe
165 170 175
Gly Ala Ala Tyr Gly Val Lys Asp Lys Glu Phe Gln Ser Glu Tyr Pro

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Thr Val Pro Ser Ile His Thr Gln Ala Pro Phe Thr Ala Glu Lys Lys  
485 490 495  
Lys His Pro Ile Leu His Pro Phe Ala Lys Val Asp Ala Thr Arg Leu  
500 505 510  
Glu Lys Leu Ala Val Trp Lys Lys Ser Arg Lys Asn Lys Pro Leu Ser  
515 520 525  
Ile Ala Gly Asn Asn Val Asp Thr Lys Trp Phe Thr Thr Leu Glu Thr  
530 535 540  
Pro Gly Lys Ala Ile Thr Ala Thr His Val Asp Ala Ala Leu Glu Leu  
545 550 555 560  
Met Lys Thr Arg Lys Glu Ser Asn Pro Glu Leu Phe Lys Asn Lys Ser  
565 570 575  
Val Val Phe Val Gly Ser Ser Phe Leu Asn Val Ile Asp Glu Ser Tyr  
580 585 590  
Met Glu Phe Leu Asp Asn Lys Glu Gly Phe Gln Phe Gln Ser Glu Glu  
595 600 605  
Ile Ser Lys Leu Ile Ile Glu Glu Glu Thr Lys Cys Ile Leu Ala Pro  
610 615 620  
Phe Cys Ile Lys Gly Lys Cys Trp Val Ala Leu Leu Ile His Leu Glu  
625 630 635 640  
Gln Lys Thr Val Cys Ile Trp Glu Cys Ala Ala Ser Tyr Leu Thr Glu  
645 650 655  
Glu Val Lys Lys Lys Tyr Val Ala Ala Tyr Ser Ile Ala Met Pro Tyr  
660 665 670  
Ile Val Arg Asn Ile Leu Lys Lys Glu Asp Met Asp Val Ser Pro Phe  
675 680 685  
Ser Ile Lys Val Leu Thr Thr Phe Pro Gln Ala Pro Arg Asn Glu Glu  
690 695 700  
Ser Gly Ile Tyr Met Leu Lys Phe Met Glu Cys Tyr Ser Met Tyr Thr  
705 710 715 720  
Ser His Ser Asn Xaa Glu Gly Asn Ile Ile Gln Asn Val Arg Asn Lys  
725 730 735  
Leu Ala Ala Asp Ile Phe Thr Glu Leu Gly Cys Phe Asp Leu Asn Gly  
740 745 750  
Lys Gly Leu  
755

(2) INFORMATION FOR SEQ ID NO:1041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 738 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..738

(D) OTHER INFORMATION: / Ceres Seq. ID 1596098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

Met Gln Gln Arg Val Lys Thr Lys Gly Ser Thr Leu Trp Phe Arg Val  
1 5 10 15  
Asp Ser Gln Pro Ile Arg Phe Ser Leu Arg Glu Phe Tyr Leu Thr Thr  
20 25 30  
Gly Ile Gln Cys Glu Pro Val His Arg Glu Leu Arg Arg Lys Gly Lys  
35 40 45  
Asp Pro Glu Gly Glu Pro Ala Val Glu Asp Glu Glu Lys Leu Cys Leu  
50 55 60  
Ala Ala Val Val Leu Ile Glu Gly Ile Leu Leu Thr Pro Tyr Gly Lys  
65 70 75 80  
Glu Lys Ile Pro Leu Pro Arg Leu Gln His Ala Ser Asp Phe Glu Met  
85 90 95  
Tyr Thr Ala Gln Pro Met Asp Glu Lys Thr Trp Ala Lys Glu Lys Tyr

DOCKET# 08668960





(2) INFORMATION FOR SEQ ID NO:1043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..568
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Glu | Ser | Asp | Lys | Ser | Ser | Val | Glu | Glu | Leu | Lys | Lys | Arg | Val |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Lys | Arg | Ser | Arg | Gly | Lys | Lys | Asn | Glu | Gln | Gln | Lys | Ala | Glu | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Thr | His | Thr | Val | Glu | Glu | Asn | Ala | Asp | Glu | Thr | Gln | Lys | Lys | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Lys | Lys | Val | Lys | Lys | Val | Arg | Gly | Lys | Ile | Glu | Glu | Glu | Glu | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Lys | Val | Glu | Ala | Met | Glu | Asp | Gly | Glu | Asp | Glu | Lys | Asn | Ile | Val | Ile |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Val | Gly | Lys | Gly | Ile | Met | Thr | Asn | Val | Thr | Phe | Asp | Ser | Leu | Asp | Leu |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Glu | Gln | Thr | Ser | Ile | Ala | Ile | Lys | Asp | Met | Gly | Phe | Gln | Tyr | Met |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Gln | Ile | Gln | Ala | Gly | Ser | Ile | Gln | Pro | Leu | Leu | Glu | Gly | Lys | Asp |
|     |     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Val | Leu | Gly | Ala | Ala | Arg | Thr | Gly | Ser | Gly | Lys | Thr | Leu | Ala | Phe | Leu |
|     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Ile | Pro | Ala | Val | Glu | Leu | Leu | Phe | Lys | Glu | Arg | Phe | Ser | Pro | Arg | Asn |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Gly | Thr | Gly | Val | Ile | Val | Ile | Cys | Pro | Thr | Arg | Glu | Leu | Ala | Ile | Gln |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Thr | Lys | Asn | Val | Ala | Glu | Glu | Leu | Leu | Lys | His | His | Ser | Gln | Thr | Val |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Met | Val | Ile | Gly | Gly | Asn | Asn | Arg | Arg | Ser | Glu | Ala | Gln | Arg | Ile |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Ser | Gly | Ser | Asn | Leu | Val | Ile | Ala | Thr | Pro | Gly | Arg | Leu | Leu | Asp |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| His | Leu | Gln | Asn | Thr | Lys | Ala | Phe | Ile | Tyr | Lys | His | Leu | Lys | Cys | Leu |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Val | Ile | Asp | Glu | Ala | Asp | Arg | Ile | Leu | Glu | Glu | Asn | Phe | Glu | Glu | Asp |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Met | Asn | Lys | Ile | Leu | Lys | Ile | Leu | Pro | Lys | Thr | Arg | Gln | Thr | Ala | Leu |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Phe | Ser | Ala | Thr | Gln | Thr | Ser | Lys | Val | Lys | Asp | Leu | Ala | Arg | Val | Ser |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Thr | Ser | Pro | Val | His | Val | Asp | Val | Asp | Asp | Gly | Arg | Arg | Lys | Val |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Thr | Asn | Glu | Gly | Leu | Glu | Gln | Gly | Tyr | Cys | Val | Val | Pro | Ser | Lys | Gln |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |     |
| Arg | Leu | Ile | Leu | Leu | Ile | Ser | Phe | Leu | Lys | Lys | Asn | Leu | Asn | Lys | Lys |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ile | Met | Val | Phe | Ser | Thr | Cys | Lys | Ser | Val | Gln | Phe | His | Thr | Glu |     |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Ile | Met | Lys | Ile | Ser | Asp | Val | Asp | Val | Ser | Asp | Ile | His | Gly | Gly | Met |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Asp | Gln | Asn | Arg | Arg | Thr | Lys | Thr | Phe | Phe | Asp | Phe | Met | Lys | Ala | Lys |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Lys | Gly | Ile | Leu | Leu | Cys | Thr | Asp | Val | Ala | Ala | Arg | Gly | Leu | Asp | Ile |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 385 |     | 390 |     | 395 |     | 400 |     |     |     |     |     |     |     |     |     |
| Pro | Ser | Val | Asp | Trp | Ile | Ile | Gln | Tyr | Asp | Pro | Pro | Asp | Lys | Pro | Thr |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Glu | Tyr | Ile | His | Arg | Val | Gly | Arg | Thr | Ala | Arg | Gly | Glu | Gly | Ala | Lys |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Gly | Lys | Ala | Leu | Leu | Val | Leu | Ile | Pro | Glu | Glu | Leu | Gln | Phe | Ile | Arg |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Tyr | Leu | Lys | Ala | Ala | Lys | Val | Pro | Val | Lys | Glu | Leu | Glu | Phe | Asn | Glu |
|     |     | 450 |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Lys | Arg | Leu | Ser | Asn | Val | Gln | Ser | Ala | Leu | Glu | Lys | Cys | Val | Ala | Lys |
|     |     | 465 |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Asp | Tyr | Asn | Leu | Asn | Lys | Leu | Ala | Lys | Asp | Ala | Tyr | Arg | Ala | Tyr | Leu |
|     |     |     | 485 |     |     |     |     | 490 |     |     |     |     |     | 495 |     |
| Ser | Ala | Tyr | Asn | Ser | His | Ser | Leu | Lys | Asp | Ile | Phe | Asn | Val | His | Arg |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Leu | Asp | Leu | Leu | Ala | Val | Ala | Glu | Ser | Phe | Cys | Phe | Ser | Ser | Pro | Pro |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Lys | Val | Asn | Leu | Asn | Ile | Glu | Ser | Gly | Ala | Gly | Lys | Val | Arg | Lys | Ala |
|     |     | 530 |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Arg | Lys | Gln | Gln | Gly | Arg | Asn | Gly | Phe | Ser | Pro | Tyr | Ser | Pro | Tyr | Gly |
|     |     | 545 |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Lys | Ser | Thr | Pro | Thr | Lys | Glu | Ala |     |     |     |     |     |     |     |     |
|     |     |     |     | 565 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1044:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 500 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..500

(D) OTHER INFORMATION: / Ceres Seq. ID 1596102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asp | Gly | Asp | Glu | Lys | Asn | Ile | Val | Ile | Val | Gly | Lys | Gly |     |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |     |
| Ile | Met | Thr | Asn | Val | Thr | Phe | Asp | Ser | Leu | Asp | Leu | Ser | Glu | Gln | Thr |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ser | Ile | Ala | Ile | Lys | Asp | Met | Gly | Phe | Gln | Tyr | Met | Thr | Gln | Ile | Gln |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ala | Gly | Ser | Ile | Gln | Pro | Leu | Glu | Gly | Lys | Asp | Val | Leu | Gly | Ala |     |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ala | Arg | Thr | Gly | Ser | Gly | Lys | Thr | Leu | Ala | Phe | Leu | Ile | Pro | Ala | Val |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| Glu | Leu | Leu | Phe | Lys | Glu | Arg | Phe | Ser | Pro | Arg | Asn | Gly | Thr | Gly | Val |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |     |
| Ile | Val | Ile | Cys | Pro | Thr | Arg | Glu | Leu | Ala | Ile | Gln | Thr | Lys | Asn | Val |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ala | Glu | Glu | Leu | Leu | Lys | His | His | Ser | Gln | Thr | Val | Ser | Met | Val | Ile |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Gly | Asn | Asn | Arg | Arg | Ser | Glu | Ala | Gln | Arg | Ile | Ala | Ser | Gly | Ser |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Leu | Val | Ile | Ala | Thr | Pro | Gly | Arg | Leu | Leu | Asp | His | Leu | Gln | Asn |
|     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |     |
| Thr | Lys | Ala | Phe | Ile | Tyr | Lys | His | Leu | Lys | Cys | Leu | Val | Ile | Asp | Glu |
|     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |     |
| Ala | Asp | Arg | Ile | Leu | Glu | Glu | Asn | Phe | Glu | Glu | Asp | Met | Asn | Lys | Ile |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Leu | Lys | Ile | Leu | Pro | Lys | Thr | Arg | Gln | Thr | Ala | Leu | Phe | Ser | Ala | Thr |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |

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Gln Thr Ser Lys Val Lys Asp Leu Ala Arg Val Ser Leu Thr Ser Pro  
210 215 220  
Val His Val Asp Val Asp Gly Arg Arg Lys Val Thr Asn Glu Gly  
225 230 235 240  
Leu Glu Gln Gly Tyr Cys Val Val Pro Ser Lys Gln Arg Leu Ile Leu  
245 250 255  
Leu Ile Ser Phe Leu Lys Lys Asn Leu Asn Lys Lys Ile Met Val Phe  
260 265 270  
Phe Ser Thr Cys Lys Ser Val Gln Phe His Thr Glu Ile Met Lys Ile  
275 280 285  
Ser Asp Val Asp Val Ser Asp Ile His Gly Gly Met Asp Gln Asn Arg  
290 295 300  
Arg Thr Lys Thr Phe Phe Asp Phe Met Lys Ala Lys Lys Gly Ile Leu  
305 310 315 320  
Leu Cys Thr Asp Val Ala Ala Arg Gly Leu Asp Ile Pro Ser Val Asp  
325 330 335  
Trp Ile Ile Gln Tyr Asp Pro Pro Asp Lys Pro Thr Glu Tyr Ile His  
340 345 350  
Arg Val Gly Arg Thr Ala Arg Gly Glu Gly Ala Lys Gly Lys Ala Leu  
355 360 365  
Leu Val Leu Ile Pro Glu Glu Leu Gln Phe Ile Arg Tyr Leu Lys Ala  
370 375 380  
Ala Lys Val Pro Val Lys Glu Leu Glu Phe Asn Glu Lys Arg Leu Ser  
385 390 395 400  
Asn Val Gln Ser Ala Leu Glu Lys Cys Val Ala Lys Asp Tyr Asn Leu  
405 410 415  
Asn Lys Leu Ala Lys Asp Ala Tyr Arg Ala Tyr Leu Ser Ala Tyr Asn  
420 425 430  
Ser His Ser Leu Lys Asp Ile Phe Asn Val His Arg Leu Asp Leu Leu  
435 440 445  
Ala Val Ala Glu Ser Phe Cys Phe Ser Ser Pro Pro Lys Val Asn Leu  
450 455 460  
Asn Ile Glu Ser Gly Ala Gly Lys Val Arg Lys Ala Arg Lys Gln Gln  
465 470 475 480  
Gly Arg Asn Gly Phe Ser Pro Tyr Ser Pro Tyr Gly Lys Ser Thr Pro  
485 490 495  
Thr Lys Glu Ala  
500

(2) INFORMATION FOR SEQ ID NO:1045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1173
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atgactgata ttaacaccaa caacgagatc gttggcaaca ccacagttgc tgagaccgcg  | 60  |
| gatgaggaag ctttgacact tgcgaaagag cttgaaatga cacagatcac cgattctgat  | 120 |
| atggataatg tgcgccgaaa tctgttcggt aatggttcaa ccaacactac cataccagcc  | 180 |
| tctgtttccc aagggatgat gtcacacttg tttgatggca aatccgggtt caaaacgtgg  | 240 |
| caagaaaaga tgcgctacta tttggtcagc ataaacatgg aaaggtaacct cccagaggat | 300 |
| ccaccaatag ttccgcaagg tgactattgt tgcaaaggtc taatcctgaa ccgcttggtg  | 360 |
| aacgatctgt ttgaccttta cagcaaggcc aagtcttcca aaacactgtg gctaacttta  | 420 |
| gagaacaagt ataagactga tgagtctaga atgcaaagat tctcaactgc gaagtttctg  | 480 |
| aatttcaaga tgggtggactc caaaccaatc atggaacagg tggaggctct tcaacgtatc | 540 |
| tgtcaagaga tagagttgga agggatgtcg atctgcaacg ttttcaagac gaattgcttg  | 600 |
| atcaagaagc taccnccggg atggtcagat ttcaagaatt accttaactt caaacgtaag  | 660 |

gcaatgactt ttgatgatct catccgaagg ttaatgattg taggcaacaa tcgtggggct 720  
cacgcgggtg ctcagaatca agggcatgat gttaatgtag ctgagcataa ggccaagctg 780  
aaaggcaagg gaaaagggtt ctctattcct cagaagaact tgaagattgg acacaaggct 840  
gatgtttgca agagcaaagc caaggatgtc aagagccagg caaacctaac tgaagaggat 900  
atggttgacg tggctactga atgtaacatg gtggacgaca accaagtga gttgtactac 960  
gacactggtg caaccacaca catctgcaca gataggacca tgttctccac ctatgtgaat 1020  
aacaagtcaa acgaacaact cttcatgggc aacacggcga tgtctaagat tgaaggtaag 1080  
ggaaaagtgg ttctgaagggt gacttcggga cgtgagctta ctctgcaaaa cgtgaagcat 1140  
gtacctgaca tgcggaagaa tctcatctct tga

(2) INFORMATION FOR SEQ ID NO:1046:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..390
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

Met Thr Asp Ile Asn Thr Asn Asn Glu Ile Val Gly Asn Thr Thr Val  
1 5 10 15  
Ala Glu Thr Ala Asp Glu Glu Ala Leu His Leu Ala Lys Glu Leu Glu  
20 25 30  
Met Thr Gln Ile Thr Asp Ser Asp Met Asp Asn Val Arg Arg Asn Leu  
35 40 45  
Phe Gly Asn Gly Ser Thr Asn Thr Thr Ile Pro Ala Ser Val Ser Gln  
50 55 60  
Gly Met Met Ser His Leu Phe Asp Gly Lys Ser Gly Phe Lys Thr Trp  
65 70 75 80  
Gln Glu Lys Met Arg Tyr Tyr Leu Val Ser Ile Asn Met Glu Arg Tyr  
85 90 95  
Leu Pro Glu Asp Pro Pro Ile Val Pro Gln Gly Asp Tyr Cys Cys Lys  
100 105 110  
Gly Leu Ile Leu Asn Arg Leu Val Asn Asp Leu Phe Asp Leu Tyr Ser  
115 120 125  
Lys Ala Lys Ser Ser Lys Thr Leu Trp Leu Thr Leu Glu Asn Lys Tyr  
130 135 140  
Lys Thr Asp Glu Ser Arg Met Gln Arg Phe Ser Thr Ala Lys Phe Leu  
145 150 155 160  
Asn Phe Lys Met Val Asp Ser Lys Pro Ile Met Glu Gln Val Glu Ala  
165 170 175  
Leu Gln Arg Ile Cys Gln Glu Ile Glu Leu Glu Gly Met Ser Ile Cys  
180 185 190  
Asn Val Phe Lys Thr Asn Cys Leu Ile Lys Lys Leu Xaa Pro Gly Trp  
195 200 205  
Ser Asp Phe Lys Asn Tyr Leu Asn Phe Lys Arg Lys Ala Met Thr Phe  
210 215 220  
Asp Asp Leu Ile Arg Arg Leu Met Ile Val Gly Asn Asn Arg Gly Ala  
225 230 235 240  
His Ala Gly Ala Gln Asn Gln Gly His Asp Val Asn Val Ala Glu His  
245 250 255  
Lys Ala Lys Leu Lys Gly Lys Gly Lys Gly Phe Ser Ile Pro Gln Lys  
260 265 270  
Asn Leu Lys Ile Gly His Lys Ala Asp Val Cys Lys Ser Lys Ala Lys  
275 280 285  
Asp Val Lys Ser Gln Ala Asn Leu Thr Glu Glu Asp Met Val Ala Val  
290 295 300  
Val Thr Glu Cys Asn Met Val Asp Asp Asn Gln Val Lys Trp Tyr Tyr  
305 310 315 320

09689580 "1046"



(2) INFORMATION FOR SEO ID NO:1048:

(A) LENGTH: 1509 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..1509

(D) OTHER INFORMATION: / Ceres Seq. ID 1596141

|             |            |            |             |             |            |      |
|-------------|------------|------------|-------------|-------------|------------|------|
| atgcggaagt  | acttagagga | ttacgttcta | cttgctgaag  | aagaaagtga  | atatctctc  | 60   |
| tctgtaataa  | acgaggaacc | ttgggattat | gctgaagcaa  | aagaaacaca  | agagtggaga | 120  |
| gaagcgtgtg  | aggacgaat  | cgcttcaatt | gagaagaaca  | agacatggga  | tttagtggaa | 180  |
| cttctccaag  | gagctaagcc | aatcgggctc | aaatgggtgt  | ttaagctaaa  | gaagaacgca | 240  |
| gaagggaaca  | taaacaagta | taaggcaaga | ctcgtggcta  | aaggttacgt  | acaacgacat | 300  |
| ggcatagatt  | ttgacgaagt | ctttgcccct | gtagcacgaa  | tcgaaacagt  | ccgcttcac  | 360  |
| attgccctag  | ctgcttcaaa | cggatgggaa | gtgcatcatc  | tcgatgtcaa  | aacagcattc | 420  |
| ttacacggtg  | aattaaaag  | gatatgattt | gtttcacaac  | cagaaggatt  | cacagagaaa | 480  |
| gggagttcta  | gcttaaagct | cattaatgac | ttcaagaagg  | gaatggcgct  | caagtttgag | 540  |
| atgagtgatc  | tcgggttact | cacatactat | cttggaaatcg | aagtaattca  | gtataatgga | 600  |
| ggaattatgt  | tgaacaag   | gagatatgca | gagaagatcc  | tagacgaaac  | caagatgagt | 660  |
| gattgcaacg  | cagttcacat | tccaatggac | tccggtttga  | agctgtcaaa  | agcgggaaca | 720  |
| gagaaaggaa  | gtcatgactc | ggagacagag | aagaacattg  | agccaaaaga  | gtatagaaga | 780  |
| aacattggat  | gtcttcggta | tctacttcac | acacgacctg  | acctctcata  | ctgtgttggt | 840  |
| gtgttgagta  | gatacgtgca | agaacctaaa | gaaggtcatg  | gagtagctat  | gaagcagatt | 900  |
| atgagatact  | tgcgtggcac | tacttctcat | ggactatctt  | tcaagcgagg  | agacaaatcg | 960  |
| gggctaatag  | gtttcagtag | tgcagtcac  | aatgtagacg  | aggtgatagg  | gaggagcaca | 1020 |
| accggacata  | tattctacct | tgatggctct | ctgataactt  | gggtgtacaca | aaagcaagaa | 1080 |
| actgtggctt  | tatcgtcttg | tgaggctgag | tttatggcag  | ccactgaagg  | agctaagcag | 1140 |
| gcaattttggt | tgcaagaatt | acttggagag | gtaacaggag  | aagcatgcaa  | gaaggtgaga | 1200 |
| ctactcattg  | acaacaaatc | ggcगतagca  | cttgccaaga  | atccagtatt  | tcacggccgg | 1260 |
| agcaaacaca  | ttcataagag | gtaccatttc | attcgtgagt  | atgttgagaa  | tgagcaaata | 1320 |
| gaagtggaa   | acgttcccgg | ggaagaacag | aaggcaaatc  | ttctaacaaa  | ggcacttgga | 1380 |
| agaatcaaat  | tcaaagagat | gagagagcta | gttggaattc  | aagagttgtc  | gaagtgtag  | 1440 |
| ttcaagctta  | agggagtga  | tgttgataag | cttgaagtta  | gcttaaggaa  | taagctaacc | 1500 |
| aaatcctaa   |            |            |             |             |            |      |

(2) INFORMATION FOR SEO ID NO:1049:

(A) LENGTH: 502 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(B) LOCATION: 1..502

(D) OTHER INFORMATION: / Ceres Seq. ID 1596142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

Met Pro Lys Tyr Leu Glu Asp Tyr Val Leu Leu Ala Glu Glu Glu Ser  
1 5 10 15  
Glu Tyr Leu Leu Ser Val Ile Asn Glu Glu Pro Trp Asp Tyr Ala Glu  
20 25 30

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Lys | Glu | Thr | Gln | Glu | Trp | Arg | Glu | Ala | Cys | Glu | Asp | Glu | Ile | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ile | Glu | Lys | Asn | Lys | Thr | Trp | Asp | Leu | Val | Glu | Leu | Pro | Gln | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Lys | Pro | Ile | Gly | Leu | Lys | Trp | Val | Phe | Lys | Leu | Lys | Lys | Asn | Ala |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Gly | Asn | Ile | Asn | Lys | Tyr | Lys | Ala | Arg | Leu | Val | Ala | Lys | Gly | Tyr |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Gln | Arg | His | Gly | Ile | Asp | Phe | Asp | Glu | Val | Phe | Ala | Pro | Val | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Ile | Glu | Thr | Val | Arg | Phe | Ile | Ile | Ala | Leu | Ala | Ala | Ser | Asn | Gly |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     |     | 125 |     |     |
| Trp | Glu | Val | His | His | Leu | Asp | Val | Lys | Thr | Ala | Phe | Leu | His | Gly | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Lys | Glu | Ile | Val | Phe | Val | Ser | Gln | Pro | Glu | Gly | Phe | Thr | Glu | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gly | Ser | Ser | Ser | Leu | Lys | Leu | Ile | Asn | Asp | Phe | Lys | Lys | Gly | Met | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Lys | Phe | Glu | Met | Ser | Asp | Leu | Gly | Gly | Leu | Leu | Thr | Tyr | Tyr | Leu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Ile | Glu | Val | Ile | Gln | Tyr | Asn | Gly | Gly | Ile | Met | Leu | Lys | Gln | Gly | Arg |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| Tyr | Ala | Glu | Lys | Ile | Leu | Asp | Glu | Thr | Lys | Met | Ser | Asp | Cys | Asn | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Val | His | Ile | Pro | Met | Asp | Ser | Gly | Leu | Lys | Leu | Ser | Lys | Ala | Gly | Thr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Glu | Lys | Gly | Ser | His | Asp | Ser | Glu | Thr | Glu | Lys | Asn | Ile | Glu | Pro | Lys |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Tyr | Arg | Arg | Asn | Ile | Gly | Cys | Leu | Arg | Tyr | Leu | Leu | His | Thr | Arg |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Pro | Asp | Leu | Ser | Tyr | Cys | Val | Gly | Val | Leu | Ser | Arg | Tyr | Met | Gln | Glu |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Pro | Lys | Glu | Gly | His | Gly | Val | Ala | Met | Lys | Gln | Ile | Met | Arg | Tyr | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Arg | Gly | Thr | Thr | Ser | Tyr | Gly | Leu | Ser | Phe | Lys | Arg | Gly | Asp | Lys | Ser |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Gly | Leu | Ile | Gly | Phe | Ser | Asp | Ser | Ser | His | Asn | Val | Asp | Glu | Asp | Asp |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Gly | Arg | Ser | Thr | Thr | Gly | His | Ile | Phe | Tyr | Leu | Asp | Gly | Ser | Leu | Ile |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Thr | Trp | Cys | Thr | Gln | Lys | Gln | Glu | Thr | Val | Ala | Leu | Ser | Ser | Cys | Glu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |
| Ala | Glu | Phe | Met | Ala | Ala | Thr | Glu | Gly | Ala | Lys | Gln | Ala | Ile | Trp | Leu |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Gln | Glu | Leu | Leu | Gly | Glu | Val | Thr | Gly | Glu | Ala | Cys | Lys | Lys | Val | Arg |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |     |
| Leu | Leu | Ile | Asp | Asn | Lys | Ser | Ala | Ile | Ala | Leu | Ala | Lys | Asn | Pro | Val |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Phe | His | Gly | Arg | Ser | Lys | His | Ile | His | Lys | Arg | Tyr | His | Phe | Ile | Arg |
|     |     | 420 |     |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Glu | Tyr | Val | Glu | Asn | Glu | Gln | Ile | Glu | Val | Glu | His | Val | Pro | Gly | Glu |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Glu | Gln | Lys | Ala | Asn | Leu | Leu | Thr | Lys | Ala | Leu | Gly | Arg | Ile | Lys | Phe |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Lys | Glu | Met | Arg | Glu | Leu | Val | Gly | Val | Gln | Glu | Leu | Ser | Lys | Cys | Glu |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     | 480 |     |
| Phe | Lys | Leu | Lys | Gly | Val | Asn | Val | Asp | Lys | Leu | Glu | Val | Ser | Leu | Arg |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Asn | Lys | Leu | Thr | Lys | Ser |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 500 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1050:

0960980 0860980









Cys Lys Arg Lys Phe Lys Ser Ser Thr Met Lys Gly Phe Pro Met Ser  
35 40 45  
Asp Val Tyr Asp Lys Leu Gly Thr Thr Lys Asp Ile Gln Ser Ile Leu  
50 55 60  
Ala Pro Thr Pro Asp Glu Lys Leu Leu Leu Glu Arg Ile Met Asp Lys  
65 70 75 80  
Glu Phe Gly Val Asn Asp Val Asp Asp Leu Ile Ala Asp Gly Trp Lys  
85 90 95  
Lys Arg Leu Val Asp Glu Glu Arg Thr Ile Cys Phe Glu Pro Leu Leu  
100 105 110  
Asn Glu Asp Val Ala His Arg Ser Phe Val Ala Asn Ile Ala Leu Ser  
115 120 125  
Thr Val Val Lys Ala Pro Arg Lys Lys Ala Val Glu Lys Lys Gly Lys  
130 135 140  
Gly Lys Ala Ala Ala Ala Leu Thr Ser Pro Ser Asp Gly Gly Leu Thr  
145 150 155 160  
Glu Val Val Asn Glu Met Lys Asn Leu Met Glu Asn Gly Phe Lys Ser  
165 170 175  
Met Asn Lys Arg Met Lys Asp Phe Asn Ala Cys Gly Ser Lys Glu Ile  
180 185 190  
Asp Asp Lys Glu Asn Glu Leu Glu Gly Ser Asp Ala Glu Thr Glu  
195 200 205  
Ile His Lys Glu Val Ala Gln Gly Asp Lys Glu Arg Glu Val Gly Glu  
210 215 220  
Thr Glu Thr Glu Xaa Asp Lys Glu Val Ala Gln Gly Asp Ser Asp Lys  
225 230 235 240  
Glu Val Ala Glu Ser Glu Lys Asp Lys Val Val Ala Glu Ser Glu Lys  
245 250 255  
Glu Lys Glu Val Ala Glu Ser Glu Ile Gly Val Ala Glu Ser Glu Lys  
260 265 270  
Asp Lys Glu Val Pro Gln Asp Asp Glu Met Asp Gly Gly Lys Val Ala  
275 280 285  
Glu Ser Asp Gly Glu Met Asp Gly Glu Lys Asp Lys Glu Val Pro Gln  
290 295 300  
Asp Asp Glu Met Asp Gly Glu Lys Glu Lys Glu Val Ala Glu Pro Ser  
305 310 315 320  
Glu Ile Gly Val Pro Glu Ser Glu Lys Asp Ile Glu Val Ala Asp Ser  
325 330 335  
Glu Lys Glu Lys Glu Val Pro Gln Asp Ala Lys Val Ala Glu Pro Ser  
340 345 350  
Lys Lys Arg Gly Lys Ala His Glu Asp Gly Asp Asp Pro Ser Lys Glu  
355 360 365  
Gly Val Lys Lys Pro Lys Val Val Lys Lys Leu Ala Glu Ser Arg Thr  
370 375 380  
Asp Ala Lys Pro Val Tyr Arg Ser Pro Ile Gln Thr Arg Tyr Arg Arg  
385 390 395 400  
Lys Lys Thr Lys Lys Asn Val  
405

(2) INFORMATION FOR SEQ ID NO:1054:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 376 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..376

(D) OTHER INFORMATION: / Ceres Seq. ID 1596156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:

Met Cys Lys Arg Lys Phe Lys Ser Ser Thr Met Lys Gly Phe Pro Met

00000000 00000000





|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Asp | Ala | Ser | Gly | Arg | Glu | Phe | Gln | Phe | Tyr | Ser | Gly | Gly | Val | Phe |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Asp | Gly | Arg | Cys | Gly | Val | Asp | Leu | Asp | His | Gly | Val | Ala | Ala | Val | Gly |
|     | 290 |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |
| Tyr | Gly | Ser | Ser | Lys | Gly | Ser | Asp | Tyr | Ile | Ile | Val | Lys | Asn | Ser | Trp |
|     | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Gly | Pro | Lys | Trp | Gly | Glu | Lys | Gly | Tyr | Ile | Arg | Leu | Lys | Arg | Asn | Thr |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Gly | Lys | Pro | Glu | Gly | Leu | Cys | Gly | Ile | Asn | Lys | Met | Ala | Ser | Phe | Pro |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Thr | Lys | Thr | Lys |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 355 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1057:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..247

(D) OTHER INFORMATION: / Ceres Seq. ID 1596161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Leu | Gly | Leu | Lys | Thr | Asp | Ile | Val | Arg | Arg | Asp | Glu | Glu | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Tyr | Ala | Glu | Phe | Ala | Tyr | Arg | Asp | Val | Glu | Ala | Val | Pro | Lys | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Asp | Trp | Arg | Lys | Lys | Gly | Ala | Val | Ala | Glu | Val | Lys | Asn | Gln | Gly |
|     |     |     | 35  |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ser | Cys | Gly | Ser | Cys | Trp | Ala | Phe | Ser | Thr | Val | Ala | Ala | Val | Glu | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Asn | Lys | Ile | Val | Thr | Gly | Asn | Leu | Thr | Thr | Leu | Ser | Glu | Gln | Glu |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Ile | Asp | Cys | Asp | Thr | Thr | Tyr | Asn | Asn | Gly | Cys | Asn | Gly | Gly | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Asp | Tyr | Ala | Phe | Glu | Tyr | Ile | Val | Lys | Asn | Gly | Gly | Leu | Arg | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Glu | Asp | Tyr | Pro | Tyr | Ser | Met | Glu | Glu | Gly | Thr | Cys | Glu | Met | Gln |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Asp | Glu | Ser | Glu | Thr | Val | Thr | Ile | Asn | Gly | His | Gln | Asp | Val | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Asn | Asp | Glu | Lys | Ser | Leu | Leu | Lys | Ala | Leu | Ala | His | Gln | Pro | Leu |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Val | Ala | Ile | Asp | Ala | Ser | Gly | Arg | Glu | Phe | Gln | Phe | Tyr | Ser | Gly |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Val | Phe | Asp | Gly | Arg | Cys | Gly | Val | Asp | Leu | Asp | His | Gly | Val | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Val | Gly | Tyr | Gly | Ser | Ser | Lys | Gly | Ser | Asp | Tyr | Ile | Ile | Val | Lys |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | Ser | Trp | Gly | Pro | Lys | Trp | Gly | Glu | Lys | Gly | Tyr | Ile | Arg | Leu | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Arg | Asn | Thr | Gly | Lys | Pro | Glu | Gly | Leu | Cys | Gly | Ile | Asn | Lys | Met | Ala |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ser | Phe | Pro | Thr | Lys | Thr | Lys |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 245 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1058:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 441 base pairs

(B) TYPE: nucleic acid

00669980 " 08668860

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..441
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1596204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| gatctttttca ttgctgtgtac tgatacatca tcaaccacta tacaatggat catggcggag | 60  |
| atcattaacc atcccaagat tcttgagagg ctaagagaag aaatcgattt tgttgtaggg   | 120 |
| aaaacaaggt tgattcaaga aactgacctc ccgaacctcc tttacttgca agcgataatc   | 180 |
| aaagaagggc taagattgca tccaccgggg ccactcttac caagaacggg ccaagaaagc   | 240 |
| ggcagaagag gttgtccagg aacaaatcta gcttatgctt ctgtaggaaac cgcgggttga  | 300 |
| gtaatgggtgc agttctttga ttggaaaatt gaaggagaga aagtcaacat gaatgaggct  | 360 |
| gctggaacaa tggatttgac catgggtcac cctcttaagt gcactcctgt tctctgaacc   | 420 |
| ctaaaccgtt taccttcgta g                                             |     |

(2) INFORMATION FOR SEQ ID NO:1059:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 146 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..146
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1596205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Leu | Phe | Ile | Ala | Gly | Thr | Asp | Thr | Ser | Thr | Thr | Ile | Gln | Trp |     |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | Met | Ala | Glu | Ile | Ile | Asn | His | Pro | Lys | Ile | Leu | Glu | Arg | Leu | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Glu | Ile | Asp | Phe | Val | Val | Gly | Lys | Thr | Arg | Leu | Ile | Gln | Glu | Thr |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Asp | Leu | Pro | Asn | Leu | Leu | Tyr | Leu | Gln | Ala | Ile | Ile | Lys | Glu | Gly | Leu |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Arg | Leu | His | Pro | Pro | Gly | Pro | Leu | Leu | Pro | Arg | Thr | Val | Gln | Glu | Ser |
|     |     |     |     |     |     |     |     | 70  |     |     |     |     | 75  |     | 80  |
| Gly | Arg | Arg | Gly | Cys | Pro | Gly | Thr | Asn | Leu | Ala | Tyr | Ala | Ser | Val | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 95  |
| Thr | Ala | Val | Gly | Val | Met | Val | Gln | Phe | Phe | Asp | Trp | Lys | Ile | Glu | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 110 |
| Glu | Lys | Val | Asn | Met | Asn | Glu | Ala | Ala | Gly | Thr | Met | Val | Leu | Thr | Met |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 125 |
| Ala | His | Pro | Leu | Lys | Cys | Thr | Pro | Val | Pro | Arg | Thr | Leu | Asn | Arg | Leu |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 140 |
| Pro | Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1060:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 129 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..129
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1596206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

Met Ala Glu Ile Ile Asn His Pro Lys Ile Leu Glu Arg Leu Arg Glu

00669960 08669960



Glu Glu Leu Lys Ala Pro Thr Pro Asp Pro Thr Ser Leu Ser Pro Gly  
100 105 110  
Gly His Arg Ser Val Glu Thr Leu Ala Asp Glu Ala Gly Val Thr Asp  
115 120 125  
Gln Ser Arg Ser Leu Leu Pro Ala Glu Asp Ile Arg Pro Ser Glu Glu  
130 135 140  
Leu Asp  
145

(2) INFORMATION FOR SEQ ID NO:1063:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..141

(D) OTHER INFORMATION: / Ceres Seq. ID 1596254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

Met Leu Ala Glu Ala Arg Gly Leu His Asp Ser Glu Val Ala Arg Ala  
1 5 10 15  
Ser Gln Thr Ala Arg Arg Glu Thr Ser Lys Val Phe Ile Ala Lys Leu  
20 25 30  
Lys Ala Ala Glu Gln Lys Val Ser Leu Leu Ala Arg Ile Asn Asp Gln  
35 40 45  
Phe Met Asn Leu Ser Gln Ala Arg Ala Asn Ala Gln Leu Ile Lys Ala  
50 55 60  
Leu Glu Glu Gly Gly Val Leu Ala Thr Glu Lys Asp Gln Val Glu Glu  
65 70 75 80  
Trp Leu Lys Asp Phe Ala Asn Thr Glu Leu Lys Glu Glu Leu Lys Ala  
85 90 95  
Pro Thr Pro Asp Pro Thr Ser Leu Ser Pro Gly Gly His Arg Ser Val  
100 105 110  
Glu Thr Leu Ala Asp Glu Ala Gly Val Thr Asp Gln Ser Arg Ser Leu  
115 120 125  
Leu Pro Ala Glu Asp Ile Arg Pro Ser Glu Glu Leu Asp  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1064:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1596255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

Met Asn Leu Ser Gln Ala Arg Ala Asn Ala Gln Leu Ile Lys Ala Leu  
1 5 10 15  
Glu Glu Gly Gly Val Leu Ala Thr Glu Lys Asp Gln Val Glu Glu Trp  
20 25 30  
Leu Lys Asp Phe Ala Asn Thr Glu Leu Lys Glu Glu Leu Lys Ala Pro  
35 40 45  
Thr Pro Asp Pro Thr Ser Leu Ser Pro Gly Gly His Arg Ser Val Glu  
50 55 60  
Thr Leu Ala Asp Glu Ala Gly Val Thr Asp Gln Ser Arg Ser Leu Leu  
65 70 75 80  
Pro Ala Glu Asp Ile Arg Pro Ser Glu Glu Leu Asp

00669980 1063



85 90

(2) INFORMATION FOR SEQ ID NO:1065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..507
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gacgtggtga tctcccaggc catcgaggga aaattggcga gagaagaggc tgagaaagaa  | 60  |
| gccttcgtca ataaggagaa tgccatcaag atggtcgagc gcgacctgaa gatggactct  | 120 |
| gaggttggtc gttgtaggcg acttctcgcc gaggcgagag gacttaggaa catcaaagtg  | 180 |
| gctcgggcta tgcaaacggc aaggcgagaa cttcggaggc cttcaccgcc aagttcaggg  | 240 |
| tggccgagga gaagatgtcg ctcttcgagg atgctaacga ccagtttata gtgggctaata | 300 |
| ccacaactga tcaaggcgct tgaagatggc agatctttgg cgaccgagaa aaaacaggtc  | 360 |
| gaggagtggc tgaaggattt tgccgatgca gaggtgaacc ttgttgcgtc cacatctgaa  | 420 |
| ctgaaggaag agctcaaagc cctgctcct gaaccagctc ctctaagccc tcgaggaat    | 480 |
| agatcggtcg agactcttgc ggattag                                      |     |

(2) INFORMATION FOR SEQ ID NO:1066:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..168
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Asp Val Val Ile Ser Gln Ala Ile Glu Gly Lys Leu Ala Arg Glu Glu |  |
| 1 5 10 15                                                       |  |
| Ala Glu Lys Glu Ala Phe Val Asn Lys Glu Asn Ala Ile Lys Met Val |  |
| 20 25 30                                                        |  |
| Glu Arg Asp Leu Lys Met Asp Ser Glu Val Val Arg Cys Arg Arg Leu |  |
| 35 40 45                                                        |  |
| Leu Ala Glu Ala Arg Gly Leu Arg Asn Ile Lys Val Ala Arg Ala Met |  |
| 50 55 60                                                        |  |
| Gln Thr Ala Arg Arg Glu Leu Arg Arg Pro Ser Pro Pro Ser Ser Gly |  |
| 65 70 75 80                                                     |  |
| Trp Pro Arg Arg Arg Cys Arg Ser Ser Arg Met Leu Thr Thr Ser Leu |  |
| 85 90 95                                                        |  |
| Ser Trp Ala Asn Pro Gln Leu Ile Lys Ala Leu Glu Asp Gly Arg Ser |  |
| 100 105 110                                                     |  |
| Leu Ala Thr Glu Lys Lys Gln Val Glu Glu Trp Leu Lys Asp Phe Ala |  |
| 115 120 125                                                     |  |
| Asp Ala Glu Val Asn Leu Val Arg Leu Thr Ser Glu Leu Lys Glu Glu |  |
| 130 135 140                                                     |  |
| Leu Lys Ala Pro Ala Pro Glu Pro Ala Pro Leu Ser Pro Arg Gly Asn |  |
| 145 150 155 160                                                 |  |
| Arg Ser Val Glu Thr Leu Ala Asp                                 |  |
| 165                                                             |  |

(2) INFORMATION FOR SEQ ID NO:1067:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

09689980-10130

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..138  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1596266  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:  
Met Val Glu Arg Asp Leu Lys Met Asp Ser Glu Val Val Arg Cys Arg  
1                  5                  10                  15  
Arg Leu Leu Ala Glu Ala Arg Gly Leu Arg Asn Ile Lys Val Ala Arg  
                  20                  25                  30  
Ala Met Gln Thr Ala Arg Arg Glu Leu Arg Arg Pro Ser Pro Pro Ser  
                  35                  40                  45  
Ser Gly Trp Pro Arg Arg Arg Cys Arg Ser Ser Arg Met Leu Thr Thr  
                  50                  55                  60  
Ser Leu Ser Trp Ala Asn Pro Gln Leu Ile Lys Ala Leu Glu Asp Gly  
65                  70                  75                  80  
Arg Ser Leu Ala Thr Glu Lys Lys Gln Val Glu Glu Trp Leu Lys Asp  
                  85                  90                  95  
Phe Ala Asp Ala Glu Val Asn Leu Val Arg Leu Thr Ser Glu Leu Lys  
                  100                  105                  110  
Glu Glu Leu Lys Ala Pro Ala Pro Glu Pro Ala Pro Leu Ser Pro Arg  
                  115                  120                  125  
Gly Asn Arg Ser Val Glu Thr Leu Ala Asp  
130                  135

(2) INFORMATION FOR SEQ ID NO:1068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1596267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

Met Asp Ser Glu Val Val Arg Cys Arg Arg Leu Leu Ala Glu Ala Arg  
1                  5                  10                  15  
Gly Leu Arg Asn Ile Lys Val Ala Arg Ala Met Gln Thr Ala Arg Arg  
                  20                  25                  30  
Glu Leu Arg Arg Pro Ser Pro Pro Ser Ser Gly Trp Pro Arg Arg Arg  
                  35                  40                  45  
Cys Arg Ser Ser Arg Met Leu Thr Thr Ser Leu Ser Trp Ala Asn Pro  
50                  55                  60  
Gln Leu Ile Lys Ala Leu Glu Asp Gly Arg Ser Leu Ala Thr Glu Lys  
65                  70                  75                  80  
Lys Gln Val Glu Glu Trp Leu Lys Asp Phe Ala Asp Ala Glu Val Asn  
                  85                  90                  95  
Leu Val Arg Leu Thr Ser Glu Leu Lys Glu Glu Leu Lys Ala Pro Ala  
                  100                  105                  110  
Pro Glu Pro Ala Pro Leu Ser Pro Arg Gly Asn Arg Ser Val Glu Thr  
115                  120                  125  
Leu Ala Asp  
130

(2) INFORMATION FOR SEQ ID NO:1069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1767 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

09669930-101300

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1767

(D) OTHER INFORMATION: / Ceres Seq. ID 1596280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

|            |             |             |            |             |             |      |
|------------|-------------|-------------|------------|-------------|-------------|------|
| atggtgaagg | tcttcatgga  | cgattttttcg | gtctatggcc | cctcttttctc | ctcatgtttg  | 60   |
| ttgaatcttg | gcagggtact  | gaccagggtgc | gaagagatca | atcttgttct  | caattgggaa  | 120  |
| aagtgtcatt | tcatggtgaa  | ggaaggcata  | atggtgggtc | acaagatatt  | agagaagggt  | 180  |
| atagagggtg | acaagggaaa  | gattgaagtg  | atgataagat | ttattaagaa  | cttctccaag  | 240  |
| atagccatgc | cgtttaaccag | actattgagc  | aaggagaccg | agtttgaatt  | cgatgaggac  | 300  |
| tgcctcaa   | at          | ctttcacac   | catcaaggaa | gctttggtat  | ctgctcctgt  | 360  |
| cctaattggg | actatgcgtt  | cgagattatg  | tgtgatgcat | cagattacgc  | cgtaggagct  | 420  |
| gttatagaca | agaagcttca  | cgtcatatat  | tacgccaggc | ggacgttggg  | tgaagctcaa  | 480  |
| ggaagatatg | caacaactga  | gaaggagctt  | ccagctgttg | aattcgcat   | taagaagttt  | 540  |
| agaagctatg | tggttggatc  | caaggtcatt  | gtctatacag | accatgcagc  | tttgaggcat  | 600  |
| ctattcttta | gtgggagcta  | caacaggaaa  | gagttccacc | aactgaacgc  | tggtgagggg  | 660  |
| agatctccat | ggtatgctaa  | tcacgtcaac  | tatttggtat | tcaaagtggg  | gcctcccaac  | 720  |
| ttgaccagtt | atgaaaggaa  | gaagtttttc  | agagacatac | accattacta  | ttgggatgaa  | 780  |
| ccttatttct | acactctttg  | taaagataag  | atctacagga | gatgcgtcct  | aaaagatgaa  | 840  |
| gtagaaggta | ttttgctgca  | ttgccatggc  | tccgcatatg | gtggccactt  | tgcaacattc  | 900  |
| aagacaatgt | caaagattct  | gcaagcaggc  | ttctggtggc | caccaatgtt  | taaggatgtt  | 960  |
| gaggagtttg | tttcaaaatg  | tgattcatgc  | cagagaaagg | gcaacatcag  | cagaagaaat  | 1020 |
| gagatgcctc | agaacccaat  | cttggaagtt  | gagatctttg | atgtatgggg  | aattgatttt  | 1080 |
| atgggtccat | tcctattttc  | atacggtaac  | aatatataat | tggtcgccgt  | agattatgta  | 1140 |
| tctaagtggg | tcgaagctat  | tgccagtcct  | accaacgatg | caaaagttat  | gctaaaactg  | 1200 |
| ttcaagacca | taactcttcc  | gagatttggg  | gttcccaggg | tagtaataag  | taatggtgga  | 1260 |
| gagcatttca | tcaacaaggg  | ttttgaaaac  | cttctgaaga | agcatggagt  | aaagcacaag  | 1320 |
| gtcgccactc | cttatcatcc  | acattcaagc  | gggcagggtg | agatttccaa  | caggagata   | 1380 |
| aaagcaattc | tgaaaacact  | gttgggatta  | caaggaaaga | ctggtctgca  | aagctcgggtg | 1440 |
| acgcactgtg | ggcttatagg  | acagctttca  | agaccccat  | tggagagAAC  | taagcttttc  | 1500 |
| catgacaaga | agatcatcac  | taaggatttc  | caggctggtg | atcagatgct  | gctattcaac  | 1560 |
| tcgcgcttga | aactctttcc  | gggaaagctt  | aagtcagat  | ggtctgggtc  | cttttgtatc  | 1620 |
| actgaagtac | gtccttatgg  | agcagtcact  | ctagctggta | agagtggaga  | tttcacagta  | 1680 |
| aatggtcaaa | ggctcaagaa  | atacttagca  | gatcaaatcc | ttccagaggt  | gacgtcgggt  | 1740 |
| catctccagg | aacttcttga  | tgattaa     |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1070:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 588 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..588

(D) OTHER INFORMATION: / Ceres Seq. ID 1596281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Lys | Val | Phe | Met | Asp | Asp | Phe | Ser | Val | Tyr | Gly | Pro | Ser | Phe |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ser | Cys | Leu | Leu | Asn | Leu | Gly | Arg | Val | Leu | Thr | Arg | Cys | Glu | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Asn | Leu | Val | Leu | Asn | Trp | Glu | Lys | Cys | His | Phe | Met | Val | Lys | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Ile | Met | Leu | Gly | His | Lys | Ile | Leu | Glu | Lys | Gly | Ile | Glu | Val | Asp |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Lys | Gly | Lys | Ile | Glu | Val | Met | Ile | Arg | Phe | Ile | Lys | Asn | Phe | Ser | Lys |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Ala | Met | Pro | Leu | Thr | Arg | Leu | Leu | Ser | Lys | Glu | Thr | Glu | Phe | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Phe | Asp | Glu | Asp | Cys | Leu | Lys | Ser | Phe | His | Thr | Ile | Lys | Glu | Ala | Leu |

00669980 10300

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     |     |     | 110 |  |  |
| Val | Ser | Ala | Pro | Val | Val | Arg | Ala | Pro | Asn | Trp | Asp | Tyr | Ala | Phe | Glu |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Ile | Met | Cys | Asp | Ala | Ser | Asp | Tyr | Ala | Val | Gly | Ala | Val | Ile | Asp | Lys |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Lys | Leu | His | Val | Ile | Tyr | Tyr | Ala | Arg | Arg | Thr | Leu | Asp | Glu | Ala | Gln |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Gly | Arg | Tyr | Ala | Thr | Thr | Glu | Lys | Glu | Leu | Pro | Ala | Val | Glu | Phe | Ala |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Phe | Lys | Lys | Phe | Arg | Ser | Tyr | Val | Val | Gly | Ser | Lys | Val | Ile | Val | Tyr |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Thr | Asp | His | Ala | Ala | Leu | Arg | His | Leu | Phe | Phe | Ser | Gly | Ser | Tyr | Asn |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |
| Arg | Lys | Glu | Phe | His | Gln | Leu | Asn | Ala | Val | Glu | Gly | Arg | Ser | Pro | Trp |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Tyr | Ala | Asn | His | Val | Asn | Tyr | Leu | Ala | Phe | Lys | Val | Glu | Pro | Pro | Asn |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Leu | Thr | Ser | Tyr | Glu | Arg | Lys | Lys | Phe | Phe | Arg | Asp | Ile | His | His | Tyr |  |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Tyr | Trp | Asp | Glu | Pro | Tyr | Phe | Tyr | Thr | Leu | Cys | Lys | Asp | Lys | Ile | Tyr |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |
| Arg | Arg | Cys | Val | Leu | Lys | Asp | Glu | Val | Glu | Gly | Ile | Leu | Leu | His | Cys |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |
| His | Gly | Ser | Ala | Tyr | Gly | Gly | His | Phe | Ala | Thr | Phe | Lys | Thr | Met | Ser |  |  |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |  |  |
| Lys | Ile | Leu | Gln | Ala | Gly | Phe | Trp | Trp | Pro | Pro | Met | Phe | Lys | Asp | Val |  |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |  |
| Glu | Glu | Phe | Val | Ser | Lys | Cys | Asp | Ser | Cys | Gln | Arg | Lys | Gly | Asn | Ile |  |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |  |
| Ser | Arg | Arg | Asn | Glu | Met | Pro | Gln | Asn | Pro | Ile | Leu | Glu | Val | Glu | Ile |  |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |  |
| Phe | Asp | Val | Trp | Gly | Ile | Asp | Phe | Met | Gly | Pro | Phe | Leu | Phe | Ser | Tyr |  |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |  |
| Gly | Asn | Lys | Tyr | Ile | Leu | Val | Ala | Val | Asp | Tyr | Val | Ser | Lys | Trp | Val |  |  |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |  |
| Glu | Ala | Ile | Ala | Ser | Pro | Thr | Asn | Asp | Ala | Lys | Val | Met | Leu | Lys | Leu |  |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |  |
| Phe | Lys | Thr | Ile | Ile | Phe | Pro | Arg | Phe | Gly | Val | Pro | Arg | Val | Val | Ile |  |  |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |  |  |
| Ser | Asn | Gly | Gly | Glu | His | Phe | Ile | Asn | Lys | Gly | Phe | Glu | Asn | Leu | Leu |  |  |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |  |
| Lys | Lys | His | Gly | Val | Lys | His | Lys | Val | Ala | Thr | Pro | Tyr | His | Pro | His |  |  |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |  |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:

| Table 1. Demographic characteristics of the study population |           |
|--------------------------------------------------------------|-----------|
| <b>Age (years)</b>                                           |           |
| Mean                                                         | 65.5      |
| SD                                                           | 10.5      |
| Range                                                        | 45-85     |
| <b>Gender</b>                                                |           |
| Male                                                         | 55 (55%)  |
| Female                                                       | 45 (45%)  |
| <b>Education (years)</b>                                     |           |
| Mean                                                         | 12.5      |
| SD                                                           | 2.5       |
| Range                                                        | 8-18      |
| <b>Marital status</b>                                        |           |
| Married                                                      | 60 (60%)  |
| Single                                                       | 10 (10%)  |
| Divorced                                                     | 15 (15%)  |
| Widowed                                                      | 15 (15%)  |
| <b>Occupation</b>                                            |           |
| Retired                                                      | 40 (40%)  |
| Homemaker                                                    | 20 (20%)  |
| Professional                                                 | 10 (10%)  |
| Managerial                                                   | 10 (10%)  |
| Unemployed                                                   | 10 (10%)  |
| <b>Income (USD/month)</b>                                    |           |
| Mean                                                         | 1,200     |
| SD                                                           | 300       |
| Range                                                        | 500-2,500 |
| <b>Health status</b>                                         |           |
| Good                                                         | 50 (50%)  |
| Fair                                                         | 30 (30%)  |
| Poor                                                         | 20 (20%)  |
| <b>Comorbidities</b>                                         |           |
| Hypertension                                                 | 30 (30%)  |
| Diabetes                                                     | 20 (20%)  |
| Cholesterol                                                  | 15 (15%)  |
| Arthritis                                                    | 10 (10%)  |
| Depression                                                   | 10 (10%)  |
| <b>Medication use</b>                                        |           |
| Yes                                                          | 40 (40%)  |
| No                                                           | 25 (25%)  |
| <b>Study duration (months)</b>                               |           |
| Mean                                                         | 12        |
| SD                                                           | 3         |
| Range                                                        | 6-18      |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Val | Asp | Ile | Pro | Leu | Asp | His | His | Val | Phe | Asn | Val | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Gly | Tyr | Asn | Ala | Pro | Gln | Gln | Val | His | Ile | Thr | Gln | Gly | Asp | Tyr |

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| ccgctgctttt | ggtctgcagg | aaatcatgaa | gtagattaca | tgccatacat | gggggaggtg | 60  |
| acacctttca  | ggaattacct | tcagcgttac | actacgcctt | acttagcctc | aaaaagtagc | 120 |
| agtcctcttt  | ggtacgctgt | taggcgtgca | tctgctcata | tcattgtcct | ctccagctat | 180 |
| tcgccttttg  | tgaagtatac | cccgcaatgg | cactggctta | gtgaagagct | tacaagagtt | 240 |

(2) INFORMATION FOR SEQ ID NO:1076:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1596337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

[illegible]

(2) INFORMATION FOR SEO ID NO:1077:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1596338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Tyr | Met | Gly | Glu | Val | Thr | Pro | Phe | Arg | Asn | Tyr | Leu | Gln | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Thr | Thr | Pro | Tyr | Leu | Ala | Ser | Lys | Ser | Ser | Ser | Pro | Leu | Trp | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Val | Arg | Arg | Ala | Ser | Ala | His | Ile | Ile | Val | Leu | Ser | Ser | Tyr | Ser |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Pro | Phe | Val | Lys | Tyr | Thr | Pro | Gln | Trp | His | Trp | Leu | Ser | Glu | Glu | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Arg | Val | Asp | Arg | Glu | Lys | Thr | Pro | Trp | Leu | Ile | Val | Leu | Met | His |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Pro | Ile | Tyr | Asn | Ser | Asn | Glu | Ala | His | Phe | Met | Glu | Gly | Glu | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Arg | Ala | Ala | Phe | Glu | Glu | Trp | Phe | Val | Gln | His | Lys | Val | Asp | Val |



(ix) FEATURE:

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:
Met Val Ile Pro Trp Gly Asp Leu Asp Ser Leu Ala Met Leu Gln Arg
1 5 10 15
Gln Leu Gly Val Asp Ile Leu Val Thr Gly His Thr His Gln Phe Thr
 20 25 30
Ala Tyr Lys His Glu Gly Gly Val Ile Asn Pro Gly Ser Ala Thr
 35 40 45
Gly Ala Tyr Ser Ser Ile Asn Gln Asp Val Asn Pro Ser Phe Val Leu
 50 55 60
Met Asp Ile Asp Gly Phe Arg Ala Val Val Tyr Val Tyr Glu Leu Ile
65 70 75 80
Asp Gly Glu Val Lys Val Asp Lys Ile Glu Phe Lys Lys Pro Pro Thr
 85 90 95
Thr Ser Ser Gly Pro
 100

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(D) OTHER INFORMATION: / Ceres Seq. ID 1596346

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(D) OTHER INFORMATION: / Ceres Seq. ID 1596350

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atggccttta | cgcaocgtt  | gttatggacg | ctactcgct  | tctgtctgac | ctggacggtg | 60  |
| ttctgcgtta | ccaacaggaa | gaagaaggcg | ccggaatttg | cagatgcggc | agcagaggag | 120 |
| agaagagaca | gtgctgctga | tgttatcatc | gtcggggctg | gtgtgggtgg | ctcggctctc | 180 |
| gcatattctc | ttgctaagga | cgggcgcoga | gtacttgtga | tagagaggga | tatgagagaa | 240 |
| ccagagagaa | tgatgggtga | gtttatgcag | ccaggaggac | gactcatgct | ttctaagctt | 300 |
| ggccttgaag | tgttcaacta | tgatttaaat | cgcagtaaaa | ctctaaccat | gattccaact | 360 |
| tcttga     |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1083:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:

Met Ala Phe Thr His Val Cys Leu Trp Thr Leu Leu Ala Phe Val Leu  
1 5 10 15  
Thr Trp Thr Val Phe Cys Val Thr Asn Arg Lys Lys Lys Ala Pro Glu  
20 25 30  
Leu Ala Asp Ala Ala Ala Glu Glu Arg Arg Asp Ser Ala Ala Asp Val  
35 40 45  
Ile Ile Val Gly Ala Gly Val Gly Gly Ser Ala Leu Ala Tyr Ser Leu  
50 55 60  
Ala Lys Asp Gly Arg Arg Val Leu Val Ile Glu Arg Asp Met Arg Glu  
65 70 75 80  
Pro Glu Arg Met Met Gly Glu Phe Met Gln Pro Gly Gly Arg Leu Met  
85 90 95  
Leu Ser Lys Leu Gly Leu Glu Val Phe Asn Tyr Asp Leu Asn Arg Ser  
100 105 110  
Lys Thr Leu Thr Met Ile Pro Thr Ser  
115 120

(2) INFORMATION FOR SEQ ID NO:1084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..483
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

atggagagag aaggcgcgctc cacaatttgc cctctcgagc tggtcagcca attgttcctg 60  
tcctgcgacg gttttgaatt gtccggtgtt ttgttccac atgttgccct ccactttcct 120  
ccgaaggata agaaagaggc gttatcgata aacaccaccg catgtgcat gagaggcagc 180  
gctcgggtct taagaggcag atgcttgagg cgcgcacatc ttgtgtggaa aggaatccaa 240  
gateccgacc atgcttcgga tgtacctccg cagttgaagt caagttcagg acctgcgtct 300  
gcgtcgggtg aagtgatccc ttctgaaagc gaagatgatg atgaaggaga agacagcaac 360  
acctggaaac acgtcaaaac caagcctaag ttggatgata agaacgaaac gtccacttcg 420  
aatgctgaac cagcgatgaa ggagtctgtt cctgagcctc ttccaaaaat gtcccogaac 480  
taa

(2) INFORMATION FOR SEQ ID NO:1085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

00559960-101300

(2) INFORMATION FOR SEQ ID NO:1086:

(A) LENGTH: 104 amino acids

(C) STRANDEDNESS:

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptide

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1596371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1087:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 975 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..975

(D) OTHER INFORMATION: / Ceres Seq. ID 1596407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

atgaatgata tatggtttat tcctctcttg atgccagggg aaacttctgg aacaacagca

(2) INFORMATION FOR SEQ ID NO:1088:

(A) LENGTH: 324 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..324

(D) OTHER INFORMATION: / Ceres Seq. ID 1596408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

[illegible]



(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

(2) INFORMATION FOR SEQ ID NO:1091:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO: 1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser                                     | Ser | Ser | Lys | Ser | Arg | Arg | Leu | Val | His | Cys | Thr | Asp | Thr | Phe |     |
| 1                                       |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Asn                                     | Gly | Glu | Met | Glu | Ile | Asn | Asn | Ser | Lys | Leu | Arg | Ser | Leu | Leu | Phe |
|                                         |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile                                     | Pro | Val | Asp | Tyr | Ser | Arg | Phe | Ser | Met | Gly | Ser | Asn | Phe | Met | Glu |
|                                         |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu                                     | Pro | Leu | Leu | Arg | Val | Leu | Asp | Leu | Ser | Phe | Ala | Asp | Phe | Glu | Gly |
|                                         | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gly                                     | Lys | Ile | Pro | Ser | Ser | Ile | Gly | Lys | Leu | Ile | His | Leu | Lys | Tyr | Leu |
| 65                                      |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser                                     | Leu | Tyr | Gln | Ala | Ser | Val | Thr | Tyr | Leu | Pro | Ser | Ser | Leu | Arg | Asn |
|                                         |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu                                     | Lys | Ser | Leu | Leu | Tyr | Leu | Asn | Leu | Arg | Ile | Asn | Ser | Gly | Gln | Leu |
|                                         |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile                                     | Asn | Val | Pro | Asn | Val | Phe | Lys | Glu | Met | Leu | Glu | Leu | Arg | Tyr | Leu |
|                                         |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |





| Variable                        | Mean           | SD               | Min | Max |
|---------------------------------|----------------|------------------|-----|-----|
| Age                             | 34.5           | 10.5             | 18  | 65  |
| Gender                          | Male           | Female           |     |     |
| Marital status                  | Married        | Single           |     |     |
| Education                       | High school    | College          |     |     |
| Occupation                      | Manager        | Worker           |     |     |
| Income                          | \$10,000       | \$20,000         |     |     |
| Health status                   | Good           | Fair             |     |     |
| Exercise frequency              | Weekly         | Monthly          |     |     |
| Stress level                    | Low            | High             |     |     |
| Sleep quality                   | Good           | Poor             |     |     |
| Dietary habits                  | Healthy        | Unhealthy        |     |     |
| Alcohol consumption             | None           | Occasional       |     |     |
| Tobacco use                     | Non-smoker     | Smoker           |     |     |
| Family size                     | 2              | 3                |     |     |
| Work hours                      | 40             | 50               |     |     |
| Commuting time                  | 30             | 45               |     |     |
| Home ownership                  | Owner          | Renter           |     |     |
| Neighborhood safety             | Safe           | Unsafe           |     |     |
| Access to green spaces          | Yes            | No               |     |     |
| Proximity to public transport   | Close          | Far              |     |     |
| Local crime rate                | Low            | High             |     |     |
| Quality of local schools        | Good           | Poor             |     |     |
| Availability of healthcare      | Yes            | No               |     |     |
| Local economy                   | Strong         | Weak             |     |     |
| Community engagement            | High           | Low              |     |     |
| Local government responsiveness | High           | Low              |     |     |
| Local infrastructure quality    | Good           | Poor             |     |     |
| Local environmental quality     | Good           | Poor             |     |     |
| Local cultural amenities        | Yes            | No               |     |     |
| Local social services           | Yes            | No               |     |     |
| Local law enforcement           | Effective      | Ineffective      |     |     |
| Local public works              | Active         | Inactive         |     |     |
| Local business development      | Active         | Inactive         |     |     |
| Local housing market            | Stable         | Volatile         |     |     |
| Local transportation network    | Well-developed | Poorly-developed |     |     |
| Local public safety             | High           | Low              |     |     |
| Local quality of life           | High           | Low              |     |     |
| Local community spirit          | High           | Low              |     |     |
| Local civic participation       | High           | Low              |     |     |
| Local political engagement      | High           | Low              |     |     |
| Local social capital            | High           | Low              |     |     |
| Local trust in government       | High           | Low              |     |     |
| Local civic responsibility      | High           | Low              |     |     |
| Local social cohesion           | High           | Low              |     |     |
| Local community resilience      | High           | Low              |     |     |
| Local social support            | High           | Low              |     |     |
| Local social network            | Strong         | Weak             |     |     |
| Local social capital            | High           | Low              |     |     |
| Local social trust              | High           | Low              |     |     |
| Local social cohesion           | High           | Low              |     |     |
| Local social support            | High           | Low              |     |     |
| Local social network            | Strong         | Weak             |     |     |
| Local social capital            | High           | Low              |     |     |
| Local social trust              | High           | Low              |     |     |
| Local social cohesion           | High           | Low              |     |     |
| Local social support            | High           | Low              |     |     |
| Local social network            | Strong         | Weak             |     |     |
| Local social capital            | High           | Low              |     |     |
| Local social trust              | High           | Low              |     |     |
| Local social cohesion           | High           | Low              |     |     |
| Local social support            | High           | Low              |     |     |
| Local social network            | Strong         | Weak             |     |     |
| Local social capital            | High           | Low              |     |     |
| Local social trust              | High           | Low              |     |     |
| Local social cohesion           | High           | Low              |     |     |
| Local social support            | High           | Low              |     |     |
| Local social network            | Strong         | Weak             |     |     |
| Local social capital            | High           | Low              |     |     |
| Local social trust              | High           | Low              |     |     |
| Local social cohesion           | High           | Low              |     |     |
| Local social support            | High           | Low              |     |     |
| Local social network            | Strong         | Weak             |     |     |
| Local social capital            | High           | Low              |     |     |
| Local social trust              | High           | Low              |     |     |
| Local social cohesion           | High           | Low              |     |     |
| Local social support            | High           | Low              |     |     |
| Local social network            | Strong         | Weak             |     |     |
| Local social capital            | High           | Low              |     |     |
| Local social trust              | High           | Low              |     |     |
| Local social cohesion           | High           | Low              |     |     |
| Local social support            | High           | Low              |     |     |
| Local social network            | Strong         | Weak             |     |     |
| Local social capital            | High           | Low              |     |     |
| Local social trust              | High           | Low              |     |     |
| Local social cohesion           | High           | Low              |     |     |
| Local social support            | High           | Low              |     |     |
| Local social network            | Strong         | Weak             |     |     |
| Local social capital            | High           | Low              |     |     |
| Local social trust              | High           | Low              |     |     |
| Local social cohesion           | High           | Low              |     |     |
| Local social support            | High           | Low              |     |     |
| Local social network            | Strong         | Weak             |     |     |
| Local social capital            | High           | Low              |     |     |
| Local social trust              | High           | Low              |     |     |
| Local social cohesion           | High           | Low              |     |     |
| Local social support            | High           | Low              |     |     |
| Local social network            | Strong         | Weak             |     |     |
| Local social capital            | High           | Low              |     |     |
| Local social trust              | High           | Low              |     |     |
| Local social cohesion           | High           | Low              |     |     |
| Local social support            |                |                  |     |     |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 amino acids

(A) LENGTH: 365 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..365

(D) OTHER INFORMATION: / Ceres Seq. ID 1596464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ser | Asn | Phe | Met | Glu | Leu | Pro | Leu | Leu | Arg | Val | Leu | Asp | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Phe | Ala | Asp | Phe | Glu | Gly | Gly | Lys | Ile | Pro | Ser | Ser | Ile | Gly | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ile | His | Leu | Lys | Tyr | Leu | Ser | Leu | Tyr | Gln | Ala | Ser | Val | Thr | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Pro | Ser | Ser | Leu | Arg | Asn | Leu | Lys | Ser | Leu | Leu | Tyr | Leu | Asn | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Ile | Asn | Ser | Gly | Gln | Leu | Ile | Asn | Val | Pro | Asn | Val | Phe | Lys | Glu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Met | Leu | Glu | Leu | Arg | Tyr | Leu | Ser | Leu | Pro | Leu | Arg | Thr | Pro | Gly | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

Thr Lys Leu Glu Phe Gly Asn Leu Leu Lys Leu Glu Thr Leu Ile Asn  
100 105 110  
Phe Ser Thr Lys Val Ser Ser Val Thr Asp Leu His Gly Met Thr Arg  
115 120 125  
Leu Arg Asn Leu Ser Ile Leu Ile Ser Gly Glu Glu Leu Arg Met Glu  
130 135 140  
Thr Leu Ser Thr Thr Pro Gly Lys Ser Leu Ser Lys Leu Gly His Leu  
145 150 155 160  
Glu Asn Leu Thr Ile Glu Tyr Ser Val Asn Ser Val Leu Leu Lys His  
165 170 175  
Leu Lys Leu Ile Phe Arg Pro Met Leu Pro Asp Met Gln His Phe Ser  
180 185 190  
Ser Gln Leu Thr Thr Ile Ser Leu Gln His Cys Leu Phe Glu Glu Asp  
195 200 205  
Pro Met Pro Ile Leu Glu Lys Leu Leu Gln Leu Lys Leu Val Tyr Leu  
210 215 220  
Thr Trp Lys Ala Tyr Val Gly Arg Arg Met Val Cys Thr Gly Gly Gly  
225 230 235 240  
Phe Pro Gln Leu His Lys Leu Ser Ile Glu Gly Leu Phe Asp Leu Glu  
245 250 255  
Glu Trp Ile Val Glu Glu Gly Ser Met Pro Arg Leu His Thr Leu Thr  
260 265 270  
Ile Asp Tyr Cys Lys Lys Leu Lys Glu Ile Pro Tyr Gly Leu Arg Phe  
275 280 285  
Ile Thr Ser Leu Lys Glu Leu Thr Ile Gly Thr Thr Asn Glu Arg Glu  
290 295 300  
Phe Gln Lys Lys Val Ser Lys Gly Gly Glu Asp Tyr Tyr Lys Ile Gln  
305 310 315 320  
His Ile Pro Ile Ile Arg Tyr Asn Trp His Pro Glu Pro Glu Asp Asn  
325 330 335  
Glu Val Lys Thr Thr Glu Ile Leu Arg Ser Met Gln Tyr Lys Gly Ser  
340 345 350  
Glu Ile Met Arg Glu Gly Ala Trp Ile Ile Phe Glu Glu  
355 360 365

(2) INFORMATION FOR SEQ ID NO:1094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 919 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..919
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atgcctctag ctaagcgagg aaggaagaga aaagccgata caaatgtttc acagagaccc  | 60  |
| ggagcctcta aaccactac tgcgaaaaga aaccctttac ctagtcaata caacttcaca   | 120 |
| cccgcgccg agattcctcc tgctaagtct tcccaagggc gagtccgagt tcaaccccaa   | 180 |
| caagcaaggt cagcagctcc acgagtctcc gactatccac ctctcaagt tcttttccag   | 240 |
| aactccgtga atcatgatct ccctgcacct ctttcgtcac aagaagtcca gaatgatgca  | 300 |
| actaatgat cgactccaca acatgacct ccaagttctc cgattcagaa ctctcatgcc    | 360 |
| agtcaaccat cttcccaagg taacaacttc caagaacgtg ttagttccgt gttaccggaa  | 420 |
| ctccaagccg ataacataaa ggctctaaac gacattcttc aagtgcctgg tctgtaggcg  | 480 |
| tggacaactg ttctttctcc catactgatg gaaaaacaa cttggtttac tctgtacaca   | 540 |
| tcttcgaggt tggttcgaaa gattactaga gtatggacaa acaaatttga tgggtgtcttc | 600 |
| tatagctggg catgtgttcc acaggatcga cgagaaagat acttcctcca gtttgcgaaa  | 660 |
| atacaccatt gggattcttt gattacagga acaattcagt actattttga agatatatgt  | 720 |
| caaagacgga tgaaagatat gattagcact gtgaggacta gtcaagagtg tcctaaatgg  | 780 |
| atcatcgatt cccatatctt ggaaacgatg tgtgcatatt gggataatga agaagcaatt  | 840 |
| gcaaagagtc tgacatatcc caagactcgc atgtttgacc ataattgggt cgtcctcac   | 900 |

00669930-10300

(2) INFORMATION FOR SEQ ID NO:1095:

(A) LENGTH: 306 amino acids

(C) STRANDEDNESS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1596523

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..435  
(D) OTHER INFORMATION: / Ceres Seq. ID 1596532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| aggaattttca tcgaacatgt tataggcaat gatgagtttg tggatgaataa tgtgtatacg | 60  |
| ctaaatatat gggatgttgg tgggcaaaag actataagat cgtattggag gaattacttt   | 120 |
| gagcagactg atgggttggg ttgggtgggt gatagttctg atcttaggag gttagatgat   | 180 |
| tgcaagatgg aacttgacaa tctcttgaaa gaagagaggc tagctgggtc atctttgctg   | 240 |
| atactagcaa ataagcagga tattcaaggt gcactaacac ctgatgaaat tggcaaggtg   | 300 |
| ctaaacttag agtccatgga taaaagccgg cactggaaga tagtgggttg cagcgcatatc  | 360 |
| acgggtgaag gtttgttggg aggattcgat tgggtgggtc aagacattgc ctccaggatt   | 420 |
| tacatgcttg actaa                                                    |     |

(2) INFORMATION FOR SEQ ID NO:1097:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..144  
(D) OTHER INFORMATION: / Ceres Seq. ID 1596533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Arg Asn Phe Ile Glu His Val Ile Gly Asn Asp Glu Phe Val Val Asn |  |
| 1 5 10 15                                                       |  |
| Asn Val Tyr Thr Leu Asn Ile Trp Asp Val Gly Gly Gln Lys Thr Ile |  |
| 20 25 30                                                        |  |
| Arg Ser Tyr Trp Arg Asn Tyr Phe Glu Gln Thr Asp Gly Leu Val Trp |  |
| 35 40 45                                                        |  |
| Val Val Asp Ser Ser Asp Leu Arg Arg Leu Asp Asp Cys Lys Met Glu |  |
| 50 55 60                                                        |  |
| Leu Asp Asn Leu Leu Lys Glu Glu Arg Leu Ala Gly Ser Ser Leu Leu |  |
| 65 70 75 80                                                     |  |
| Ile Leu Ala Asn Lys Gln Asp Ile Gln Gly Ala Leu Thr Pro Asp Glu |  |
| 85 90 95                                                        |  |
| Ile Gly Lys Val Leu Asn Leu Glu Ser Met Asp Lys Ser Arg His Trp |  |
| 100 105 110                                                     |  |
| Lys Ile Val Gly Cys Ser Ala Tyr Thr Gly Glu Gly Leu Leu Glu Gly |  |
| 115 120 125                                                     |  |
| Phe Asp Trp Leu Val Gln Asp Ile Ala Ser Arg Ile Tyr Met Leu Asp |  |
| 130 135 140                                                     |  |

(2) INFORMATION FOR SEQ ID NO:1098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..82  
(D) OTHER INFORMATION: / Ceres Seq. ID 1596534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Glu Leu Asp Asn Leu Leu Lys Glu Glu Arg Leu Ala Gly Ser Ser |  |
| 1 5 10 15                                                       |  |
| Leu Leu Ile Leu Ala Asn Lys Gln Asp Ile Gln Gly Ala Leu Thr Pro |  |
| 20 25 30                                                        |  |
| Asp Glu Ile Gly Lys Val Leu Asn Leu Glu Ser Met Asp Lys Ser Arg |  |

00559950-104300

(2) INFORMATION FOR SEQ ID NO:1099:

(A) LENGTH: 1248 base pairs

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..1248

(D) OTHER INFORMATION: / Ceres Seq. ID 1596611

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:10594 |            |            |             |            |             |      |
|--------------------------------------------|------------|------------|-------------|------------|-------------|------|
| atggcaaccg                                 | tggaatccaa | gaaacaagag | aagaagtctga | gaacgagcaa | accaaagaag  | 60   |
| gataacatcg                                 | ggatgaggat | gttaatgaaa | ttggtaatga  | ctttgagact | agtaatagct  | 120  |
| tggagaaacac                                | taacacatgt | acgggaactc | aagaagcggg  | aacagaaagc | tcaagtgtct  | 180  |
| acggccaagt                                 | acaattcaat | ggactcgagg | gattggatgt  | tagcatgtga | agacgaaatc  | 240  |
| tattcgataa                                 | agaagaacga | gactcggagt | cttgtagatc  | ttccatttgg | aataaagccg  | 300  |
| attggtttaa                                 | aatgggtatt | caaactcaaa | cgaaattctg  | atgtaagtat | caataaatac  | 360  |
| aaagctcgac                                 | ttgttgctaa | gggttacgtg | caacgttatg  | ggactgattt | ctatgaagtc  | 420  |
| tttgttccag                                 | tagcttgtat | tgagaaaata | attcttctgc  | acattgaggc | ttcaaattgat | 480  |
| tgggagatac                                 | aacttgatgt | taaaacagct | ttcttatcatg | gagagttaaa | ggaaactggt  | 540  |
| tatgtcacgc                                 | gaccagaaga | ttttgtagaa | aaggggagaag | aaggaaaaga | accgtcgggt  | 600  |
| tatcggaaaa                                 | ctataagtg  | tgagtttctt | cttgtagcag  | tttacgtgga | tgacttattt  | 660  |
| gttacaggaa                                 | caaatacaac | cattattgat | gagttcaaag  | gagagatgac | ttcaaatttc  | 720  |
| aacatgagca                                 | accttgggaa | attaacttat | tatctcggaa  | ttgaagtgtt | tcaacgaaaa  | 780  |
| gaagaaataa                                 | ggttgaatca | aactcgttat | gagatgaaga  | tattagaaga | gactgcaatg  | 840  |
| gccggaccta                                 | tcttactctg | tgggagtaat | gagtcgttat  | atgcaaagtc | caagagaatc  | 900  |
| acatggagcg                                 | gctatgaggc | actgcttaag | gcattgaaac  | ggcaagataa | gcaatttggc  | 960  |
| tccaagattt                                 | gctcagtgaa | gtcacccggg | taccaagcaa  | aagagtgtgt | atacggattg  | 1020 |
| acaataaatc                                 | agcgatatct | ctcacgaaga | acctgtattt  | tactggcgag | ggcaaacaca  | 1080 |
| tccataggcg                                 | aagtcgaaca | tgttctggga | attgacgaaa  | gggcagacat | gttaacaaag  | 1140 |
| gcccttgtaa                                 | gaatgaagtt | taagagatg  | agagatctca  | ttggtgttca | agatgtgtgt  | 1200 |
| gaagggatag                                 | agcttaggat | ctttaggagt | tatctaagat  | gtgtttag   |             |      |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 415 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..415

(D) OTHER INFORMATION: / Ceres Seq. ID 1596612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

| (X1) SEQUENCE DESCRIPTION: 321 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|--------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met                            | Ala | Thr | Val | Glu | Ser | Lys | Lys | Gln | Glu | Lys | Lys | Ser | Arg | Thr | Ser |  |
| 1                              |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys                            | Pro | Lys | Lys | Asp | Asn | Met | Arg | Met | Arg | Met | Leu | Met | Lys | Leu | Val |  |
|                                |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Met                            | Thr | Leu | Arg | Leu | Val | Ile | Ala | Trp | Arg | Thr | Leu | Thr | His | Val | Arg |  |
|                                |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Glu                            | Leu | Lys | Lys | Arg | Glu | Gln | Lys | Ala | Gln | Val | Leu | Thr | Ala | Lys | Tyr |  |
|                                | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Asn                            | Ser | Met | Asp | Ser | Arg | Asp | Trp | Met | Leu | Ala | Cys | Glu | Asp | Glu | Ile |  |

| Table 1. (continued) |        |
|----------------------|--------|
| 10                   | 0.0000 |
| 11                   | 0.0000 |
| 12                   | 0.0000 |
| 13                   | 0.0000 |
| 14                   | 0.0000 |
| 15                   | 0.0000 |
| 16                   | 0.0000 |
| 17                   | 0.0000 |
| 18                   | 0.0000 |
| 19                   | 0.0000 |
| 20                   | 0.0000 |
| 21                   | 0.0000 |
| 22                   | 0.0000 |
| 23                   | 0.0000 |
| 24                   | 0.0000 |
| 25                   | 0.0000 |
| 26                   | 0.0000 |
| 27                   | 0.0000 |
| 28                   | 0.0000 |
| 29                   | 0.0000 |
| 30                   | 0.0000 |
| 31                   | 0.0000 |
| 32                   | 0.0000 |
| 33                   | 0.0000 |
| 34                   | 0.0000 |
| 35                   | 0.0000 |
| 36                   | 0.0000 |
| 37                   | 0.0000 |
| 38                   | 0.0000 |
| 39                   | 0.0000 |
| 40                   | 0.0000 |
| 41                   | 0.0000 |
| 42                   | 0.0000 |
| 43                   | 0.0000 |
| 44                   | 0.0000 |
| 45                   | 0.0000 |
| 46                   | 0.0000 |
| 47                   | 0.0000 |
| 48                   | 0.0000 |
| 49                   | 0.0000 |
| 50                   | 0.0000 |
| 51                   | 0.0000 |
| 52                   | 0.0000 |
| 53                   | 0.0000 |
| 54                   | 0.0000 |
| 55                   | 0.0000 |
| 56                   | 0.0000 |
| 57                   | 0.0000 |
| 58                   | 0.0000 |
| 59                   | 0.0000 |
| 60                   | 0.0000 |
| 61                   | 0.0000 |
| 62                   | 0.0000 |
| 63                   | 0.0000 |
| 64                   | 0.0000 |
| 65                   | 0.0000 |
| 66                   | 0.0000 |
| 67                   | 0.0000 |
| 68                   | 0.0000 |
| 69                   | 0.0000 |
| 70                   | 0.0000 |
| 71                   | 0.0000 |
| 72                   | 0.0000 |
| 73                   | 0.0000 |
| 74                   | 0.0000 |
| 75                   | 0.0000 |
| 76                   | 0.0000 |
| 77                   | 0.0000 |
| 78                   | 0.0000 |
| 79                   | 0.0000 |
| 80                   | 0.0000 |
| 81                   | 0.0000 |
| 82                   | 0.0000 |
| 83                   | 0.0000 |
| 84                   | 0.0000 |
| 85                   | 0.0000 |
| 86                   | 0.0000 |
| 87                   | 0.0000 |
| 88                   | 0.0000 |
| 89                   | 0.0000 |
| 90                   | 0.0000 |
| 91                   | 0.0000 |
| 92                   | 0.0000 |
| 93                   | 0.0000 |
| 94                   | 0.0000 |
| 95                   | 0.0000 |
| 96                   | 0.0000 |
| 97                   | 0.0000 |
| 98                   | 0.0000 |
| 99                   | 0.0000 |
| 100                  | 0.0000 |

(i) SEQUENCE CHARACTERISTICS:

- (ix) FEATURE:

- (D) OTHER INFORMATION: / Ceres Seq. ID 1596614

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Met | Arg | Met | Leu | Met | Lys | Leu | Val | Met | Thr | Leu | Arg | Leu | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Ala | Trp | Arg | Thr | Leu | Thr | His | Val | Arg | Glu | Leu | Lys | Lys | Arg | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Lys | Ala | Gln | Val | Leu | Thr | Ala | Lys | Tyr | Asn | Ser | Met | Asp | Ser | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

Asp Trp Met Leu Ala Cys Glu Asp Glu Ile Tyr Ser Ile Lys Lys Asn  
50 55 60  
Glu Thr Arg Ser Leu Val Asp Leu Pro Phe Gly Ile Lys Pro Ile Gly  
65 70 75 80  
Leu Lys Trp Val Phe Lys Leu Lys Arg Asn Ser Asp Val Ser Ile Asn  
85 90 95  
Lys Tyr Lys Ala Arg Leu Val Ala Lys Gly Tyr Val Gln Arg Tyr Gly  
100 105 110  
Thr Asp Phe Tyr Glu Val Phe Val Pro Val Ala Cys Ile Glu Lys Ile  
115 120 125  
Ile Leu Val Asp Leu Glu Ala Ser Asn Asp Trp Glu Ile Gln Leu Asp  
130 135 140  
Val Lys Thr Ala Phe Leu His Gly Glu Leu Lys Glu Thr Val Tyr Val  
145 150 155 160  
Thr Arg Pro Glu Asp Phe Val Glu Lys Gly Glu Glu Gly Lys Glu Pro  
165 170 175  
Ser Val Tyr Arg Lys Thr Ile Ser Gly Glu Phe Leu Leu Val Ala Val  
180 185 190  
Tyr Val Asp Asp Leu Phe Val Thr Gly Thr Asn Thr Thr Ile Ile Asp  
195 200 205  
Glu Phe Lys Gly Glu Met Thr Ser Asn Phe Asn Met Ser Asn Leu Gly  
210 215 220  
Lys Leu Thr Tyr Tyr Leu Gly Ile Glu Val Phe Gln Arg Lys Glu Glu  
225 230 235 240  
Ile Arg Leu Asn Gln Thr Arg Tyr Glu Met Lys Ile Leu Glu Glu Thr  
245 250 255  
Ala Met Ala Gly Pro Ile Leu Leu Cys Gly Ser Asn Glu Ser Leu Tyr  
260 265 270  
Ala Lys Ser Lys Arg Ile Thr Trp Ser Gly Tyr Glu Ala Leu Leu Lys  
275 280 285  
Ala Leu Lys Arg Gln Asp Lys Gln Phe Gly Ser Lys Ile Cys Ser Val  
290 295 300  
Lys Ser Pro Gly Tyr Gln Ala Lys Glu Leu Leu Tyr Gly Leu Thr Ile  
305 310 315 320  
Asn Gln Arg Tyr Leu Ser Arg Arg Thr Leu Tyr Phe Met Ala Arg Ala  
325 330 335  
Asn Thr Ser Ile Gly Glu Val Glu His Val Leu Gly Ile Glu Gln Arg  
340 345 350  
Ala Asp Ile Leu Thr Lys Ala Leu Val Arg Met Lys Phe Lys Glu Met  
355 360 365  
Arg Asp Leu Ile Gly Val Gln Asp Val Cys Glu Gly Ile Glu Leu Arg  
370 375 380  
Ile Phe Arg Ser Tyr Leu Arg Cys Val  
385 390

(2) INFORMATION FOR SEQ ID NO:1102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1500
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atggagctca atgtctacgg attgtgggct tatgatgcaa tcaccgcgct ggcaatggct  | 60  |
| attgaagaag ctggaataga taacatgact ttcagtaatg cagatccttg gaaaaatgta  | 120 |
| tctgaacttg aagctcttgg tttatctcag tttgggtccaa agcttctcca gacgctctca | 180 |
| acaattcagt tcagaggact tgcaggagat ttctggtttg tcaatgggca actgcaacca  | 240 |
| tcggtgtttg agattgttaa tgtgatcggg accggagtaa ggtcagtagg attctggacg  | 300 |

0068980-10100

(2) INFORMATION FOR SEQ ID NO:1103:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Asn | Val | Tyr | Gly | Leu | Trp | Ala | Tyr | Asp | Ala | Ile | Thr | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ala | Met | Ala | Ile | Glu | Glu | Ala | Gly | Ile | Asp | Asn | Met | Thr | Phe | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Ala | Asp | Pro | Gly | Lys | Asn | Val | Ser | Glu | Leu | Glu | Ala | Leu | Gly | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Gln | Phe | Gly | Pro | Lys | Leu | Gln | Thr | Leu | Ser | Thr | Ile | Gln | Phe |     |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Gly | Leu | Ala | Gly | Asp | Phe | Cys | Phe | Val | Asn | Gly | Gln | Leu | Gln | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Val | Phe | Glu | Ile | Val | Asn | Val | Ile | Gly | Thr | Gly | Val | Arg | Ser | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Phe | Trp | Thr | Glu | Glu | Asn | Gly | Leu | Val | Lys | Lys | Leu | Glu | Gln | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Ser | Cys | Met | Ser | Asn | Leu | Ser | Thr | Trp | Asn | Asp | His | Leu | Lys | Tyr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Ile | Trp | Pro | Gly | Glu | Ala | Gly | Ser | Ile | Pro | Thr | Gly | Ser | Lys | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Thr | Asn | Asp | Lys | Arg | Leu | Arg | Ile | Gly | Val | Pro | Lys | Arg | Ile | Gly |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Phe | Thr | Asp | Leu | Val | Lys | Val | Thr | Arg | Asp | Pro | Ile | Thr | Asn | Ser | Thr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Val | Thr | Gly | Phe | Cys | Ile | Asp | Tyr | Phe | Glu | Ala | Val | Val | Gln | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Met | Pro | Tyr | Asp | Val | Ser | Tyr | Glu | Phe | Ile | Pro | Phe | Glu | Lys | Pro | Asn |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Glu | Pro | Ala | Gly | Ser | Tyr | Asn | Asp | Leu | Val | His | Gln | Val | Tyr | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |



Gly Arg Tyr Asp Ala Val Val Gly Asp Thr Thr Ile Leu Ser Lys Arg  
225 230 235 240  
Ser Leu Tyr Val Glu Phe Thr Leu Pro Phe Ile Lys Ser Gly Val Gly  
245 250 255  
Leu Val Val Ser Ile Glu Asp Gln Val Lys Arg Asp Ser Val Pro Phe  
260 265 270  
Leu Lys Pro Leu Ser Trp Glu Leu Trp Leu Thr Ser Phe Val Leu Phe  
275 280 285  
Phe Leu Ile Gly Phe Thr Val Trp Ala Leu Glu His Arg Asp Asn Pro  
290 295 300  
Asp Phe His Gly Pro Pro Asn Tyr Gln Ala Ser Thr Ile Leu Trp Phe  
305 310 315 320  
Ala Phe Ser Thr Met Val Phe Ala Pro Ser Thr Leu Asn Leu Pro Ser  
325 330 335  
Pro Ser Thr Ser Leu His Ile Leu Lys Phe Leu Tyr Ile Ser Thr Ser  
340 345 350  
Gln Ile Leu Met Leu Thr Leu Lys Leu Leu Ser Ala Gly Glu Arg Val  
355 360 365  
Tyr Ser Phe Glu Ala Arg Val Leu Val Ile Thr Trp Tyr Phe Ile Val  
370 375 380  
Leu Val Leu Thr Leu Ser Tyr Thr Ala Ser Leu Ala Ser Leu Leu Thr  
385 390 395 400  
Ser Gln Gln Leu Asn Pro Thr Ile Thr Ser Met Ser Ser Leu Leu Gln  
405 410 415  
Arg Gly Glu Arg Val Gly Tyr Gln Arg Thr Ser Phe Ile Leu Gly Lys  
420 425 430  
Leu Lys Asp Thr Xaa Phe Pro Gln Ser Ser Leu Val Pro Phe Asp Thr  
435 440 445  
Ala Glu Glu Cys Asp Glu Leu Leu Ser Lys Gly Ser Lys Lys Gly Gly  
450 455 460  
Val Ser Ala Ala Phe Leu Glu Ile Pro Tyr Leu Arg Ile Phe Leu Ser  
465 470 475 480  
Asn Tyr Cys Asn Thr Tyr Lys Ile Val Glu Val Pro Phe Lys Val Asp  
485 490 495  
Gly Phe Gly Phe  
500

(2) INFORMATION FOR SEQ ID NO:1104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..482
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

Met Ala Ile Glu Glu Ala Gly Ile Asp Asn Met Thr Phe Ser Asn Ala  
1 5 10 15  
Asp Pro Gly Lys Asn Val Ser Glu Leu Glu Ala Leu Gly Leu Ser Gln  
20 25 30  
Phe Gly Pro Lys Leu Leu Gln Thr Leu Ser Thr Ile Gln Phe Arg Gly  
35 40 45  
Leu Ala Gly Asp Phe Cys Phe Val Asn Gly Gln Leu Gln Pro Ser Val  
50 55 60  
Phe Glu Ile Val Asn Val Ile Gly Thr Gly Val Arg Ser Val Gly Phe  
65 70 75 80  
Trp Thr Glu Glu Asn Gly Leu Val Lys Lys Leu Glu Gln Gln Pro Ser  
85 90 95  
Cys Met Ser Asn Leu Ser Thr Trp Asn Asp His Leu Lys Tyr Ile Ile

09689900-10100

[illegible]

- ```
(2) INFORMATION FOR SEQ ID NO:1105:
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 705 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: DNA (genomic)
  (ix) FEATURE:
      (A) NAME/KEY: -
      (B) LOCATION: 1..705
      (D) OTHER INFORMATION: / Ceres Seq. ID 1596784
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:
```


Val Val Ile Gly Gly Glu Asp Gly His Asp Tyr Tyr Leu Ser Asp Val
130 135 140
His Ile Leu Asp Thr Gly Glu Lys Ala Ser
145 150

(2) INFORMATION FOR SEQ ID NO:1109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1003
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

gaagttttta tctttgagga aaggtacaaa aantgacgtt gctgctgctt tagaacagga 60
acttcacact tcgaggtcta tgtttgagca agctcggttc aaccttggtga ctgctctatc 120
aaatgttgaa gctaagaaaa ggtttgaatt tttggaagca gtcagtggaa caatggatgc 180
acatcttcgg tacttcaaac aggtcttgac atatgcgcaa caatccagag aaagatcaaa 240
ttatgaacaa gcagcactta atgaaaagat gcaggagtac aaaagacagg ttgatcgaga 300
gagcaggtgg gggtcaaagt gttctaattg atcaccaa at ggagatggca tacaagcaat 360
cggtagaagc tctcacaaaa tgatagacgc cgtaatgcaa tctgctgcaa gaggaaaggt 420
gcaaacaata aggcaaggtt atctctctaa acgatcttca aacctgagag gagactggaa 480
aagaaggttt tttgttcttg acagccgggg aatgctctat tattaccgaa aacagtgtag 540
caaaccatct gggctctggaa gccagctttc tggacagaga aatagctccg agcttgggtc 600
tggactgctt agtaggtggc tttcttcgaa taatcatgga catggtggtg tccatgatga 660
gaagtctgta gctcgtcata cagtgaactt actcacctca acaattaaag tcgacgctga 720
tcaatcagat ctgaggtttt gctttaggat catatcacct acaaaaaact acacgttgca 780
ggctgagagt gcactcgatc aaatggattg gatagaaaag atcactgggg ttattgcatc 840
actacttagt tctcaggtcc ctgaacaggc tcatattaaa taccaatgca actttgggtg 900
ttgtccatcg gctacatttc agcgtcttcc tggtagtccc atgggaagtg gccaccatcg 960
atctgctagt gaaagtagct catatgaaag ttctgaatat gat

(2) INFORMATION FOR SEQ ID NO:1110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..334
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

Lys Phe Leu Ser Leu Arg Lys Gly Thr Lys Xaa Asp Val Ala Ala Ala
1 5 10 15
Leu Glu Gln Glu Leu His Thr Ser Arg Ser Met Phe Glu Gln Ala Arg
20 25 30
Phe Asn Leu Val Thr Ala Leu Ser Asn Val Glu Ala Lys Lys Arg Phe
35 40 45
Glu Phe Leu Glu Ala Val Ser Gly Thr Met Asp Ala His Leu Arg Tyr
50 55 60
Phe Lys Gln Val Leu Thr Tyr Ala Gln Gln Ser Arg Glu Arg Ser Asn
65 70 75 80
Tyr Glu Gln Ala Ala Leu Asn Glu Lys Met Gln Glu Tyr Lys Arg Gln
85 90 95
Val Asp Arg Glu Ser Arg Trp Gly Ser Asn Gly Ser Asn Gly Ser Pro
100 105 110
Asn Gly Asp Gly Ile Gln Ala Ile Gly Arg Ser Ser His Lys Met Ile
115 120 125

09689980 101300

Asp	Ala	Val	Met	Gln	Ser	Ala	Ala	Arg	Gly	Lys	Val	Gln	Thr	Ile	Arg
130						135					140				
Gln	Gly	Tyr	Leu	Ser	Lys	Arg	Ser	Ser	Asn	Leu	Arg	Gly	Asp	Trp	Lys
145					150				155						160
Arg	Arg	Phe	Phe	Val	Leu	Asp	Ser	Arg	Gly	Met	Leu	Tyr	Tyr	Tyr	Arg
				165					170						175
Lys	Gln	Cys	Ser	Lys	Pro	Ser	Gly	Ser	Gly	Ser	Gln	Leu	Ser	Gly	Gln
			180					185					190		
Arg	Asn	Ser	Ser	Glu	Leu	Gly	Ser	Gly	Leu	Leu	Ser	Arg	Trp	Leu	Ser
			195				200					205			
Ser	Asn	Asn	His	Gly	His	Gly	Gly	Val	His	Asp	Glu	Lys	Ser	Val	Ala
			210			215					220				
Arg	His	Thr	Val	Asn	Leu	Leu	Thr	Ser	Thr	Ile	Lys	Val	Asp	Ala	Asp
225					230					235					240
Gln	Ser	Asp	Leu	Arg	Phe	Cys	Phe	Arg	Ile	Ile	Ser	Pro	Thr	Lys	Asn
				245					250						255
Tyr	Thr	Leu	Gln	Ala	Glu	Ser	Ala	Leu	Asp	Gln	Met	Asp	Trp	Ile	Glu
			260					265					270		
Lys	Ile	Thr	Gly	Val	Ile	Ala	Ser	Leu	Leu	Ser	Ser	Gln	Val	Pro	Glu
			275					280				285			
Gln	Ala	His	Ile	Lys	Tyr	Gln	Cys	Asn	Phe	Gly	Asp	Cys	Pro	Ser	Ala
			290			295					300				
Thr	Phe	Gln	Arg	Leu	Pro	Gly	Ser	Pro	Met	Gly	Ser	Gly	His	His	Arg
305					310					315					320
Ser	Ala	Ser	Glu	Ser	Ser	Ser	Tyr	Glu	Ser	Ser	Glu	Tyr	Asp		
				325					330						

(2) INFORMATION FOR SEQ ID NO:1111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..308

(D) OTHER INFORMATION: / Ceres Seq. ID 1596802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

Met	Phe	Glu	Gln	Ala	Arg	Phe	Asn	Leu	Val	Thr	Ala	Leu	Ser	Asn	Val
1				5					10					15	
Glu	Ala	Lys	Lys	Arg	Phe	Glu	Phe	Leu	Glu	Ala	Val	Ser	Gly	Thr	Met
			20					25					30		
Asp	Ala	His	Leu	Arg	Tyr	Phe	Lys	Gln	Val	Leu	Thr	Tyr	Ala	Gln	Gln
		35					40					45			
Ser	Arg	Glu	Arg	Ser	Asn	Tyr	Glu	Gln	Ala	Ala	Leu	Asn	Glu	Lys	Met
		50				55					60				
Gln	Glu	Tyr	Lys	Arg	Gln	Val	Asp	Arg	Glu	Ser	Arg	Trp	Gly	Ser	Asn
65					70				75					80	
Gly	Ser	Asn	Gly	Ser	Pro	Asn	Gly	Asp	Gly	Ile	Gln	Ala	Ile	Gly	Arg
			85					90						95	
Ser	Ser	His	Lys	Met	Ile	Asp	Ala	Val	Met	Gln	Ser	Ala	Ala	Arg	Gly
			100					105					110		
Lys	Val	Gln	Thr	Ile	Arg	Gln	Gly	Tyr	Leu	Ser	Lys	Arg	Ser	Ser	Asn
		115					120					125			
Leu	Arg	Gly	Asp	Trp	Lys	Arg	Arg	Phe	Phe	Val	Leu	Asp	Ser	Arg	Gly
		130					135				140				
Met	Leu	Tyr	Tyr	Tyr	Arg	Lys	Gln	Cys	Ser	Lys	Pro	Ser	Gly	Ser	Gly
145					150					155					160
Ser	Gln	Leu	Ser	Gly	Gln	Arg	Asn	Ser	Ser	Glu	Leu	Gly	Ser	Gly	Leu
				165					170					175	
Leu	Ser	Arg	Trp	Leu	Ser	Ser	Asn	Asn	His	Gly	His	Gly	Gly	Val	His

00669900 101300

Asp	Glu	Lys	Ser	Val	Ala	Arg	His	Thr	Val	Asn	Leu	Leu	Thr	Ser	Thr
		180						185							190
		195					200					205			
Ile	Lys	Val	Asp	Ala	Asp	Gln	Ser	Asp	Leu	Arg	Phe	Cys	Phe	Arg	Ile
		210				215					220				
Ile	Ser	Pro	Thr	Lys	Asn	Tyr	Thr	Leu	Gln	Ala	Glu	Ser	Ala	Leu	Asp
225					230					235				240	
Gln	Met	Asp	Trp	Ile	Glu	Lys	Ile	Thr	Gly	Val	Ile	Ala	Ser	Leu	Leu
			245						250					255	
Ser	Ser	Gln	Val	Pro	Glu	Gln	Ala	His	Ile	Lys	Tyr	Gln	Cys	Asn	Phe
		260						265					270		
Gly	Asp	Cys	Pro	Ser	Ala	Thr	Phe	Gln	Arg	Leu	Pro	Gly	Ser	Pro	Met
		275					280					285			
Gly	Ser	Gly	His	His	Arg	Ser	Ala	Ser	Glu	Ser	Ser	Ser	Tyr	Glu	Ser
		290				295					300				
Ser	Glu	Tyr	Asp												
305															

(2) INFORMATION FOR SEQ ID NO:1112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..277
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

Met	Asp	Ala	His	Leu	Arg	Tyr	Phe	Lys	Gln	Val	Leu	Thr	Tyr	Ala	Gln
1			5					10						15	
Gln	Ser	Arg	Glu	Arg	Ser	Asn	Tyr	Glu	Gln	Ala	Ala	Leu	Asn	Glu	Lys
		20						25					30		
Met	Gln	Glu	Tyr	Lys	Arg	Gln	Val	Asp	Arg	Glu	Ser	Arg	Trp	Gly	Ser
		35				40						45			
Asn	Gly	Ser	Asn	Gly	Ser	Pro	Asn	Gly	Asp	Gly	Ile	Gln	Ala	Ile	Gly
	50				55					60					
Arg	Ser	Ser	His	Lys	Met	Ile	Asp	Ala	Val	Met	Gln	Ser	Ala	Ala	Arg
65				70				75					80		
Gly	Lys	Val	Gln	Thr	Ile	Arg	Gln	Gly	Tyr	Leu	Ser	Lys	Arg	Ser	Ser
			85					90					95		
Asn	Leu	Arg	Gly	Asp	Trp	Lys	Arg	Arg	Phe	Phe	Val	Leu	Asp	Ser	Arg
		100						105					110		
Gly	Met	Leu	Tyr	Tyr	Tyr	Arg	Lys	Gln	Cys	Ser	Lys	Pro	Ser	Gly	Ser
		115				120						125			
Gly	Ser	Gln	Leu	Ser	Gly	Gln	Arg	Asn	Ser	Ser	Glu	Leu	Gly	Ser	Gly
	130				135						140				
Leu	Leu	Ser	Arg	Trp	Leu	Ser	Ser	Asn	Asn	His	Gly	His	Gly	Gly	Val
145				150						155				160	
His	Asp	Glu	Lys	Ser	Val	Ala	Arg	His	Thr	Val	Asn	Leu	Leu	Thr	Ser
			165						170					175	
Thr	Ile	Lys	Val	Asp	Ala	Asp	Gln	Ser	Asp	Leu	Arg	Phe	Cys	Phe	Arg
		180					185						190		
Ile	Ile	Ser	Pro	Thr	Lys	Asn	Tyr	Thr	Leu	Gln	Ala	Glu	Ser	Ala	Leu
		195				200						205			
Asp	Gln	Met	Asp	Trp	Ile	Glu	Lys	Ile	Thr	Gly	Val	Ile	Ala	Ser	Leu
	210				215						220				
Leu	Ser	Ser	Gln	Val	Pro	Glu	Gln	Ala	His	Ile	Lys	Tyr	Gln	Cys	Asn
225				230						235				240	
Phe	Gly	Asp	Cys	Pro	Ser	Ala	Thr	Phe	Gln	Arg	Leu	Pro	Gly	Ser	Pro
			245						250					255	

00669980-1030

Met Gly Ser Gly His His Arg Ser Ala Ser Glu Ser Ser Ser Tyr Glu
260 265 270
Ser Ser Glu Tyr Asp
275

(2) INFORMATION FOR SEQ ID NO:1113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1044 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1044
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

aagtttttat	ctttgaggaa	aggtacaaaa	antgacgttg	ctgctgcttt	agaacaggaa	60
cttcacactt	cgaggtctat	gtttgagcaa	gctcggttca	acottgtgac	tgctctatca	120
aatgttgaag	ctaagaaaag	gtttgaattt	ttggaagcag	tcagtggaac	aatggatgca	180
catcttcggt	acttcaaaca	gggttacgaa	ttactgcatc	agatggaacc	atatatcaat	240
caggtcttga	catatgcgca	acaatccaga	gaaagatcaa	attatgaaca	agcagcactt	300
aatgaaaaga	tgcaggagta	caaaagacag	gttgatcgag	agagcaggtg	gggttcaaat	360
ggttctaata	gatcaccaaa	tggagatggc	atacaagcaa	tcggtagaag	ctctcacaaa	420
atgatagacg	ccgtaatgca	atctgctgca	agaggaaagg	tgcaaacaat	aaggcaaggt	480
tatctctcta	aacgatcttc	aaacctgaga	ggagactgga	aaagaagggt	ttttgttctt	540
gacagccggg	gaatgctcta	ttattaccga	aaacagtgtg	gcaaaccatc	tgggtctgga	600
agccagcttt	ctggacagag	aaatagctcc	gagcttgggg	ctggactgct	tagtaggttg	660
ctttcttcga	ataatcatgg	acatggtggt	gtccatgatg	agaagtctgt	agctcgtcat	720
acagtgaact	tactcacctc	aacaattaaa	gtcgacgctg	atcaatcaga	tctgagggtt	780
tgcttttagga	tcatatcacc	tacaaaaaac	tacacgttgc	aggctgagag	tgcactcgat	840
caaatggatt	ggatagaaaa	gatcactggg	gttattgcat	cactacttag	ttctcagggtc	900
cctgaacagg	ctcatattaa	ataccaatgc	aactttgggtg	attgtccatc	ggctacattt	960
cagcgtcttc	ctggtagtcc	catgggaagt	ggccaccatc	gatctgctag	tgaaagtagc	1020
tcatatgaaa	gttctgaata	tgat				

(2) INFORMATION FOR SEQ ID NO:1114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..348
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

Lys	Phe	Leu	Ser	Leu	Arg	Lys	Gly	Thr	Lys	Xaa	Asp	Val	Ala	Ala	Ala
1				5					10					15	
Leu	Glu	Gln	Glu	Leu	His	Thr	Ser	Arg	Ser	Met	Phe	Glu	Gln	Ala	Arg
				20				25					30		
Phe	Asn	Leu	Val	Thr	Ala	Leu	Ser	Asn	Val	Glu	Ala	Lys	Lys	Arg	Phe
		35					40					45			
Glu	Phe	Leu	Glu	Ala	Val	Ser	Gly	Thr	Met	Asp	Ala	His	Leu	Arg	Tyr
		50				55				60					
Phe	Lys	Gln	Gly	Tyr	Glu	Leu	Leu	His	Gln	Met	Glu	Pro	Tyr	Ile	Asn
65					70				75					80	
Gln	Val	Leu	Thr	Tyr	Ala	Gln	Gln	Ser	Arg	Glu	Arg	Ser	Asn	Tyr	Glu
				85				90					95		
Gln	Ala	Ala	Leu	Asn	Glu	Lys	Met	Gln	Glu	Tyr	Lys	Arg	Gln	Val	Asp
			100				105						110		
Arg	Glu	Ser	Arg	Trp	Gly	Ser	Asn	Gly	Ser	Asn	Gly	Ser	Pro	Asn	Gly

SEQUENCE DESCRIPTION: SEQ ID NO: 1																
Met	Phe	Glu	Gln	Ala	Arg	Phe	Asn	Leu	Val	Thr	Ala	Leu	Ser	Asn	Val	
1				5					10					15		
Glu	Ala	Lys	Lys	Arg	Phe	Glu	Phe	Leu	Glu	Ala	Val	Ser	Gly	Thr	Met	
			20					25					30			
Asp	Ala	His	Leu	Arg	Tyr	Phe	Lys	Gln	Gly	Tyr	Glu	Leu	Leu	His	Gln	
		35					40					45				
Met	Glu	Pro	Tyr	Ile	Asn	Gln	Val	Leu	Thr	Tyr	Ala	Gln	Gln	Ser	Arg	
	50				55						60					
Glu	Arg	Ser	Asn	Tyr	Glu	Gln	Ala	Ala	Leu	Asn	Glu	Lys	Met	Gln	Glu	
65				70						75					80	
Tyr	Lys	Arg	Gln	Val	Asp	Arg	Glu	Ser	Arg	Trp	Gly	Ser	Asn	Gly	Ser	
			85						90					95		
Asn	Gly	Ser	Pro	Asn	Gly	Asp	Gly	Ile	Gln	Ala	Ile	Gly	Arg	Ser	Ser	
			100					105					110			
His	Lys	Met	Ile	Asp	Ala	Val	Met	Gln	Ser	Ala	Ala	Arg	Gly	Lys	Val	
		115					120					125				
Gln	Thr	Ile	Arg	Gln	Gly	Tyr	Leu	Ser	Lys	Arg	Ser	Ser	Asn	Leu	Arg	
	130					135					140					
Gly	Asp	Trp	Lys	Arg	Arg	Phe	Phe	Val	Leu	Asp	Ser	Arg	Gly	Met	Leu	
145				150						155					160	

210 215 220
Met Asp Trp Ile Glu Lys Ile Thr Gly Val Ile Ala Ser Leu Leu Ser
225 230 235 240
Ser Gln Val Pro Glu Gln Ala His Ile Lys Tyr Gln Cys Asn Phe Gly
245 250 255
Asp Cys Pro Ser Ala Thr Phe Gln Arg Leu Pro Gly Ser Pro Met Gly
260 265 270
Ser Gly His His Arg Ser Ala Ser Glu Ser Ser Ser Tyr Glu Ser Ser
275 280 285
Glu Tyr Asp
290

(2) INFORMATION FOR SEQ ID NO:1117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..412
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

tttggctatg cgttatccta ggagacttgt gttggctggt tgtttatcgg ctctgattgt 60
tatgactatc ctctctgcta ctcttggatg ggctgctcct aatctgatct ctcgcaaagt 120
gactcatcac ataacaacat tgttgttctt tggttttggg ctatggtctt tgtgggacgg 180
tttcaaagaa ggaggagggg gttcggaaga attggctgaa gtcgaagcag aactgagaga 240
agatgaaaac aaaaagcaga atagggcgtt cctcacgcaa tttttctctc caatttttct 300
caaggctttt tcgattaatt tctttggaga atggggtgac aagagtcagc ttgctacaat 360
tggttttagct gcagatgaaa atccatttgg ggtggtcctt ggtggagttg tg

(2) INFORMATION FOR SEQ ID NO:1118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..137
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

Leu Ala Met Arg Tyr Pro Arg Arg Leu Val Leu Ala Gly Cys Leu Ser
1 5 10 15
Ala Leu Ile Val Met Thr Ile Leu Ser Ala Thr Leu Gly Trp Ala Ala
20 25 30
Pro Asn Leu Ile Ser Arg Lys Trp Thr His His Ile Thr Thr Leu Leu
35 40 45
Phe Phe Gly Phe Gly Leu Trp Ser Leu Trp Asp Gly Phe Lys Glu Gly
50 55 60
Gly Gly Gly Ser Glu Glu Leu Ala Glu Val Glu Ala Glu Leu Arg Glu
65 70 75 80
Asp Glu Asn Lys Lys Gln Asn Arg Ala Phe Leu Thr Gln Phe Phe Ser
85 90 95
Pro Ile Phe Leu Lys Ala Phe Ser Ile Asn Phe Phe Gly Glu Trp Gly
100 105 110
Asp Lys Ser Gln Leu Ala Thr Ile Gly Leu Ala Ala Asp Glu Asn Pro
115 120 125
Phe Gly Val Val Leu Gly Gly Val Val
130 135

(2) INFORMATION FOR SEQ ID NO:1119:

0968980-10130

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2361 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..2361
(D) OTHER INFORMATION: / Ceres Seq. ID 1596933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

atgagctaca aaaatacaaaa taactctcac ttgattctct tcaagctggt acttcttctg 60
atccttttatt ctgcagatct cacagcttca agctcatgtc gaagtgaatg tggaggatgc 120
aaatgtggag gaattgcgat cccataccct tttggaatcg gtaagggctg ctatctcgag 180
aagtcatacg aaatcgaatg tcttaatact tcaggaaagc ttgtccctt tctttctgta 240
attagcaaaag aagttgttag tatccatctt cctggtaggc aatcctttgg gtcagttcgt 300
gtcagaagtc cgataacatc cgcaggatgt tctagtgatg gaaaagactc cgcaccagta 360
atgaacttga cggatagtc tttttctgtt agtgacataa acaaccttgt gggagttggt 420
tgcagcagca aggtgtcgtt ggagcatata aagcaaaaaca tgggtgggatg tgagttgaac 480
tgcagtagca ctaacgcgtc ggatagcaac agcatccctt tcttcgacaa aacgggggtgc 540
tctttttctt atacttttgc ccaggtttgt acaggaaaca aaccggaaga tatgggatgc 600
gatggtaggg gatgttgcga agcgagtcta cctagagagc ctcaacaagt tattgggtatc 660
agaatagaga gcaatgatgg aaagtcaaca acaagtggag actgtagagt cgccttctta 720
actgatgaat tcttcagttt gtcgaagctg accaaaccag aacagttaca tgctaagaga 780
tatgtctacat taagtctagg atggataatg cagacgagga atacttctt cgtcaactcc 840
ttggcctgca aaatcagaaa agacacggac actgcttact ctaatgacca gagtataaag 900
tgtatatgcg actacaccat gagcatcatt tctgatatta ggtatgccaa ttgtgaatgc 960
aacctagggt acaaaggtaa cccatatgat tcggacggat gtagagatat tgatgaatgt 1020
aaagagaatc ccaaattattg taaagaaaca gacacttgtg tgaatttcga gggaggctat 1080
cgctgtgtgg gcgataagac taaagcaata atgatagggt cgggtactgg ttttggggtc 1140
ttagtcttag ttggtggagt atggtggtt agaaagtctc tagtgaagag aaggatggca 1200
aagaggaaga agaagttctt caaacgtaat ggaggactac tgttgcaaca agaattgaat 1260
acaagacaag gcgttgtcga aaaagcaaga atcttcacct cgaaagagct agagaaagcc 1320
actgaaaact tcagcgaaaa cagagttctt ggacatggtg gtcaaggtag tgtgtacaaa 1380
ggtatgcttg tagatggtag aaccgttgca gtcaagaaat caaaagttat agatgaagac 1440
aaacttcaag agttcatcaa tgaggtcgtg attctctccc agataaaacca tagacatgta 1500
gtcaaaactct tgggatggtt tcttgagaca gaagttccta ttctggttta cgagtttatc 1560
atcaacggaa acctctttta gcatatccac gaagaagaag attgcaggag ctctttctta tcttcattct 1620
tggggaatgc gtctacgcat tgctgtggat attgcaggag ctctttctta tcttcattct 1680
gctgcatctt ctccaattta tcatagagac atcaagtcaa caaatatatt actagacgaa 1740
aagtaccgag ccaagggtggc tgatttttga acatcaaggt cagtaacct agatcaaact 1800
cattggacaa cggttatctt aggtacggtt gggtagtggt atccagagta ttaccggtcc 1860
agccaatata ctgaaaagag tgatgtttat agctttggag tcattctagc ggaacttatc 1920
actggagata agcctgtcat aatggtacaa aacactcaag agataatagc cttggcagag 1980
catttcagag ttgccatgaa agagagaaga ctttctgaca tcatggatgc tagaataaga 2040
gatgatagca aaccggaaca agtgatggca gtagcaaatc tggcaatgaa gtggttgagt 2100
tctagaggaa ggaatcgctc gaatatgaga gaagttttta cagagtttga aaggatttgc 2160
acgtctccgg aagattcaca ggtgcagaac cggattgacg aagaagaaga agaagatgga 2220
gtagaagaag aagaagaagt tgtgacaata gtacacagag gagattcttg gagcattggt 2280
gttactgctc cagcctcaag tattgtcgtc tcacctccat cttcagatgt tgaaccattg 2340
aatcctcttc tcacatggtg a

(2) INFORMATION FOR SEQ ID NO:1122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..786
(D) OTHER INFORMATION: / Ceres Seq. ID 1596934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

Met Ser Tyr Lys Asn Thr Asn Asn Ser His Leu Ile Leu Phe Lys Leu

09659500-0100

1													5					10					15
Leu	Leu	Leu	Leu	Ile	Leu	Tyr	Ser	Ala	Asp	Leu	Thr	Ala	Ser	Ser	Ser								
			20				25				30												
Cys	Arg	Ser	Glu	Cys	Gly	Gly	Cys	Lys	Cys	Gly	Gly	Ile	Ala	Ile	Pro								
		35				40				45													
Tyr	Pro	Phe	Gly	Ile	Gly	Lys	Gly	Cys	Tyr	Leu	Glu	Lys	Ser	Tyr	Glu								
		50				55				60													
Ile	Glu	Cys	Leu	Asn	Thr	Ser	Gly	Lys	Leu	Val	Pro	Phe	Leu	Ser	Val								
65				70				75				80											
Ile	Ser	Lys	Glu	Val	Ser	Ile	His	Leu	Pro	Gly	Arg	Gln	Ser	Phe									
			85				90				95												
Gly	Ser	Val	Arg	Val	Arg	Ser	Pro	Ile	Thr	Ser	Ala	Gly	Cys	Ser	Ser								
			100				105				110												
Asp	Gly	Lys	Asp	Ser	Ala	Pro	Val	Met	Asn	Leu	Thr	Asp	Ser	Pro	Phe								
		115				120				125													
Phe	Val	Ser	Asp	Ile	Asn	Asn	Leu	Val	Gly	Val	Gly	Cys	Ser	Ser	Lys								
		130				135				140													
Val	Ser	Leu	Glu	His	Ile	Lys	Gln	Asn	Met	Val	Gly	Cys	Glu	Leu	Asn								
145				150				155				160											
Cys	Ser	Thr	Thr	Asn	Ala	Ser	Asp	Ser	Asn	Ser	Ile	Pro	Phe	Phe	Asp								
			165				170				175												
Lys	Thr	Gly	Cys	Ser	Phe	Ser	Tyr	Thr	Phe	Ala	Gln	Val	Cys	Thr	Gly								
			180				185				190												
Asn	Lys	Pro	Glu	Asp	Met	Gly	Cys	Asp	Gly	Arg	Gly	Cys	Cys	Gln	Ala								
		195				200				205													
Ser	Leu	Pro	Arg	Glu	Pro	Gln	Gln	Val	Ile	Gly	Ile	Arg	Ile	Glu	Ser								
		210				215				220													
Asn	Asp	Gly	Lys	Ser	Thr	Thr	Ser	Gly	Asp	Cys	Arg	Val	Ala	Phe	Leu								
225				230				235				240											
Thr	Asp	Glu	Phe	Phe	Ser	Leu	Ser	Lys	Leu	Thr	Lys	Pro	Glu	Gln	Leu								
			245				250				255												
His	Ala	Lys	Arg	Tyr	Ala	Thr	Leu	Ser	Leu	Gly	Trp	Ile	Met	Gln	Thr								
			260				265				270												
Arg	Asn	Thr	Ser	Phe	Val	Asn	Ser	Leu	Ala	Cys	Lys	Ile	Arg	Lys	Asp								
		275				280				285													
Thr	Asp	Thr	Ala	Tyr	Ser	Asn	Asp	Gln	Ser	Ile	Lys	Cys	Ile	Cys	Asp								
		290				295				300													
Tyr	Thr	Met	Ser	Ile	Ile	Ser	Asp	Ile	Arg	Tyr	Ala	Asn	Cys	Glu	Cys								
305				310				315				320											
Asn	Leu	Gly	Tyr	Lys	Gly	Asn	Pro	Tyr	Asp	Ser	Asp	Gly	Cys	Arg	Asp								
			325				330				335												
Ile	Asp	Glu	Cys	Lys	Glu	Asn	Pro	Lys	Tyr	Cys	Lys	Glu	Thr	Asp	Thr								
			340				345				350												
Cys	Val	Asn	Phe	Glu	Gly	Gly	Tyr	Arg	Cys	Val	Gly	Asp	Lys	Thr	Lys								
		355				360				365													
Ala	Ile	Met	Ile	Gly	Ala	Gly	Thr	Gly	Phe	Gly	Val	Leu	Val	Leu	Val								
		370				375				380													
Gly	Gly	Val	Trp	Trp	Leu	Arg	Lys	Phe	Leu	Val	Lys	Arg	Arg	Met	Ala								
385				390				395				400											
Lys	Arg	Lys	Lys	Lys	Phe	Phe	Lys	Arg	Asn	Gly	Gly	Leu	Leu	Leu	Gln								
			405				410				415												
Gln	Glu	Leu	Asn																				

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 666 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..666

(D) OTHER INFORMATION: / Ceres Seq. ID 1596936

Asn Leu Thr Asp Ser Pro Phe Phe Val Ser As

(x1) SEQUENCE DESCRIPTION: SEQ INFORMATION															
Met	Asn	Leu	Thr	Asp	Ser	Pro	Phe	Phe	Val	Ser	Asp	Ile	Asn	Asn	Leu
1				5					10					15	
Val	Gly	Val	Gly	Cys	Ser	Ser	Lys	Val	Ser	Leu	Glu	His	Ile	Lys	Gln
			20					25					30		
Asn	Met	Val	Gly	Cys	Glu	Leu	Asn	Cys	Ser	Thr	Thr	Asn	Ala	Ser	Asp
		35					40					45			
Ser	Asn	Ser	Ile	Pro	Phe	Phe	Asp	Lys	Thr	Gly	Cys	Ser	Phe	Ser	Tyr
	50					55					60				
Thr	Phe	Ala	Gln	Val	Cys	Thr	Gly	Asn	Lys	Pro	Glu	Asp	Met	Gly	Cys
65					70				75					80	
Asp	Gly	Arg	Gly	Cys	Cys	Gln	Ala	Ser	Leu	Pro	Arg	Glu	Pro	Gln	Gln

													85			90				95		
Val	Ile	Gly	Ile	Arg	Ile	Glu	Ser	Asn	Asp	Gly	Lys	Ser	Thr	Thr	Ser							
			100					105					110									
Gly	Asp	Cys	Arg	Val	Ala	Phe	Leu	Thr	Asp	Glu	Phe	Phe	Ser	Leu	Ser							
			115					120					125									
Lys	Leu	Thr	Lys	Pro	Glu	Gln	Leu	His	Ala	Lys	Arg	Tyr	Ala	Thr	Leu							
			130					135					140									
Ser	Leu	Gly	Trp	Ile	Met	Gln	Thr	Arg	Asn	Thr	Ser	Phe	Val	Asn	Ser							
145								150					155									
Leu	Ala	Cys	Lys	Ile	Arg	Lys	Asp	Thr	Asp	Thr	Ala	Tyr	Ser	Asn	Asp							
							165					170										
Gln	Ser	Ile	Lys	Cys	Ile	Cys	Asp	Tyr	Thr	Met	Ser	Ile	Ile	Ser	Asp							
							180					185										
Ile	Arg	Tyr	Ala	Asn	Cys	Glu	Cys	Asn	Leu	Gly	Tyr	Lys	Gly	Asn	Pro							
							195					200										
Tyr	Asp	Ser	Asp	Gly	Cys	Arg	Asp	Ile	Asp	Glu	Cys	Lys	Glu	Asn	Pro							
							210					215										
Lys	Tyr	Cys	Lys	Glu	Thr	Asp	Thr	Cys	Val	Asn	Phe	Glu	Gly	Gly	Tyr							
225								230					235									
Arg	Cys	Val	Gly	Asp	Lys	Thr	Lys	Ala	Ile	Met	Ile	Gly	Ala	Gly	Thr							
							245					250										
Gly	Phe	Gly	Val	Leu	Val	Leu	Val	Gly	Gly	Val	Trp	Trp	Leu	Arg	Lys							
							260					265										
Phe	Leu	Val	Lys	Arg	Arg	Met	Ala	Lys	Arg	Lys	Lys	Lys	Phe	Phe	Lys							
							275					280										
Arg	Asn	Gly	Gly	Leu	Leu	Leu	Gln	Gln	Glu	Leu	Asn	Thr	Arg	Gln	Gly							
							290					295										
Val	Val	Glu	Lys	Ala	Arg	Ile	Phe	Thr	Ser	Lys	Glu	Leu	Glu	Lys	Ala							
305								310					315									
Thr	Glu	Asn	Phe	Ser	Glu	Asn	Arg	Val	Leu	Gly	His	Gly	Gly	Gln	Gly							
							325					330										
Thr	Val	Tyr	Lys	Gly	Met	Leu	Val	Asp	Gly	Arg	Thr	Val	Ala	Val	Lys							
							340					345										
Lys	Ser	Lys	Val	Ile	Asp	Glu	Asp	Lys	Leu	Gln	Glu	Phe	Ile	Asn	Glu							
							355					360										
Val	Val	Ile	Leu	Ser	Gln	Ile	Asn	His	Arg	His	Val	Val	Lys	Leu	Leu							
							370					375										
Gly	Cys	Cys	Leu	Glu	Thr	Glu	Val	Pro	Ile	Leu	Val	Tyr	Glu	Phe	Ile							
385								390					395									
Ile	Asn	Gly	Asn	Leu	Phe	Lys	His	Ile	His	Glu	Glu	Glu	Ala	Asp	Asp							
							405					410										
Tyr	Thr	Met	Ile	Trp	Gly	Met	Arg	Leu	Arg	Ile	Ala	Val	Asp	Ile	Ala							
							420					425										
Gly	Ala	Leu	Ser	Tyr	Leu	His	Ser	Ala	Ala	Ser	Ser	Pro	Ile	Tyr	His							
							435					440										
Arg	Asp	Ile	Lys	Ser	Thr	Asn	Ile	Leu	Leu	Asp	Glu	Lys	Tyr	Arg	Ala							
							450					455										
Lys	Val	Ala	Asp	Phe	Gly	Thr	Ser	Arg	Ser	Val	Thr	Ile	Asp	Gln	Thr							
465								470					475									
His	Trp	Thr	Thr	Val	Ile	Ser	Gly	Thr	Val	Gly	Tyr	Val	Asp	Pro	Glu							
							485					490										
Tyr	Tyr	Arg	Ser	Ser	Gln	Tyr	Thr	Glu	Lys	Ser	Asp	Val	Tyr	S								

Val Thr Gly Lys Tyr Lys Ile Val Arg Met Cys Phe His Asp Cys Tyr
50 55 60
Glu Phe Gly Ile Leu Asp Ile Glu Ser Gly Glu Trp Ser Lys Leu Met
65 70 75 80
Ser Pro Pro His Ile Met Arg Val Gly Ser Lys Ser Val Cys Val Asn
85 90 95
Gly Ser Ile Tyr Trp Leu Gln Ile Ser Val Ser Tyr Ile Ile Leu Ala
100 105 110
Leu Asp Leu His Gln Glu Thr Phe Asn Gly Val Tyr His Leu Pro Ala
115 120 125
Thr Trp Val Thr Gln Asp Thr Gln Leu Val Asn Leu Glu Asp Arg Leu
130 135 140
Ala Met Ala Met Thr Thr Lys Val Gly Pro Glu Trp Ile Leu Glu Ile
145 150 155 160
Trp Ser Met Asp Ile Glu Glu Lys Gly Trp Ser Lys Arg Tyr Thr Trp
165 170 175
Ser Lys Ala Tyr Ser Ile Ser Leu Ala His Arg Val Val Val Ser Trp
180 185 190
Pro Trp Gln Lys Arg Trp Phe Thr Pro Val Ser Val Ser Lys Gln Gly
195 200 205
Asn Leu Val Phe Tyr Asp Asn His Lys Arg Leu Phe Lys Tyr Tyr Ser
210 215 220
Gly Thr Asp Glu Ile Arg Cys Leu Ser Ser Asn Ile Asn Val Ile Ser
225 230 235 240
Ser Tyr Val Glu Asn Leu Ala Pro Leu Pro Leu Lys Pro Ser His Thr
245 250 255
His His Asp Leu Gly Asn Ser Asn Ser Lys Phe Ser Thr Ser Arg Cys
260 265 270
His Leu Phe Pro Thr Arg Ala Asn Phe
275 280

(2) INFORMATION FOR SEQ ID NO:1127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1116
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

atgtttaaga atgctcaaga atttatctcg aaatgtgact catgtcagag aagaggggaac	60
atcagcagaa ggaatgagat gcctaagaat ctgatcttag aagttgagat ctttgacgtt	120
tggggaatcg attttatggg tccgtttcct ttttcttacg ggaacgatta catactggtc	180
gcagtagact atgtatcaaa atgggtggaa gccatagcca gccccaccaa tgatgttaga	240
gttgtgctaa agctgttcaa gacaattatt ttccctagat ttggagtctc gagagttaag	300
catggagtaa agcacaaggt agccactcct tatcatccac agacgagcgg gcagggtggaa	360
atctccaaca gggagataaa agtaattcta gagaaaacag tggggattac gaggaaagat	420
tgggtctgcga agctctatga cgcactatgg gcttacagaa caactttcaa gactcctatt	480
ggcacgactc ctttcaacct tctctatgga aagtcctgtc acttacctgt ggaactcaag	540
tataaagcca tgtgggcagt taaactcctg aacttcgaca ttaaaaccgc cgaagagaag	600
cggttgatcc aactgaacga tctcaacgag attcgcttag aagcttatga gagttccaaa	660
atctacaagg agcgaaccaa gtctttccat gacaagaaga tagtctcaag agattttaag	720
tatgaagagc tgagggaat agattctggt tttgagggaa caacaataca ctcgaccaca	780
gagcaatcaa actcaacatt gttctggctt cttcacccca ggaaatcact cgaccacacc	840
ctacagggac cgaatgacga tgtggtcgag tatagcgaac gatgcagtca taacttctcc	900
atgtcagtaa ttactcgac cgcggtgctg gtcgcagcag aagaagagag gtcgagtatc	960
atcagagcgg tgctggccgc gacgaaggag cagaggtcga gtacccccag ggggaagctg	1020
agacacaaca gggagattct tcgatggcct gggagcaatc acaggcggct attgacgacc	1080
aatccgctg cttcttccac tgagtggact gtgtga	

00609900 "1013100

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2554

(D) OTHER INFORMATION: / Ceres Seq. ID 1596976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

atggagacat	cttggagatt	tctcagaagt	gtttgcttac	tttcatttgt	ccttgggtcg	60
ttttctgttt	accaaaccct	ttgtcttgtt	gacgctcaag	aagacgccat	tgtaacactg	120
caagtagatg	cttctaactg	gacacggcga	ccgattcccg	aaactctatt	tgggatcttc	180
tttgaggaaa	taaatactgc	tggagcaggt	ggactatggg	ctgaacttgt	tagcaataga	240
ggatttgaag	ctgggtggaca	aatcattcct	tccaatatct	ggccttggtc	cattattgga	300
gatgaatcat	ccatttatgt	tgttacagac	cgttcttcgt	gttttgagcg	taacaagatt	360
gctcttagaa	tggaagtcct	ttgtgacagc	aattcttgtc	caacaggagg	cgtcgggggt	420
tataaccggg	gttactgggg	catgaacatt	gaaaaaggga	agaaatacaa	agtgggtgtc	480
tatgtgcgtt	cgactggcga	catcgatgtt	tctgtgtcgt	ttacaagttc	gaatggatca	540
tgcactcttg	cgtcagaaaa	tactatagct	ttggcttctg	atgtttccag	ttggacaaaa	600
atggaaatgc	ttttagaagc	aaatggaaca	gataatgggt	caagacttca	atttacaact	660
acaaaaaaag	gttcaatttg	gtttgaccaa	gtctcagcca	tacctatgga	tacttacaag	720
ggacatgggt	tcagaaatga	ccttttccaa	atgatggtcg	atctaaaacc	gcggtttatc	780
cgattcccg	gcaatgcatt	ccgctggaaa	gaaaccgtgg	gagcttggga	agagagacct	840
ggccattatg	gtgatgtttg	gaagtactgg	actgatgatg	cccttggcca	ctttgaattc	900
tttcaacttg	cagaagacct	tggtgcatcc	ccaatatggg	tgtttaacaa	tgggataagt	960
cacaatgatc	aagttgaaac	aaaaaatgtc	atgccttttg	ttcaagaagc	gattgacggt	1020
atagagtttg	ctcgtggaga	ttctaattct	acatggggat	cggttcgcgc	tgcaatggga	1080
catccagagc	cttttgaact	aaaatatgtt	gcggttggga	atgaagattg	ttttaaaagt	1140
ttctacagag	gaaactatct	tgaattctac	gatgctatca	aaaaagctta	tccagacatt	1200
aaaatcactc	ccaactgcga	tgcactgtct	aaaccgctcg	atcaccctgc	tgattacttt	1260
gattaccaca	tttactactc	tgcaagagac	ttgttttcca	agtcccatga	ttttgacaat	1320
acaccgcgca	acggaccaaa	ggcttttgtt	agcgaatacg	ctgtaagcaa	aacggatgct	1380
aaaaatggaa	accttttggc	cgctctcggg	gaagcagctt	tcctccttgg	tttggaagg	1440
aacagtggca	ttgtaggaat	ggtagctat	gcacctctct	ttgtcaacac	aaacgataga	1500
aggtggatcc	cggatgcaat	agtttttaac	tcgtctcatc	tatatggaac	tcctagctat	1560
tgggtccaac	agttcttcac	cgagtcaagc	ggagcaactc	ttctcaattc	tacacttaat	1620
ggagacactt	cttctgttga	agcatctgcc	atctctttcc	aaaccaatgg	caaagattac	1680
atacagatca	aggctgtaaa	ctttgggaaa	caatcagtaa	atctaaaggt	agcagtgaac	1740
ggactgatcg	caaaatttta	tggatcgaag	aagaaaaatac	ttacatctgc	caatgtgatg	1800
gatgagaact	ctttttcaaa	cccaaagatg	attgtgccac	aagaaagtgt	gctggagatg	1860
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ttgaaagaat	ctgaaaatgt	cctcaagatg	ccaaaatctg	attcatacaa	gaaaacttca	1980
acaatgagca	agatggctcc	cttgatcgcc	ttattcactg	gcctttgcgg	cttcaagaaa	2040
aacgctcggc	cattgggaac	gatcgagaca	atgaatcagt	catctccacg	ggagacaaaa	2100
gaaagagAAC	aaacaaggaa	tgacttccag	aacaaggaaa	ctgatgactt	gtggaacaag	2160
gaaagcgatg	atcgagatac	taatgcattt	aatgacgata	gtagtgaagc	ggactctgag	2220
cttccggttg	ctccaggaag	aaaaggaaca	atacgtggaa	catattcgtg	taacaacatg	2280
gtgttaagaa	gatccttgtc	tactaagaag	aaactgagtg	cgagccctaac	gatccaaata	2340
ccgagatcat	tgtccattgt	cctcaaactg	gacaaggagg	aggataaatc	tgtgaggaag	2400
aagaaactga	acgcaaatga	ttcgattctg	gtacgtccaa	ttatacttgg	agagagatgt	2460
agggttcttg	atgcggaacc	aggagatgaa	gatcanagcc	aaagaatggc	agagaacaga	2520
atatatcgtc	ctagatccat	gagttcgatc	tcga			

(2) INFORMATION FOR SEQ ID NO:1131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 851 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..851

(D) OTHER INFORMATION: / Ceres Seq. ID 1596977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

0969990-101300

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..728

(D) OTHER INFORMATION: / Ceres Seq. ID 1596979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

(X1) SEQUENCE DESCRIPTION: SEQ ID NUMBER: 1

Met	Glu	Val	Leu	Cys	Asp	Ser	Asn	Ser	Cys	Pro	Thr	Gly	Gly	Val	Gly
1				5					10					15	

Val	Tyr	Asn	Pro	Gly	Tyr	Trp	Gly	Met	Asn	Ile	Glu	Lys	Gly	Lys	Lys
			20					25					30		
Tyr	Lys	Val	Val	Phe	Tyr	Val	Arg	Ser	Thr	Gly	Asp	Ile	Asp	Val	Ser
		35					40					45			
Val	Ser	Phe	Thr	Ser	Ser	Asn	Gly	Ser	Ser	Thr	Leu	Ala	Ser	Glu	Asn
	50					55					60				
Thr	Ile	Ala	Leu	Ala	Ser	Asp	Val	Ser	Ser	Trp	Thr	Lys	Met	Glu	Met
65					70					75					80
Leu	Leu	Glu	Ala	Asn	Gly	Thr	Asp	Asn	Gly	Ala	Arg	Leu	Gln	Phe	Thr
				85					90					95	
Thr	Thr	Lys	Lys	Gly	Ser	Ile	Trp	Phe	Asp	Gln	Val	Ser	Ala	Ile	Pro
			100					105					110		
Met	Asp	Thr	Tyr	Lys	Gly	His	Gly	Phe	Arg	Asn	Asp	Leu	Phe	Gln	Met
		115					120					125			
Met	Val	Asp	Leu	Lys	Pro	Arg	Phe	Ile	Arg	Phe	Pro	Gly	Asn	Ala	Phe
	130					135					140				
Arg	Trp	Lys	Glu	Thr	Val	Gly	Ala	Trp	Glu	Glu	Arg	Pro	Gly	His	Tyr
145					150					155					160
Gly	Asp	Val	Trp	Lys	Tyr	Trp	Thr	Asp	Asp	Ala	Leu	Gly	His	Phe	Glu
				165					170					175	
Phe	Phe	Gln	Leu	Ala	Glu	Asp	Leu	Gly	Ala	Ser	Pro	Ile	Trp	Val	Phe
			180					185					190		
Asn	Asn	Gly	Ile	Ser	His	Asn	Asp	Gln	Val	Glu	Thr	Lys	Asn	Val	Met
		195					200					205			
Pro	Phe	Val	Gln	Glu	Ala	Ile	Asp	Gly	Ile	Glu	Phe	Ala	Arg	Gly	Asp
	210					215					220				
Ser	Asn	Ser	Thr	Trp	Gly	Ser	Val	Arg	Ala	Ala	Met	Gly	His	Pro	Glu
225					230					235					240
Pro	Phe	Glu	Leu	Lys	Tyr	Val	Ala	Val	Gly	Asn	Glu	Asp	Cys	Phe	Lys
				245					250					255	
Ser	Phe	Tyr	Arg	Gly	Asn	Tyr	Leu	Glu	Phe	Tyr	Asp	Ala	Ile	Lys	Lys
			260					265					270		
Ala	Tyr	Pro	Asp	Ile	Lys	Ile	Ile	Ser	Asn	Cys	Asp	Ala	Ser	Ser	Lys
		275					280					285			
Pro	Leu	Asp	His	Pro	Ala	Asp	Tyr	Phe	Asp	Tyr	His	Ile	Tyr	Thr	Leu
	290					295					300				
Ala	Arg	Asp	Leu	Phe	Ser	Lys	Ser	His	Asp	Phe	Asp	Asn	Thr	Pro	Arg
305					310					315					320
Asn	Gly	Pro	Lys	Ala	Phe	Val	Ser	Glu	Tyr	Ala	Val	Ser	Lys	Thr	Asp
				325					330					335	
Ala	Lys	Asn	Gly	Asn	Leu	Leu	Ala	Ala	Leu	Gly	Glu	Ala	Ala	Phe	Leu
			340					345					350		
Leu	Gly	Leu	Glu	Lys	Asn	Ser	Gly	Ile	Val	Gly	Met	Val	Ser	Tyr	Ala
		355					360					365			
Pro	Leu	Phe	Val												

500 505 510
Ser Ser Phe Asp Leu Leu Lys Glu Ser Glu Asn Val Leu Lys Met Pro
515 520 525
Lys Ser Asp Ser Tyr Lys Lys Thr Ser Thr Met Ser Lys Met Ala Pro
530 535 540
Leu Ile Ala Leu Phe Thr Gly Leu Cys Gly Phe Lys Lys Asn Ala Arg
545 550 555 560
Pro Leu Gly Thr Ile Glu Thr Met Asn Gln Ser Ser Pro Arg Glu Thr
565 570 575
Lys Glu Arg Glu Gln Thr Arg Asn Asp Phe Gln Asn Lys Glu Thr Asp
580 585 590
Asp Leu Trp Asn Lys Glu Ser Asp Asp Arg Asp Thr Asn Ala Phe Asn
595 600 605
Asp Asp Ser Ser Glu Ala Asp Ser Glu Leu Pro Leu Pro Pro Gly Arg
610 615 620
Lys Gly Thr Ile Arg Gly Thr Tyr Ser Cys Asn Asn Met Val Leu Arg
625 630 635 640
Arg Ser Leu Ser Thr Lys Lys Lys Leu Ser Ala Ser Leu Thr Ile Gln
645 650 655
Ile Pro Arg Ser Leu Ser Met Val Leu Lys Arg Asp Lys Glu Glu Asp
660 665 670
Lys Ser Val Arg Lys Lys Lys Leu Asn Ala Asn Asn Ser Ile Leu Val
675 680 685
Arg Pro Ile Ile Leu Gly Glu Arg Cys Arg Val Leu Asp Ala Glu Pro
690 695 700
Gly Asp Glu Asp Xaa Ser Gln Arg Met Ala Glu Asn Arg Ile Tyr Arg
705 710 715 720
Pro Arg Ser Met Ser Ser Ile Ser
725

(2) INFORMATION FOR SEQ ID NO:1133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..729
- (D) OTHER INFORMATION: / Ceres Seq. ID 1596980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

atgtccggtg	cacaatctag	tgattcggtt	ccagagattt	cacggccgac	tgcaacagaa	60
tgtcaagagg	tgaaatccga	tgaagcactc	actgaacca	accctgattg	ggctctagtt	120
ctcgtcaaa	acccatcgcc	tccactcatc	atcgaggttg	aggatgagac	tctgccttca	180
atcgacagtg	ttcagaacct	taaaccgaag	gatcatgagg	ctgccccctc	gcaaccctct	240
gttgcatctc	gattgcgcaa	gaggaagtca	tctgctgctg	atccacgcat	caaaaggatg	300
aagcagggaa	agggagttac	cggactgatt	cgaacggtta	ttaagttcaa	cccgttcact	360
gagaatctag	tgtttgagtt	ctgggcta	ctgcccacta	tgaaggtaga	cacgtataag	420
gtcagagtct	tggtgcgcaa	tcgggagt	gagctctcac	ctgggaagat	caacgagatg	480
tatggtctcc	cttttgttga	tgctagacag	cagcgaatgg	atatcgctgg	tctgggtgat	540
gaacaagtgg	ctgaatttct	cactgggtgg	aaagtcagtg	ttctgagcaa	gcttcagaca	600
tggtatgcgag	agcaaacgtg	gcaagctaag	gcggatgatg	tgagagacca	aggatggaag	660
ctgacttgcc	gtggtgtcaa	agacaagaat	taccaagaag	atatggaaga	tatcatctcg	720
aagatttag						

(2) INFORMATION FOR SEQ ID NO:1134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

00569980 08569980

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..242

(D) OTHER INFORMATION: / Ceres Seq. ID 1596981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

Met Ser Gly Ala Gln Ser Ser Asp Ser Leu Pro Glu Ile Ser Arg Pro
1 5 10 15
Thr Ala Thr Glu Cys Gln Glu Val Lys Ser Asp Glu Ala Leu Thr Glu
20 25 30
Pro Asn Pro Asp Trp Ala Leu Val Lys Asp Pro Ser Pro Pro
35 40 45
Leu Ile Ile Glu Val Glu Asp Glu Thr Leu Pro Ser Ile Asp Ser Val
50 55 60
Gln Asn Pro Lys Pro Lys Asp His Glu Ala Ala Pro Ser Gln Pro Ser
65 70 75 80
Val Ala Ser Arg Leu Arg Lys Arg Lys Ser Ser Ala Ala Asp Pro Arg
85 90 95
Ile Lys Arg Met Lys Gln Gly Lys Gly Val Thr Gly Leu Ile Arg Thr
100 105 110
Val Ile Lys Phe Asn Pro Phe Thr Glu Asn Leu Val Phe Glu Phe Trp
115 120 125
Ala Asn Leu Pro Thr Met Lys Val Asp Thr Tyr Lys Val Arg Val Leu
130 135 140
Val Arg Asn Arg Glu Tyr Glu Leu Ser Pro Gly Lys Ile Asn Glu Met
145 150 155 160
Tyr Gly Leu Pro Phe Val Asp Ala Arg Gln Gln Arg Met Asp Ile Ala
165 170 175
Gly Leu Val Asp Glu Gln Val Ala Glu Phe Leu Thr Gly Gly Lys Val
180 185 190
Ser Val Leu Ser Lys Leu Gln Thr Trp Met Arg Glu Gln Thr Trp Gln
195 200 205
Ala Lys Ala Asp Asp Val Glu Ser Gln Gly Trp Lys Leu Thr Trp Arg
210 215 220
Gly Val Lys Asp Lys Asn Tyr Gln Glu Asp Met Glu Asp Ile Ile Ser
225 230 235 240
Lys Ile

(2) INFORMATION FOR SEQ ID NO:1135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1596983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

Met Lys Gln Gly Lys Gly Val Thr Gly Leu Ile Arg Thr Val Ile Lys
1 5 10 15
Phe Asn Pro Phe Thr Glu Asn Leu Val Phe Glu Phe Trp Ala Asn Leu
20 25 30
Pro Thr Met Lys Val Asp Thr Tyr Lys Val Arg Val Leu Val Arg Asn
35 40 45
Arg Glu Tyr Glu Leu Ser Pro Gly Lys Ile Asn Glu Met Tyr Gly Leu
50 55 60
Pro Phe Val Asp Ala Arg Gln Gln Arg Met Asp Ile Ala Gly Leu Val
65 70 75 80
Asp Glu Gln Val Ala Glu Phe Leu Thr Gly Gly Lys Val Ser Val Leu
85 90 95

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Ser Lys Leu Gln Thr Trp Met Arg Glu Gln Thr Trp Gln Ala Lys Ala
100 105 110
Asp Asp Val Glu Ser Gln Gly Trp Lys Leu Thr Trp Arg Gly Val Lys
115 120 125
Asp Lys Asn Tyr Gln Glu Asp Met Glu Asp Ile Ile Ser Lys Ile
130 135 140

(2) INFORMATION FOR SEQ ID NO:1136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1107

(D) OTHER INFORMATION: / Ceres Seq. ID 1596991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:

ccgacgaggg agaaacactt ggtccttaat ggcggcaaca gaaaccctac tggagaagtg 60
gtcgctagaa gtgcagccag agattatcaa aacagtagca agaaacgata atccaagaac 120
ctcatcaaag ggcaatggac ggcggaagaa gacaggaagt tgataagggt ggtgaggcaa 180
catggggaga ggaaatgggc aatgatattc gagaaacttg agggaagagc aggcaaacaa 240
tgtcgtgaga gatggcataa tcatctccgt cctgatatta agaaagatgg atggagttaa 300
gaagaagaga gggttcttgt ggaatcacac atgagaatcg ggaacaaatg ggcagagatc 360
gctaaactca taccaggacg gactgagaat tctatcaaga accattggaa tgcgaccaag 420
agacgtcaaa attcaaaacg caaacacaaa cgcgaatcaa acgctgataa caatgataga 480
gatgcctctc catcagctaa aagaccatgc attctccaag actacatcaa aagtatcgag 540
agaaataaca ttaacaagga caatgacgag aagaagaatg agaacaccaa cagtgttatt 600
tctacaccta atcttgatca gatctattct gatggtgatt ccgctgtctc catccttggc 660
ggtccatatg acgaagagct agattacttt caaaatatct ttgcaaacca tccgatttct 720
cttgagaatt taggtttgag ccaaacttcg gatgaggtaa ctcagtcttc atcatctggg 780
ttcatgatca agaaccctaa ccctaacttg cagcacagtg ttggaattca tcatcaagag 840
gcaacgatca cagctccggc gaatacacc cacccttgcgt ctgatattct cttatcttat 900
ttattgaacg gtacgacgct ttcatactcc gacactcatt ttccgtcttc ctcatcttcc 960
acgtcatcca ccaccgtaga gcatggaggc cacaacgagt ttcttgagcc tcaagctaac 1020
tctacaagtg aaagaagaga aatggatctg atagagatgc tctctgggtc tattcaagg 1080
agcaacatct gcttcccgtt ggtctag

(2) INFORMATION FOR SEQ ID NO:1137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..368

(D) OTHER INFORMATION: / Ceres Seq. ID 1596992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:

Pro Thr Arg Glu Lys His Leu Val Leu Asn Gly Gly Asn Arg Asn Pro
1 5 10 15
Thr Gly Glu Val Val Ala Arg Ser Ala Ala Arg Asp Tyr Gln Asn Ser
20 25 30
Thr Lys Lys Arg Ser Ser Lys Asn Leu Ile Lys Gly Gln Trp Thr Ala
35 40 45
Glu Glu Asp Arg Lys Leu Ile Arg Leu Val Arg Gln His Gly Glu Arg
50 55 60
Lys Trp Ala Met Ile Ser Glu Lys Leu Glu Gly Arg Ala Gly Lys Gln
65 70 75 80
Cys Arg Glu Arg Trp His Asn His Leu Arg Pro Asp Ile Lys Lys Asp
85 90 95

09689950-10300

	100		105		110
Glu Arg Asn Asn Ile Asn Lys Asp Asn Asp Glu Lys Lys Asn Glu Asn					
115			120		125
Thr Ile Ser Val Ile Ser Thr Pro Asn Leu Asp Gln Ile Tyr Ser Asp					
130			135		140
Gly Asp Ser Ala Ser Ser Ile Leu Gly Gly Pro Tyr Asp Glu Glu Leu					
145			150		155
Asp Tyr Phe Gln Asn Ile Phe Ala Asn His Pro Ile Ser Leu Glu Asn					
	165		170		175
Leu Gly Leu Ser Gln Thr Ser Asp Glu Val Thr Gln Ser Ser Ser Ser					
	180		185		190
Gly Phe Met Ile Lys Asn Pro Asn Pro Asn Leu His Asp Ser Val Gly					
195			200		205
Ile His His Gln Glu Ala Thr Ile Thr Ala Pro Ala Asn Thr Pro His					
210			215		220
Leu Ala Ser Asp Ile Tyr Leu Ser Tyr Leu Leu Asn Gly Thr Thr Ser					
225			230		235
Ser Tyr Ser Asp Thr His Phe Pro Ser Ser Ser Ser Thr Ser Ser					
	245		250		255
Thr Thr Val Glu His Gly Gly His Asn Glu Phe Leu Glu Pro Gln Ala					
	260		265		270
Asn Ser Thr Ser Glu Arg Arg Glu Met Asp Leu Ile Glu Met Leu Ser					
	275		280		285
Gly Ser Ile Gln Gly Ser Asn Ile Cys Phe Pro Leu Val					
290			295		300

(2) INFORMATION FOR SEQ ID NO:1139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..258

(D) OTHER INFORMATION: / Ceres Seq. ID 1596994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

Met Arg Ile Gly Asn Lys Trp Ala Glu Ile Ala Lys Leu Ile Pro Gly					
1	5		10		15
Arg Thr Glu Asn Ser Ile Lys Asn His Trp Asn Ala Thr Lys Arg Arg					
	20		25		30
Gln Asn Ser Lys Arg Lys His Lys Arg Glu Ser Asn Ala Asp Asn Asn					
	35		40		45
Asp Arg Asp Ala Ser Pro Ser Ala Lys Arg Pro Cys Ile Leu Gln Asp					
	50		55		60
Tyr Ile Lys Ser Ile Glu Arg Asn Asn Ile Asn Lys Asp Asn Asp Glu					
	65		70		75
Lys Lys Asn Glu Asn Thr Ile Ser Val Ile Ser Thr Pro Asn Leu Asp					
	85		90		95
Gln Ile Tyr Ser Asp Gly Asp Ser Ala Ser Ser Ile Leu Gly Gly Pro					
	100		105		110
Tyr Asp Glu Glu Leu Asp Tyr Phe Gln Asn Ile Phe Ala Asn His Pro					
	115		120		125
Ile Ser Leu Glu Asn Leu Gly Leu Ser Gln Thr Ser Asp Glu Val Thr					
	130		135		140
Gln Ser Ser Ser Ser Gly Phe Met Ile Lys Asn Pro Asn Pro Asn Leu					
	145		150		155
His Asp Ser Val Gly Ile His His Gln Glu Ala Thr Ile Thr Ala Pro					
	165		170		175
Ala Asn Thr Pro His Leu Ala Ser Asp Ile Tyr Leu Ser Tyr Leu Leu					
	180		185		190

00669990-10300

65					70					75					80
Gln	Thr	Ser	Asn	Val	Asn	Glu	Ser	Asp	Gly	Glu	Gly	Met	Phe	Leu	Lys
				85					90					95	
Lys	Asp	Asp	Pro	Lys	Val	Thr	Ala	Leu	Met	Gln	Gln	Ala	Glu	Leu	Leu
			100					105					110		
Ser	Ser	Leu	Ala	Gln	Lys	Val	Asn	Ala	Asp	Asn	Thr	Glu	Gln	Ser	Met
		115					120					125			
Glu	Asn	Ala	Trp	Lys	Val	Leu	Gln	Asp	Phe	Leu	Asn	Lys	Gly	Lys	Glu
	130					135					140				
Asn	Asp	Leu	Phe	Arg	Tyr	Gly	Ile	Pro	Asp	Ile	Asp	Phe	Lys	Ile	Glu
145					150					155					160
Glu	Phe	Lys	Asp	Leu	Ile	Glu	Asp	Leu	Arg	Ser	Gly	Tyr	Glu	Asp	Asn
				165				170						175	
Gln	Leu	Ser	Trp	Arg	Gln	Pro	Asp	Leu	His	Asp	Ser	Pro	Ala	Ser	Ser
			180					185					190		
Glu	Tyr	Ser	Ser	Gly	Ser	Thr	Ile	Met	Val	Asp	Gln	Ser	Gly	Asp	Lys
	195					200						205			
Thr	Gln	Pro	Phe	Ser	Ala	Asp	Thr	Gln	Thr	Glu	His	Lys	Gln	Val	Gly
	210					215					220				
Glu	Glu	Leu	Leu	Val	Pro	Lys	Asn	Pro	Asp	Glu	Asn	Met	Pro	Ile	Ser
225					230					235					240
Gly	Glu	Glu	Lys	Phe	Ser	Ser	Pro	Ile	Gln	Val	Thr	Pro	Leu	Phe	Arg
				245					250					255	
Ser	Leu	Ala	Asp	Gly	Ile	Pro	Ser	Pro	Gln	Phe	Ser	Glu	Ser	Val	Ser
		260					265						270		
Phe	Ala	Pro	Ser	Leu	Phe	Ile	Ile	Gln	Tyr	Leu	Gly	Phe	Glu	Lys	Ser
		275				280					285				
Met	Ser	Leu	Lys	Arg	Leu	Ile	Ala	Phe	Val	Gly	Glu	Glu	Leu	Pro	Ala
	290					295					300				
Lys	Asn	Thr	Arg	Asp	Arg	Val	Leu	Ile	Ser	Met	Ser	Lys	Cys		
305					310				315						

(2) INFORMATION FOR SEQ ID NO:1142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..307

(D) OTHER INFORMATION: / Ceres Seq. ID 1597001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:

Met	Leu	Phe	Leu	Asp	Gly	Ile	Ser	Thr	Pro	Arg	Lys	Ser	Glu	Asn	Glu
1				5					10					15	
Thr	Pro	Ile	Ala	Lys	Lys	Leu	Lys	Arg	Ser	His	Ile	Leu	Asp	Leu	Thr
		20						25				30			
Glu	Ile	Ser	Asn	Tyr	Gly	Arg	Ala	Glu	Ala	Cys	Val	Asn	Gln	Gln	Ile
	35					40					45				
Arg	Ser	Pro	Phe	Ser	Val	Leu	Ala	Arg	Asn	Ala	Thr	Gly	Ile	Asp	Ser
	50					55				60					
Leu	Glu	Glu	Gln	Asn	Gln	Thr	Ser	Asn	Val	Asn	Glu	Ser	Asp	Gly	Glu
65				70					75					80	
Gly	Met	Phe	Leu	Lys	Lys	Asp	Asp	Pro	Lys	Val	Thr	Ala	Leu	Met	Gln
			85					90					95		
Gln	Ala	Glu	Leu	Leu	Ser	Ser	Leu	Ala	Gln	Lys	Val	Asn	Ala	Asp	Asn
	100						105					110			
Thr	Glu	Gln	Ser	Met	Glu	Asn	Ala	Trp	Lys	Val	Leu	Gln	Asp	Phe	Leu
	115					120					125				
Asn	Lys	Gly	Lys	Glu	Asn	Asp	Leu	Phe	Arg	Tyr	Gly	Ile	Pro	Asp	Ile
130						135					140				

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210
Lys Cys
225

215

220

(2) INFORMATION FOR SEQ ID NO:1144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1098
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:

tcaagctcaa	actctaaagg	tgtaggtgaa	gtcatcatta	taagaccaga	gtgaactgat	60
aatgctgtga	agaacaggtt	tacaacactt	tgtagaaga	gagccaagca	tgaagctatg	120
actaaagaca	gcaactcaaa	cacaaaaaga	atgttgttct	tagacggtat	cagtacaccg	180
cgaaaaatccg	agaatgaaac	tcctattgct	aagaaattga	agagaagtca	cattctagat	240
ctcacagaga	tcagtaacta	tggaagggcc	gaggcatgtg	tgaatcagca	gataaggtct	300
ccatttttcgg	ttttagctcg	aaatgccact	ggtattgata	gcttggaaga	acagaatcaa	360
acaagcaatg	tgaatgagag	tgatggtgaa	gggatgtttc	ttaagaagga	tgatccaaaa	420
gttacagctt	tgatgcaaca	agctgaactt	ttaagctcct	tggcgcagaa	agttaatgca	480
gacaacacag	aacagagtat	ggagaatgct	tggaaggttc	ttcaggactt	cttgaataaa	540
ggcaaggaga	atgattttatt	cagatatgga	atacctgata	tagatttttaa	gatcgaggaa	600
tttaaggacc	ttatagagga	tttgaggagt	ggttatgaag	acaatcaatt	atcttgagg	660
caacctgac	ttcatgactc	accagctagc	tctgagtata	gttcgggac	aaccatcatg	720
gtggatcagt	ctggtgataa	aacacaacca	ttctcagcag	atactcagac	agaacataag	780
caagttggag	aggagttgct	cgtcccga	aatcctgatg	agaatatgcc	catctcgggc	840
gaagaaaagt	tcagctcgcc	tattcaggtc	acgccattgt	tcagatcttt	ggcagacggt	900
ataccaagtc	cacagttctc	cgaaagtgag	aggagcttcc	tgctaaaaac	actagggatc	960
gagtcctcat	ctccatgtcc	aagtgcta	ccttcaaac	caccccttg	caaaagagtc	1020
cttctccata	gcttgaagcc	atctacaaa	gaaggcacca	gtgtgtcttt	aagaaaaaat	1080
tctttggttt	gtctctaa					

(2) INFORMATION FOR SEQ ID NO:1145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

Met	Thr	Lys	Asp	Ser	Asn	Ser	Asn	Thr	Lys	Arg	Met	Leu	Phe	Leu	Asp
1				5				10						15	
Gly	Ile	Ser	Thr	Pro	Arg	Lys	Ser	Glu	Asn	Glu	Thr	Pro	Ile	Ala	Lys
				20				25						30	
Lys	Leu	Lys	Arg	Ser	His	Ile	Leu	Asp	Leu	Thr	Glu	Ile	Ser	Asn	Tyr
				35				40						45	
Gly	Arg	Ala	Glu	Ala	Cys	Val	Asn	Gln	Gln	Ile	Arg	Ser	Pro	Phe	Ser
				50				55						60	
Val	Leu	Ala	Arg	Asn	Ala	Thr	Gly	Ile	Asp	Ser	Leu	Glu	Glu	Gln	Asn
				65				70						75	
Gln	Thr	Ser	Asn	Val	Asn	Glu	Ser	Asp	Gly	Glu	Gly	Met	Phe	Leu	Lys
				85				90						95	
Lys	Asp	Asp	Pro	Lys	Val	Thr	Ala	Leu	Met	Gln	Gln	Ala	Glu	Leu	Leu
				100				105						110	
Ser	Ser	Leu	Ala	Gln	Lys	Val	Asn	Ala	Asp	Asn	Thr	Glu	Gln	Ser	Met

09659800 "08659860

115 120 125
Glu Asn Ala Trp Lys Val Leu Gln Asp Phe Leu Asn Lys Gly Lys Glu
130 135 140
Asn Asp Leu Phe Arg Tyr Gly Ile Pro Asp Ile Asp Phe Lys Ile Glu
145 150 155 160
Glu Phe Lys Asp Leu Ile Glu Asp Leu Arg Ser Gly Tyr Glu Asp Asn
165 170 175
Gln Leu Ser Trp Arg Gln Pro Asp Leu His Asp Ser Pro Ala Ser Ser
180 185 190
Glu Tyr Ser Ser Gly Ser Thr Ile Met Val Asp Gln Ser Gly Asp Lys
195 200 205
Thr Gln Pro Phe Ser Ala Asp Thr Gln Thr Glu His Lys Gln Val Gly
210 215 220
Glu Glu Leu Leu Val Pro Lys Asn Pro Asp Glu Asn Met Pro Ile Ser
225 230 235 240
Gly Glu Glu Lys Phe Ser Ser Pro Ile Gln Val Thr Pro Leu Phe Arg
245 250 255
Ser Leu Ala Asp Gly Ile Pro Ser Pro Gln Phe Ser Glu Ser Glu Arg
260 265 270
Ser Phe Leu Leu Lys Thr Leu Gly Ile Glu Ser Ser Ser Pro Cys Pro
275 280 285
Ser Ala Asn Pro Ser Lys Pro Pro Pro Cys Lys Arg Val Leu Leu His
290 295 300
Ser Leu Lys Pro Ser Thr Lys Glu Gly Thr Ser Val Ser Leu Arg Lys
305 310 315 320
Asn Ser Leu Val Cys Leu
325

(2) INFORMATION FOR SEQ ID NO:1146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..315
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

Met Leu Phe Leu Asp Gly Ile Ser Thr Pro Arg Lys Ser Glu Asn Glu
1 5 10 15
Thr Pro Ile Ala Lys Lys Leu Lys Arg Ser His Ile Leu Asp Leu Thr
20 25 30
Glu Ile Ser Asn Tyr Gly Arg Ala Glu Ala Cys Val Asn Gln Gln Ile
35 40 45
Arg Ser Pro Phe Ser Val Leu Ala Arg Asn Ala Thr Gly Ile Asp Ser
50 55 60
Leu Glu Glu Gln Asn Gln Thr Ser Asn Val Asn Glu Ser Asp Gly Glu
65 70 75 80
Gly Met Phe Leu Lys Lys Asp Asp Pro Lys Val Thr Ala Leu Met Gln
85 90 95
Gln Ala Glu Leu Ser Ser Leu Ala Gln Lys Val Asn Ala Asp Asn
100 105 110
Thr Glu Gln Ser Met Glu Asn Ala Trp Lys Val Leu Gln Asp Phe Leu
115 120 125
Asn Lys Gly Lys Glu Asn Asp Leu Phe Arg Tyr Gly Ile Pro Asp Ile
130 135 140
Asp Phe Lys Ile Glu Glu Phe Lys Asp Leu Ile Glu Asp Leu Arg Ser
145 150 155 160
Gly Tyr Glu Asp Asn Gln Leu Ser Trp Arg Gln Pro Asp Leu His Asp
165 170 175

DOCKET# 00668960

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3173
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

ctaataagaac	taaaaactct	ttgagatttt	tggttgatga	gaatggcaat	gaacacactt	60
tgaatagaga	gaaaggcaat	gaacacactt	tgaatagaga	gaaaggcaat	attgcttctg	120
tttactttga	gaatctgttc	atgtcttctt	atcctgctaa	ctctcagtcg	gctttggatg	180
gttttaaaac	tcgagtttca	gaggagatga	atcaagaatt	aactcaagct	gttactgaat	240
tggaaattca	ttctgctaga	gtgctcctgg	tccagatggg	tactgcctt	attcttccag	300
aaaaatggga	atgttgtcaa	ggatcagatt	atatagagat	tctgggtttt	tttgagacgg	360
gggttctgcc	tcaagactgg	aatcatactc	acctctgttt	gattccaaaa	tttactaacc	420
ctcagagaa	gtccgatatt	agaccaatta	gtctatgctc	agtcttatat	aagattatct	480
ccaaaatcct	atctttcaga	ttaaagaagc	atctcccatc	tatcgtttca	ccttctcaat	540
ctgcgttttt	tgttgaaagg	ttaatctctc	acaatattct	cattgctcat	gaaattgtgc	600
atagcttaag	aactaatggc	aggatctcca	aagagtttat	ggttttcaaa	actgatattg	660
ctaaagccta	tgatagggtg	gaatggtctt	tcttacaaga	aattttgggt	gctttgggct	720
tcaatgataa	atggaattct	tggattatgg	gctgtgtgac	ttctgttacc	tattcagttc	780
tgataaatgg	tcaacatttt	gggcatatta	ctcccgagag	aggatcaga	caaggtgatc	840
ccatctctcc	atttctgttt	gtgctttgtg	cggagactct	tattcatatt	ctacaacaag	900
ctgagaattc	taagaaagtt	agtggcattc	agtttaattg	ttctgggcct	tcagttaatc	960
atttattggt	tgttgatgac	actcagttag	tctgtcgagc	aacaaaatcg	gattgtgaac	1020
agatgatgct	ttgtttatct	cagtatgggc	atatctcagg	acaactgatt	aatgtggaga	1080
aatcttctgat	cactttttgga	gttaaggtag	atgaggatag	taaacagtgg	atcaagaatc	1140
gttctggtat	tcatctagaa	gggtgggacag	ggaagtatct	ggggttacct	gagaacttga	1200
gtggttccaa	acaggatttg	tttggtctata	tcaaagaaaa	attgcaatct	catttgtctg	1260
gttggtatga	taaaactctc	tcacaaggag	gcaaggagat	cttggttaaag	tcaattgctt	1320
tggccttgcc	tgtgtatatt	atgacntggt	ttaggcttcc	taaagggtta	tgcactaagc	1380
ttacaagtgt	aatgatggat	ttttggtgga	actctatgga	attttcaaat	aaaattcatt	1440
ggataggtgg	taagaagtta	actctgccta	agagcttagg	gggttttggt	ttcaaagact	1500
tncaatggtt	taaccaggca	ctattggcca	aacaagcttg	gagattatc	agtgattcga	1560
agagcattgt	ttctcaaata	ttcaagagcc	gagaattatt	aaatggtggt	ctgaagagac	1620
ttataggaaa	tgggtgagcaa	accaatgtgt	ggattgataa	atggctgttt	gatggacata	1680
gtcaacgacc	tatgaatttg	cattcattga	tgaatattca	tatgaagggt	agtcatttaa	1740
ttgatcctct	ctctcggaat	tggaaactga	agaagctgac	agagttatct	catgagaaaag	1800
atgttcaatt	aattatgcat	cagagacctc	tcatctctag	cgaagactct	tattgttggg	1860
ctgggactaa	taatggttta	tacacggtga	agtctggata	tgaaagaagt	agcagggaga	1920
ctttcaagaa	tctcttcaag	gaggctgatg	tttatccttc	tgttaatctg	ttgtttgaca	1980
agggttgggt	tcttgaaacg	gttccaaaaa	ttaaagtctt	catgtggaaa	gctttaaaag	2040
gtgctcttgc	agtagaagac	atattaagat	caagaggcat	tcgaactgca	gatggatgct	2100
tattttgtaa	agaggaaatt	gaaacaatta	atcatctatt	gtttcaatgt	ccttttgcta	2160
gacaagtatg	gacactttca	cttattcagg	cacctgcaac	gggttttggg	acatctatct	2220
tctccaatat	aaatcatgtg	attcaaaatt	ctcagaattt	tggaaatcct	cgatcatatga	2280
gaactgtgag	tccatgggtta	ttgtgggaga	tatggaaaaa	caggaaataag	actttgtttc	2340
agggtactgg	tttaacgagt	agtgaattg	tagctaaagc	ttatgaagag	tgcaatcttt	2400
ggatcgctaa	gagtgtcatc	actgagttca	cgggagagct	ggatctcttg	tctgtgctac	2460
gaagggaacc	ctggcctttac	aatagttggg	ttgtcacggc	tcacgttggt	gaggtaaaact	2520
cggccttttg	atacttgtct	aacattgagt	tgtgggttca	aatgcgtggg	attcctctcc	2580
tctatgtttg	tgaagccaca	gtgacagaga	tagctcttgg	tttagggcaa	attatatcat	2640
tggattttca	tgatgtact	acaacccaaa	tagcttttat	tagagtgaga	atccgatttg	2700
agatcactga	tcgtataagg	ttcttccaaa	gaattacctt	tgattctggt	gagactgcgc	2760
tgataaggct	gactcatcat	aggaattact	gcccttatcg	acaacctgag	cctcgttcta	2820
tcattogtgg	tcctaccaac	aatctcacta	ggtctagaag	agaaggagtg	tgtacccggg	2880
atgaatatca	tcgttcttcc	ctgaactccc	aatcacagat	gtctgagaac	gcctttccag	2940
caoctattga	acctcctcca	agagtggcag	ctcctccttt	gaatcctgat	gaatttaggg	3000

DOCKET "08060950"

850	855	860
Ala Thr Val Thr Glu Ile	Ala Leu Gly Leu Gly Gln Ile Ile Ser Leu	
865	870	875
Asp Phe His Asp Ala Thr Thr Thr Gln Ile Ala Phe Ile Arg Val Arg		880
	885	890
Ile Arg Phe Glu Ile Thr Asp Arg Ile Arg Phe Phe Gln Arg Ile Thr		895
	900	905
Phe Asp Ser Gly Glu Thr Ala Leu Ile Arg Leu Thr His Arg Asn		910
	915	920
Tyr Cys Pro Tyr Arg Gln Pro Glu Pro Arg Ser Ile Ile Arg Gly Pro		925
	930	935
Thr Asn Asn Leu Thr Arg Ser Arg Arg Glu Gly Val Cys Thr Arg Asp		940
	945	950
Glu Tyr His Arg Ser Ser Leu Asn Ser Gln Ser Gln Met Ser Glu Asn		955
	965	970
Ala Phe Pro Ala Pro Ile Glu Pro Pro Pro Arg Val Ala Ala Pro Pro		975
	980	985
Leu Asn Pro Asp Glu Phe Arg Ala Ala Tyr Phe Pro Glu Gly Arg Ala		990
	995	1000
Gly Ser Leu Pro Asn Ile Gly Thr Leu Asn Leu Asn Pro Pro Ser Arg		1005
	1010	1015
Arg Gln Glu Ala Ser Arg Asn Ser Asp Val Gln Pro Phe Thr Gly Pro		1020
	1025	1030
Ala Phe Gly Ala Asn Val Pro Arg Val Val Glu Val Gly Glu Cys Ser		1035
	1045	1050
		1055

(2) INFORMATION FOR SEQ ID NO:1150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..1010
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:

Met Ser Ser Tyr Pro Ala Asn Ser Gln Ser Ala Leu Asp Gly Phe Lys	
1	15
Thr Arg Val Ser Glu Glu Met Asn Gln Glu Leu Thr Gln Ala Val Thr	
20	30
Glu Leu Glu Ile His Ser Ala Arg Val Leu Leu Val Gln Met Val His	
35	45
Cys Leu Ile Leu Pro Glu Lys Trp Glu Cys Cys Gln Gly Ser Asp Tyr	
50	60
Ile Glu Ile Leu Gly Phe Phe Glu Thr Gly Val Leu Pro Gln Asp Trp	
65	80
Asn His Thr His Leu Cys Leu Ile Pro Lys Phe Thr Asn Pro Gln Arg	
85	95
Met Ser Asp Ile Arg Pro Ile Ser Leu Cys Ser Val Leu Tyr Lys Ile	
100	110
Ile Ser Lys Ile Leu Ser Phe Arg Leu Lys Lys His Leu Pro Ser Ile	
115	125
Val Ser Pro Ser Gln Ser Ala Phe Phe Ala Glu Arg Leu Ile Ser His	
130	140
Asn Ile Leu Ile Ala His Glu Ile Val His Ser Leu Arg Thr Asn Gly	
145	160
Arg Ile Ser Lys Glu Phe Met Val Phe Lys Thr Asp Met Ala Lys Ala	
165	175

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[illegible]

Lys	Trp	Glu	Cys	Cys	Gln	Gly	Ser	Asp	Tyr	Ile	Glu	Ile	Leu	Gly	Phe
		35					40					45			
Phe	Glu	Thr	Gly	Val	Leu	Pro	Gln	Asp	Trp	Asn	His	Thr	His	Leu	Cys
		50				55					60				
Leu	Ile	Pro	Lys	Phe	Thr	Asn	Pro	Gln	Arg	Met	Ser	Asp	Ile	Arg	Pro
65					70				75					80	
Ile	Ser	Leu	Cys	Ser	Val	Leu	Tyr	Lys	Ile	Ile	Ser	Lys	Ile	Leu	Ser
				85				90						95	
Phe	Arg	Leu	Lys	Lys	His	Leu	Pro	Ser	Ile	Val	Ser	Pro	Ser	Gln	Ser
			100					105					110		
Ala	Phe	Phe	Ala	Glu	Arg	Leu	Ile	Ser	His	Asn	Ile	Leu	Ile	Ala	His
		115					120					125			
Glu	Ile	Val	His	Ser	Leu	Arg	Thr	Asn	Gly	Arg	Ile	Ser	Lys	Glu	Phe
		130				135					140				
Met	Val	Phe	Lys	Thr	Asp	Met	Ala	Lys	Ala	Tyr	Asp	Arg	Val	Glu	Trp
145					150					155					160
Ser	Phe	Leu	Gln	Glu	Ile	Leu	Val	Ala	Leu	Gly	Phe	Asn	Asp	Lys	Trp
				165					170					175	
Asn	Ser	Trp	Ile	Met	Gly	Cys	Val	Thr	Ser	Val	Thr	Tyr	Ser	Val	Leu
			180					185						190	
Ile	Asn	Gly	Gln	His	Phe	Gly	His	Ile	Thr	Pro	Glu	Arg	Gly	Ile	Arg
		195					200					205			
Gln	Gly	Asp	Pro	Ile	Ser	Pro	Phe	Leu	Phe	Val	Leu	Cys	Thr	Glu	Ala
		210				215					220				
Leu	Ile	His	Ile	Leu	Gln	Gln	Ala	Glu	Asn	Ser	Lys	Lys	Val	Ser	Gly
225					230					235					240
Ile	Gln	Phe	Asn	Gly	Ser	Gly	Pro	Ser	Val	Asn	His	Leu	Leu	Phe	Val
				245					250					255	
Asp	Asp	Thr	Gln	Leu	Val	Cys	Arg	Ala	Thr	Lys	Ser	Asp	Cys	Glu	Gln
			260					265					270		
Met	Met	Leu	Cys	Leu	Ser	Gln	Tyr	Gly	His	Ile	Ser	Gly	Gln	Leu	Ile
		275					280					285			
Asn	Val	Glu	Lys	Ser	Ser	Ile	Thr	Phe	Gly	Val	Lys	Val	Asp	Glu	Asp
		290				295					300				
Thr	Lys	Gln	Trp	Ile	Lys	Asn	Arg	Ser	Gly	Ile	His	Leu	Glu	Gly	Gly
305					310					315					320
Thr	Gly	Lys	Tyr	Leu	Gly	Leu	Pro	Glu	Asn	Leu	Ser	Gly	Ser	Lys	Gln
				325					330					335	
Asp	Leu	Phe	Gly	Tyr	Ile	Lys	Glu	Lys	Leu	Gln	Ser	His	Leu	Ser	Gly
			340					345					350		
Trp	Tyr	Asp	Lys	Thr	Leu	Ser	Gln	Gly	Gly	Lys	Glu	Ile	Leu	Leu	Lys
		355					360					365			
Ser	Ile	Ala	Leu	Ala	Leu	Pro	Val	Tyr	Ile	Met	Xaa	Cys	Phe	Arg	Leu
		370				375					380				
Pro	Lys	Gly	Leu	Cys	Thr	Lys	Leu	Thr	Ser	Val	Met	Met	Asp	Phe	Trp
385					390					395					400
Trp	Asn	Ser	Met	Glu	Phe	Ser	Asn	Lys	Ile	His	Trp	Ile	Gly	Gly	Lys
			405						410					415	
Lys	Leu	Thr	Leu	Pro	Lys	Ser	Leu	Gly	Gly	Phe	Gly	Phe	Lys	Asp	Xaa
			420					425					430		
Gln	Cys	Phe	Asn	Gln	Ala	Leu	Leu	Ala	Lys	Gln	Ala	Trp	Arg	Leu	Phe
		435					440					445			
Ser	Asp	Ser	Lys	Ser	Ile	Val	Ser	Gln	Ile	Phe	Lys	Ser	Arg	Glu	Leu
		450				455					460				
Leu	Asn	Gly	Gly	Leu	Lys	Arg	Leu	Ile	Gly	Asn	Gly	Glu	Gln	Thr	Asn
465					470					475					480
Val	Trp	Ile	Asp	Lys	Trp	Leu	Phe	Asp	Gly	His	Ser	Gln	Arg	Pro	Met
			485						490					495	
Asn	Leu	His	Ser	Leu	Met	Asn	Ile	His	Met	Lys	Val	Ser	His	Leu	Ile
			500					505					510		
Asp	Pro	Leu	Ser	Arg	Asn	Trp	Asn	Leu	Lys	Lys	Leu	Thr	Glu	Leu	Phe

DOCKET "08669950"

(2) INFORMATION FOR SEQ ID NO:1152:
(i) SEQUENCE CHARACTERISTICS:


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(2) INFORMATION FOR SEQ ID NO:1156:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 525 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: DNA (genomic)
      (ix) FEATURE:
            (A) NAME/KEY: -
```

[illegible]

(B) LOCATION: 1..209

(D) OTHER INFORMATION: / Ceres Seq. ID 1597079

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:

Met	Phe	Gly	Met	Arg	Thr	Met	Ile	Ala	Leu	Glu	Glu	Lys	Gly	Val	Lys
1			5					10						15	
Tyr	Glu	Tyr	Arg	Glu	Glu	Asp	Val	Ile	Asn	Asn	Lys	Ser	Pro	Leu	Leu
			20					25					30		
Leu	Glu	Met	Asn	Pro	Ile	His	Lys	Thr	Ile	Pro	Val	Leu	Ile	His	Asn
		35					40					45			
Gly	Lys	Pro	Val	Leu	Glu	Ser	Leu	Ile	Gln	Ile	Gln	Tyr	Ile	Asp	Glu
	50					55					60				
Val	Trp	Ser	Asp	Asn	Asn	Ser	Phe	Leu	Pro	Ser	Asp	Pro	Tyr	His	Arg
65					70					75				80	
Ala	Gln	Ala	Leu	Phe	Trp	Ala	Asp	Phe	Ile	Asp	Lys	Lys	Glu	Gln	Leu
			85					90						95	
Tyr	Val	Cys	Gly	Arg	Lys	Thr	Arg	Ala	Thr	Lys	Gly	Glu	Glu	Leu	Glu
			100					105					110		
Ala	Ala	Asn	Lys	Glu	Phe	Ile	Glu	Ile	Leu	Lys	Thr	Leu	Gln	Cys	Glu
		115					120					125			
Leu	Gly	Glu	Lys	Pro	Tyr	Phe	Gly	Gly	Asp	Lys	Phe	Gly	Phe	Val	Asp
	130						135					140			
Ile	Val	Leu	Ile	Gly	Phe	Tyr	Ser	Trp	Phe	Pro	Ala	Tyr	Gln	Lys	Phe
145					150					155				160	
Gly	Asn	Phe	Ser	Ile	Glu	Pro	Glu	Cys	Leu	Lys	Leu	Ile	Ala	Trp	Gly
			165					170						175	
Lys	Arg	Cys	Met	Gln	Arg	Glu	Ser	Val	Ala	Lys	Ala	Leu	Pro	Asp	Ser
			180					185					190		
Glu	Lys	Val	Val	Gly	Tyr	Val	Leu	Gln	Leu	Lys	Lys	Leu	Tyr	Gly	Ile
		195					200						205		
Glu															

(2) INFORMATION FOR SEQ ID NO:1163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1786 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1786

(D) OTHER INFORMATION: / Ceres Seq. ID 1597092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:

totacagagg	ctgatttttg	atagacctcc	agaaggaatt	aggaaaatag	tactggccac	60
caatatggct	gagacaagta	tcaccatcaa	tgatgttgta	tatgtgattg	attgtgggaa	120
agcaaaaagaa	acatcttatg	atgcgcttaa	caataccctt	tgtctgcttc	catcttggat	180
ttcaaaggca	gctgctcgcc	aaagaagagg	aagagctggt	cgtgttatgc	ctggagaatg	240
ttatcacctc	tatcctagat	gtgtctacga	agcttttgct	gactaccagc	agccggaact	300
totaaggacg	ccgttgcagt	ctctgtgttt	acaaattaaa	agcctaggac	ttggaagcat	360
ttcggagttc	ctctccaggg	cattgcaacc	tcctgaagca	ttatcgggtc	aaaatgctgt	420
tgagtatcta	aaaatcattg	gggctcttga	tgacgatgaa	aatttaacac	cttttaggaac	480
tcataatatg	ctctatgcag	ggaaaaatct	gtcaatgctt	cctgtggagc	ctaaacttgg	540
aaaaatgctt	atttttagggg	ctatcttcaa	ctgtctagat	ccagtaattga	cagttgttgc	600
tggtcttagt	gtcagagacc	cattccttat	gccatttgac	aaaaaagatc	tagcagaaac	660
agcaagggtc	aagttctctg	gccgtgatta	cagtgatcat	ttgacattgg	ttcgagcata	720
caatggttgg	aaagatgctg	aaagaacaca	ttctggttac	gactattgct	ggaagaactt	780
tctctcttct	caaactctta	aggccatgga	ctctatgcgg	aaacaattct	tcaatctcct	840
caaggaggct	tctctgattg	ataacattga	aggttgcagt	aagctgagtc	atgatgaaca	900
tcttgtagcg	gcaatcattt	gtgctggcat	gttccttgga	gtctgttctg	ttgtttttta	960
ccctacaata	aacaattctc	cctgcagaaa	taaggaaaag	tcaattacgc	tcaagacaat	1020
ggaagatgga	caagtgcctc	tatacnagag	ttctgtgaat	ggcaatgtac	caatgattcc	1080

00569930 00569930

290	295	300
Ile Ile Cys Ala Gly Met Phe Pro Gly Val Cys Ser Val Val Phe Tyr		
305	310	315
Pro Thr Ile Asn Asn Ser Pro Ser Gln Asn Lys Glu Lys Ser Ile Thr		
	325	330
Leu Lys Thr Met Glu Asp Gly Gln Val Leu Leu Tyr Xaa Ser Ser Val		
	340	345
Asn Gly Asn Val Pro Met Ile Pro Phe Pro Trp Leu Val Phe Asn Asp		
	355	360
Lys Val Lys Val Asn Ser Val Phe Leu Arg Asp Ser Thr Ala Val Ser		
	370	375
Asp Ser Val Leu Leu Leu Phe Gly Asp Lys Ile Ser Ser Gly Gly Phe		
385	390	395
Asp Gly His Leu Lys Met Leu Gly Gly Tyr Leu Glu Phe Phe Met Lys		
	405	410
Pro Thr Leu Ala Tyr Thr Tyr Leu Ser Leu Lys Arg Glu Leu Asp Glu		
	420	425
Leu Ile Gln Asn Lys Leu Val Asn Pro Lys Leu Asp Ile Gln Leu Tyr		
	435	440
Asp Lys Leu Met Thr Ala Ile Arg Leu Leu Val Ser Glu Asp Gln Cys		
	450	455
Glu Gly Arg Phe Val Tyr Gly Arg Lys Ala Leu Ser Pro Thr Pro Thr		
465	470	475
Lys Lys Leu Lys Asp Val Gly Ala Gln Leu Gln Asn Ser Gly Gly Glu		
	485	490
Asn Asn Lys Asn Gln Leu Gln Thr Leu Leu Ala Arg Ala Gly His Gly		
	500	505
Ser Pro Val Tyr Lys Thr Arg Gln Leu Lys Asn Asn Gln Phe Arg Ser		
	515	520
Met Val Thr Phe Asn Gly Leu Asp Phe Met Gly Lys Pro Cys Gly Ser		
	530	535
Lys Lys Asn Ala Glu Lys Asp Ala Ala His Glu Ala Leu Leu Trp Leu		
545	550	555
Gln Gly Glu Ser Lys Ser Ser Leu Asn Asp Leu Asn His Met Ser Met		
	565	570
Leu Leu Lys Lys Asn Lys Ser Lys Asn His Ala Lys Ala Ser Thr Lys		
	580	585
Trp Gly		

(2) INFORMATION FOR SEQ ID NO:1165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..573

(D) OTHER INFORMATION: / Ceres Seq. ID 1597094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165:

Met Ala Glu Thr Ser Ile Thr Ile Asn Asp Val Val Tyr Val Ile Asp	
1	5
Cys Gly Lys Ala Lys Glu Thr Ser Tyr Asp Ala Leu Asn Asn Thr Pro	
	20
Cys Leu Leu Pro Ser Trp Ile Ser Lys Ala Ala Ala Arg Gln Arg Arg	
	35
Gly Arg Ala Gly Arg Val Met Pro Gly Glu Cys Tyr His Leu Tyr Pro	
	50
Arg Cys Val Tyr Glu Ala Phe Ala Asp Tyr Gln Gln Pro Glu Leu Leu	
65	70

DOCKET "08668960"

570

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..519

- (D) OTHER INFORMATION: / Ceres Seq. ID 1597095

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166:

Met 1	Pro	Gly	Glu	Cys 5	Tyr	His	Leu	Tyr	Pro 10	Arg	Cys	Val	Tyr	Glu 15	Ala
Phe	Ala	Asp	Tyr	Gln	Gln	Pro	Glu	Leu	Leu	Arg	Thr	Pro	Leu	Gln	Ser
			20					25					30		
Leu	Cys	Leu	Gln	Ile	Lys	Ser	Leu	Gly	Leu	Gly	Ser	Ile	Ser	Glu	Phe
		35					40					45			
Leu	Ser	Arg	Ala	Leu	Gln	Pro	Pro	Glu	Ala	Leu	Ser	Val	Gln	Asn	Ala
	50					55					60				
Val	Glu	Tyr	Leu	Lys	Ile	Ile	Gly	Ala	Leu	Asp	Asp	Asp	Glu	Asn	Leu
65					70					75				80	
Thr	Pro	Leu	Gly	Thr	His	Asn	Met	Leu	Tyr	Ala	Gly	Lys	Asn	Leu	Ser
				85					90					95	
Met	Leu	Pro	Val	Glu	Pro	Lys	Leu	Gly	Lys	Met	Leu	Ile	Leu	Gly	Ala
			100					105					110		
Ile	Phe	Asn	Cys	Leu	Asp	Pro	Val	Met	Thr	Val	Val	Ala	Gly	Leu	Ser
		115					120					125			
Val	Arg	Asp	Pro	Phe	Leu	Met	Pro	Phe	Asp	Lys	Lys	Asp	Leu	Ala	Glu
	130					135					140				
Thr	Ala	Arg	Ser	Lys	Phe	Ser	Gly	Arg	Asp	Tyr	Ser	Asp	His	Leu	Thr
145				150					155					160	
Leu	Val	Arg	Ala	Tyr	Asn	Gly	Trp	Lys	Asp	Ala	Glu	Arg	Thr	His	Ser
				165					170					175	
Gly	Tyr	Asp	Tyr	Cys	Trp	Lys	Asn	Phe	Leu	Ser	Ser	Gln	Thr	Leu	Lys
			180					185					190		
Ala	Met	Asp	Ser	Met	Arg	Lys	Gln	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ala
		195					200					205			
Ser	Leu	Ile	Asp	Asn	Ile	Glu	Gly	Cys	Ser	Lys	Leu	Ser	His	Asp	Glu
	210					215					220				
His	Leu	Val	Arg	Ala	Ile	Ile	Cys	Ala	Gly	Met	Phe	Pro	Gly	Val	Cys
225				230					235					240	
Ser	Val	Val	Phe	Tyr	Pro	Thr	Ile	Asn	Asn	Ser	Pro	Ser	Gln	Asn	Lys
				245					250					255	
Glu	Lys	Ser	Ile	Thr	Leu	Lys	Thr	Met	Glu	Asp	Gly	Gln	Val	Leu	Leu
			260					265					270		
Tyr	Xaa	Ser	Ser	Val	Asn	Gly	Asn	Val	Pro	Met	Ile	Pro	Phe	Pro	Trp
		275					280						285		
Leu	Val	Phe	Asn	Asp	Lys	Val	Lys	Val	Asn	Ser	Val	Phe	Leu	Arg	Asp
	290					295					300				
Ser	Thr	Ala	Val	Ser	Asp	Ser	Val	Leu	Leu	Leu	Phe	Gly	Asp	Lys	Ile
				310						315				320	
Ser	Ser	Gly	Gly	Phe	Asp	Gly	His	Leu	Lys	Met	Leu	Gly	Gly	Tyr	Leu
				325					330					335	
Glu	Phe	Phe	Met	Lys	Pro	Thr	Leu	Ala	Tyr	Thr	Tyr	Leu	Ser	Leu	Lys
			340					345					350		
Arg	Glu	Leu	Asp	Glu	Leu	Ile	Gln	Asn	Lys	Leu	Val	Asn	Pro	Lys	

Ser Glu Asp Gln Cys Glu Gly Arg Phe Val Tyr Gly Arg Lys Ala Leu
385 390 395 400
Ser Pro Thr Pro Thr Lys Lys Leu Lys Asp Val Gly Ala Gln Leu Gln
405 410 415
Asn Ser Gly Gly Glu Asn Asn Lys Asn Gln Leu Gln Thr Leu Leu Ala
420 425 430
Arg Ala Gly His Gly Ser Pro Val Tyr Lys Thr Arg Gln Leu Lys Asn
435 440 445
Asn Gln Phe Arg Ser Met Val Thr Phe Asn Gly Leu Asp Phe Met Gly
450 455 460
Lys Pro Cys Gly Ser Lys Lys Asn Ala Glu Lys Asp Ala Ala His Glu
465 470 475 480
Ala Leu Leu Trp Leu Gln Gly Glu Ser Lys Ser Ser Leu Asn Asp Leu
485 490 495
Asn His Met Ser Met Leu Leu Lys Lys Asn Lys Ser Lys Asn His Ala
500 505 510
Lys Ala Ser Thr Lys Trp Gly
515

(2) INFORMATION FOR SEQ ID NO:1167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..780
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:

atgcaaacaa taataatttc tccacttggt tctcatcgtc tctgtcttgc tcgtgctgtt	60
ccttgcaacc gtctttctcaa caaccaccac cgtgctcctc cttcgatccg cctctcaaac	120
caccgttcaa ccacctcact ccgcctcttc tctcgcgcgc ggtctctctg tgtttgcaaa	180
tctgacgccg agtatcttgc taaagcagca gccagtcggg acagtgaat gccgactgaa	240
gatgtgcaag atcccagaat cgctaagatt gcctcttcca ttagagtcac cccgacttc	300
cctaaaccag gaatcatggt tcaggacata acgacgcttc ttctcgacac tgaggccttt	360
aaggatacta ttgcttttgt ttgttgataga taaaagata aaggcatatc tgttgttgca	420
ggtgttgaag ctgagaggtt catttttggc cctcctattg cgttggctat tggtgccaaa	480
tttgttccca tgaggacgcc caagaagcta cctgggaagg ttatttcgga ggagtattcg	540
ttggagtatg gaccagatac gattgagatg cacgtagggt cagtagagcc tggtagcgct	600
gctattatta ttgatgncct cattgccacg ggtgggactc tcgctgctgc aatccgacta	660
cttgaacgag taggagtgna gattgttgaa tgtgcttgcg taattgagtt accagagctt	720
aagggaagag agaaactagg agagacgtcg ctatttgctc ttgttaaagtc ggctgcttaa	780

(2) INFORMATION FOR SEQ ID NO:1168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..259
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:

Met Gln Thr Ile Ile Ile Ser Pro Leu Val Ser His Arg Leu Cys Leu
1 5 10 15
Ala Arg Ala Val Pro Cys Asn Arg Leu Leu Asn Asn His His Arg Ala
20 25 30
Pro Pro Ser Ile Arg Leu Ser Asn His Arg Ser Thr Thr Ser Leu Arg

00559301 02559350

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 1																
Met	Ala	Thr	Glu	Asp	Val	Gln	Asp	Pro	Arg	Ile	Ala	Lys	Ile	Ala	Ser	
1				5					10					15		
Ser	Ile	Arg	Val	Ile	Pro	Asp	Phe	Pro	Lys	Pro	Gly	Ile	Met	Phe	Gln	
			20					25					30			
Asp	Ile	Thr	Thr	Leu	Leu	Leu	Asp	Thr	Glu	Ala	Phe	Lys	Asp	Thr	Ile	
			35				40					45				
Ala	Leu	Phe	Val	Asp	Arg	Tyr	Lys	Asp	Lys	Gly	Ile	Ser	Val	Val	Ala	
			50			55					60					
Gly	Val	Glu	Ala	Arg	Gly	Phe	Ile	Phe	Gly	Pro	Ile	Ala	Leu	Ala		
65				70					75				80			
Ile	Gly	Ala	Lys	Phe	Val	Pro	Met	Arg	Thr	Pro	Lys	Lys	Leu	Pro	Gly	
				85					90				95			
Lys	Val	Ile	Ser	Glu	Glu	Tyr	Ser	Leu	Glu	Tyr	Gly	Pro	Asp	Thr	Ile	
			100					105					110			
Glu	Met	His	Val	Gly	Ala	Val	Glu	Pro	Gly	Glu	Arg	Ala	Ile	Ile	Ile	
			115				120					125				
Asp	Xaa	Leu	Ile	Ala	Thr	Gly	Gly	Thr	Leu	Ala	Ala	Ala	Ile	Arg	Leu	
			130			135						140				
Leu	Glu	Arg	Val	Gly	Val	Xaa	Ile	Val	Glu	Cys	Ala	Cys	Val	Ile	Glu	
145				150						155					160	

Leu Pro Glu Leu Lys Gly Lys Glu Lys Leu Gly Glu Thr Ser Leu Phe
165 170 175
Val Leu Val Lys Ser Ala Ala
180

(2) INFORMATION FOR SEQ ID NO:1170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 870 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..870
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170:

atggcgactc	tcttcactgc	gacggttcct	tctcaccacc	gtttcgtctc	tccatcccaa	60
catccgaaac	agagtcttct	atcgagtcg	ctaagcgtca	cattcacgga	gaatccacaa	120
ccaacggcgg	tggtcacatt	gcaggagcag	caattgacgg	attggattac	ttctccggtg	180
acgcgacggg	tcggaatcgg	cgccgggttt	acctgggctg	ggtttttagc	tttcggtggt	240
gtctccgagc	agatgaagaa	gtcacgactc	gatgtgtttc	aggaagagga	taacacaaga	300
ggtttagaaa	agcaagaaga	gatcatctta	ccaaacggca	taagggtacta	tgatctacaa	360
gttggaagtg	gagctaactc	aagctcagga	tacttggtag	tgtttgatgt	aaagggacaa	420
gtacatggca	ctgaacaagt	gttcgtggac	acatttgagg	gcaaaggcaa	gtcactagcg	480
atggtaatgg	actcaagacc	gtatagcaag	ggactatgcc	aaggtataga	gcatgttctc	540
aggtcaatga	aggctggagg	taaacgtaga	gtgataattc	caccgtcctt	aggatttgga	600
gacagaaatg	tcgaatttgg	acagggtttg	gagattcctc	catctgcaac	acttgactat	660
atcatcgagg	ttgatacagt	ttattgtttc	caaactattg	tggtttacca	gttcatattc	720
ttcgtaatca	cggctctttt	caaatttgat	caagtcactg	actttgtgtg	tagcacaac	780
ttcgttatac	ttgctgtgtt	aacacttggt	ctcaaagcct	cttggcattt	tcgacaggat	840
cttgcaatgg	ggggaagatc	gtcgccttga				

(2) INFORMATION FOR SEQ ID NO:1171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..289
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:

Met	Ala	Thr	Leu	Phe	Thr	Ala	Thr	Val	Pro	Ser	His	His	Arg	Phe	Val
1			5					10						15	
Ser	Pro	Ser	Gln	His	Pro	Lys	Gln	Ser	Leu	Leu	Ser	Gln	Ser	Leu	Ser
			20					25					30		
Val	Thr	Phe	Thr	Glu	Asn	Pro	Gln	Pro	Thr	Ala	Val	Val	Thr	Leu	Gln
			35				40					45			
Glu	Gln	Gln	Leu	Thr	Asp	Trp	Ile	Thr	Ser	Pro	Val	Thr	Arg	Arg	Phe
			50			55					60				
Gly	Ile	Gly	Ala	Gly	Phe	Thr	Trp	Ala	Gly	Phe	Leu	Ala	Phe	Gly	Val
			65			70			75					80	
Val	Ser	Glu	Gln	Met	Lys	Lys	Ser	Arg	Leu	Asp	Val	Phe	Gln	Glu	Glu
			85					90					95		
Asp	Asn	Thr	Arg	Gly	Leu	Glu	Lys	Gln	Glu	Glu	Ile	Ile	Leu	Pro	Asn
			100					105					110		
Gly	Ile	Arg	Tyr	Tyr	Asp	Leu	Val	Gly	Ser	Gly	Ala	Thr	Pro	Ser	
			115			120					125				
Ser	Gly	Tyr	Leu	Val	Val	Phe	Asp	Val	Lys	Gly	Gln	Val	His	Gly	Thr
			130			135					140				

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- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..126
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1597173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:

Trp	Gly	Arg	Val	Thr	Ser	Trp	Lys	Lys	Ser	Ala	Thr	Ser	Thr	Thr	Thr
1				5					10					15	
Arg	Val	Ala	Thr	Lys	Asp	Thr	Thr	Thr	Ser	Lys	Pro	Thr	Ile	Pro	Thr
			20					25					30		
Ser	Pro	Thr	Val	Ala	Pro	Ala	Leu	Leu	Ile	Leu	Arg	Ile	Arg	Cys	Ile
		35					40				45				
Pro	Cys	Asn	Asn	Asn	Lys	Val	Arg	Thr	Asn	Leu	Leu	Phe	Ser	Thr	Thr
	50				55						60				
Lys	Val	Ser	Phe	Leu	Ser	Asn	Xaa	Trp	Gly	Thr	Thr	Ser	Arg	His	
65				70				75						80	
His	His	Leu	Asp	Leu	His	Ile	Ser	Lys	Thr	Met	Met	Glu	Thr	Leu	Asn
			85					90						95	
Thr	Lys	Val	Arg	Tyr	Leu	Glu	Gly	His	Ser	Ala	Ser	Ser	Ser	Ala	Pro
			100					105						110	
Thr	Gln	Thr	Ser	Gln	Thr	Thr	Gln	Ala	Lys	Gln	Phe	Arg	Ile		
			115				120					125			

(2) INFORMATION FOR SEQ ID NO:1176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1026
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:

gaagaacccc	gtaacgttta	tctcgggttg	tgtretgatg	ggttcaatcc	atttggcatg	60
tctcgtaatc	attcgttgtg	gcctgtgatc	ctaactcctt	ataatttacc	ccctgggatg	120
tgcataaata	cagagtactt	atttcttacc	attctgaatt	ctggtccaaa	tcatcctcga	180
gctagtcttg	atgtcttcct	ccaacctcct	attgaggagt	taaaagagtt	gtgggtctact	240
ggagtcgatg	cgtacgatgt	ttcattgagt	cagaatttta	atctaaaagc	agtactacta	300
tggacgatta	gcgactttcc	ggcgtatagc	atgttatcag	gatggactac	tcagttttgt	360
aaatgtagta	tgttcgaaga	ttatctttct	gcgaaatata	catgcttgcc	cgaaaaagaa	420
ctctacgcga	gaagagcgaa	agaatatcat	ctatgggtta	aagaatatgt	aacatactgg	480
aacactactt	ctccatttcc	tacttgggtt	caagagattg	tgcaaggacc	tttgaacaag	540
gttaaaactt	ggccaatgta	tttcacaaga	ggatatttgt	ttcatacgca	aaatcacggc	600
gctggacgaa	agacatgtaa	ctatggggtc	tgtgttaaag	gtggaaatta	cgctgattca	660
tctgatgaag	cggatttcta	cggtacctta	actgataata	tagaactcga	gtatgaggat	720
caagtttgtt	atattcogta	tccatatacg	aagaaaccaa	agaacatttg	gctcaatggt	780
ctaaaagtca	atccgagggg	aaatatctct	ggagaatatg	aaaacaatga	tccaactcct	840
ttgcaaacag	aaaatgatga	tgatgttttg	ctcactacaa	ttgaagatct	tgttcttgaa	900
actccggtag	ccaacttaaa	ccaataatc	cttgattacg	atgtcgggga	tgctgaacca	960
gaagacgaat	tccgatgtaa	tttatcgctc	tcggacgaag	atgaagtaga	agatgaagat	1020
gtataa						

(2) INFORMATION FOR SEQ ID NO:1177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

00669800 00669800

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..341

(D) OTHER INFORMATION: / Ceres Seq. ID 1597193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177:

Glu Glu Pro Arg Asn Val Tyr Leu Gly Leu Cys Xaa Asp Gly Phe Asn
1 5 10 15
Pro Phe Gly Met Ser Arg Asn His Ser Leu Trp Pro Val Ile Leu Thr
20 25 30
Pro Tyr Asn Leu Pro Pro Gly Met Cys Met Asn Thr Glu Tyr Leu Phe
35 40 45
Leu Thr Ile Leu Asn Ser Gly Pro Asn His Pro Arg Ala Ser Leu Asp
50 55 60
Val Phe Leu Gln Pro Leu Ile Glu Glu Leu Lys Glu Leu Trp Ser Thr
65 70 75 80
Gly Val Asp Ala Tyr Asp Val Ser Leu Ser Gln Asn Phe Asn Leu Lys
85 90 95
Ala Val Leu Leu Trp Thr Ile Ser Asp Phe Pro Ala Tyr Ser Met Leu
100 105 110
Ser Gly Trp Thr Thr Gln Phe Cys Lys Cys Ser Met Phe Glu Asp Tyr
115 120 125
Leu Ser Ala Lys Tyr Pro Cys Leu Pro Glu Lys Glu Leu Tyr Ala Arg
130 135 140
Arg Ala Lys Glu Tyr His Leu Trp Val Lys Glu Tyr Val Thr Tyr Trp
145 150 155 160
Asn Thr Thr Ser Pro Phe Pro Thr Trp Val Gln Glu Ile Val Gln Gly
165 170 175
Pro Leu Asn Lys Val Lys Thr Trp Pro Met Tyr Phe Thr Arg Gly Tyr
180 185 190
Leu Phe His Thr Gln Asn His Gly Ala Gly Arg Lys Thr Cys Asn Tyr
195 200 205
Gly Val Cys Val Lys Gly Gly Asn Tyr Ala Asp Ser Ser Asp Glu Ala
210 215 220
Asp Phe Tyr Gly Thr Leu Thr Asp Asn Ile Glu Leu Glu Tyr Glu Asp
225 230 235 240
Gln Val Cys Tyr Ile Pro Tyr Pro Tyr Thr Lys Lys Pro Lys Asn Ile
245 250 255
Trp Leu Asn Val Leu Lys Val Asn Pro Arg Gly Asn Ile Ser Gly Glu
260 265 270
Tyr Glu Asn Asn Asp Pro Thr Leu Leu Gln Thr Glu Asn Asp Asp Asp
275 280 285
Val Leu Leu Thr Thr Ile Glu Asp Leu Val Leu Glu Thr Pro Val Ala
290 295 300
Asn Leu Asn Pro Ile Ile Leu Asp Tyr Asp Val Gly Asp Ala Glu Pro
305 310 315 320
Glu Asp Glu Phe Arg Cys Asn Leu Ser Ser Ser Asp Glu Asp Glu Val
325 330 335
Glu Asp Glu Asp Val
340

(2) INFORMATION FOR SEQ ID NO:1178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 322 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..322

(D) OTHER INFORMATION: / Ceres Seq. ID 1597194

DOCKET "08668960"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:

Met Ser Arg Asn His Ser Leu Trp Pro Val Ile Leu Thr Pro Tyr Asn
1 5 10 15
Leu Pro Pro Gly Met Cys Met Asn Thr Glu Tyr Leu Phe Leu Thr Ile
20 25 30
Leu Asn Ser Gly Pro Asn His Pro Arg Ala Ser Leu Asp Val Phe Leu
35 40 45
Gln Pro Leu Ile Glu Glu Leu Lys Glu Leu Trp Ser Thr Gly Val Asp
50 55 60
Ala Tyr Asp Val Ser Leu Ser Gln Asn Phe Asn Leu Lys Ala Val Leu
65 70 75 80
Leu Trp Thr Ile Ser Asp Phe Pro Ala Tyr Ser Met Leu Ser Gly Trp
85 90 95
Thr Thr Gln Phe Cys Lys Cys Ser Met Phe Glu Asp Tyr Leu Ser Ala
100 105 110
Lys Tyr Pro Cys Leu Pro Glu Lys Glu Leu Tyr Ala Arg Arg Ala Lys
115 120 125
Glu Tyr His Leu Trp Val Lys Glu Tyr Val Thr Tyr Trp Asn Thr Thr
130 135 140
Ser Pro Phe Pro Thr Trp Val Gln Glu Ile Val Gln Gly Pro Leu Asn
145 150 155 160
Lys Val Lys Thr Trp Pro Met Tyr Phe Thr Arg Gly Tyr Leu Phe His
165 170 175
Thr Gln Asn His Gly Ala Gly Arg Lys Thr Cys Asn Tyr Gly Val Cys
180 185 190
Val Lys Gly Gly Asn Tyr Ala Asp Ser Ser Asp Glu Ala Asp Phe Tyr
195 200 205
Gly Thr Leu Thr Asp Asn Ile Glu Leu Glu Tyr Glu Asp Gln Val Cys
210 215 220
Tyr Ile Pro Tyr Pro Tyr Thr Lys Lys Pro Lys Asn Ile Trp Leu Asn
225 230 235 240
Val Leu Lys Val Asn Pro Arg Gly Asn Ile Ser Gly Glu Tyr Glu Asn
245 250 255
Asn Asp Pro Thr Leu Leu Gln Thr Glu Asn Asp Asp Asp Val Leu Leu
260 265 270
Thr Thr Ile Glu Asp Leu Val Leu Glu Thr Pro Val Ala Asn Leu Asn
275 280 285
Pro Ile Ile Leu Asp Tyr Asp Val Gly Asp Ala Glu Pro Glu Asp Glu
290 295 300
Phe Arg Cys Asn Leu Ser Ser Ser Asp Glu Asp Glu Val Glu Asp Glu
305 310 315 320
Asp Val

(2) INFORMATION FOR SEQ ID NO:1179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..302
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:

Met Cys Met Asn Thr Glu Tyr Leu Phe Leu Thr Ile Leu Asn Ser Gly
1 5 10 15
Pro Asn His Pro Arg Ala Ser Leu Asp Val Phe Leu Gln Pro Leu Ile
20 25 30
Glu Glu Leu Lys Glu Leu Trp Ser Thr Gly Val Asp Ala Tyr Asp Val
35 40 45

09669980 08668960

SEQUENCE DESCRIPTION: 322 Amino Acids																
Met	Gly	Leu	Gln	Glu	Asn	Leu	Leu	Arg	Gly	Ile	Tyr	Ala	Tyr	Gly	Phe	
1				5					10					15		
Glu	Lys	Pro	Ser	Ala	Ile	Gln	Gln	Arg	Gly	Ile	Val	Pro	Phe	Cys	Lys	
			20					25					30			
Gly	Leu	Asp	Val	Ile	Gln	Gln	Ala	Gln	Ser	Gly	Thr	Gly	Lys	Thr	Ala	
		35					40					45				
Thr	Phe	Cys	Ser	Gly	Val	Leu	Gln	Gln	Leu	Asp	Tyr	Ala	Leu	Leu	Gln	
	50					55					60					
Cys	Gln	Ala	Leu	Val	Leu	Ala	Pro	Thr	Arg	Glu	Leu	Ala	Gln	Gln	Ile	
65					70					75					80	
Glu	Lys	Val	Met	Arg	Ala	Leu	Gly	Asp	Tyr	Gln	Gly	Val	Lys	Val	His	
				85					90					95		
Ala	Cys	Val	Gly	Gly	Thr	Ser	Val	Arg	Xaa	Asp	Gln	Arg	Ile	Leu	Gln	
			100					105					110			
Ala	Gly	Val	His	Val	Val	Val	Gly	Thr	Pro	Gly	Arg	Val	Phe	Asp	Met	
		115					120					125				
Leu	Arg	Arg	Gln	Ser	Leu	Arg	Pro	Asp	Cys	Ile	Lys	Met	Phe	Val	Leu	
	130					135					140					
Asp	Glu	Ala	Asp	Glu	Met	Leu	Ser	Arg	Gly	Phe	Lys	Asp	Gln	Ile	Tyr	
145					150					155					160	
Asp	Ile	Phe	Gln	Leu	Leu	Pro	Pro	Lys	Ile	Gln	Val	Gly	Val	Phe	Ser	
			165						170					175		
Ala	Thr	Met	Pro	Pro	Glu	Ala	Leu	Glu	Ile	Thr	Arg	Lys	Phe	Met	Ser	
		180						185					190			
Lys	Pro	Val	Arg	Ile	Leu	Val	Lys	Arg	Asp	Glu	Leu	Thr	Leu	Glu	Xaa	
		195					200					205				
Tyr	Gln	Ala	Ile	Leu	Arg	Glu	Xaa	Trp	Arg	Lys	Lys	Thr	Gly	Xaa	Leu	
	210					215					220					
Glu	Thr	Leu	Cys	Asp	Leu	Tyr	Xaa	Asp	Ser	Ser	His	His	Ser	Glu	Cys	
225					230					235					240	
His	Leu	Cys	Gln	His	Ser	Ser	Gln	Gly	Arg	Xaa	Gly	Xaa	Thr	Asp	Lys	
			245						250					255		
Met	Arg	Ser	Arg	Asp	His	Thr	Val	Ser	Xaa	Xaa	Ser	Trp	Arg	His	Gly	
		260						265					270			
Pro	Lys	His	Gln	Arg	His	His	His	Glu	Arg	Val	Gln	Val	Xaa	Ala	Arg	
		275					280					285				

Leu Val Phe
290

(2) INFORMATION FOR SEQ ID NO:1187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..208
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:

Met Arg Ala Leu Gly Asp Tyr Gln Gly Val Lys Val His Ala Cys Val
1 5 10 15
Gly Gly Thr Ser Val Arg Xaa Asp Gln Arg Ile Leu Gln Ala Gly Val
20 25 30
His Val Val Val Gly Thr Pro Gly Arg Val Phe Asp Met Leu Arg Arg
35 40 45
Gln Ser Leu Arg Pro Asp Cys Ile Lys Met Phe Val Leu Asp Glu Ala
50 55 60
Asp Glu Met Leu Ser Arg Gly Phe Lys Asp Gln Ile Tyr Asp Ile Phe
65 70 75 80
Gln Leu Leu Pro Pro Lys Ile Gln Val Gly Val Phe Ser Ala Thr Met
85 90 95
Pro Pro Glu Ala Leu Glu Ile Thr Arg Lys Phe Met Ser Lys Pro Val
100 105 110
Arg Ile Leu Val Lys Arg Asp Glu Leu Thr Leu Glu Xaa Tyr Gln Ala
115 120 125
Ile Leu Arg Glu Xaa Trp Arg Lys Lys Thr Gly Xaa Leu Glu Thr Leu
130 135 140
Cys Asp Leu Tyr Xaa Asp Ser Ser His His Ser Glu Cys His Leu Cys
145 150 155 160
Gln His Ser Ser Gln Gly Arg Xaa Gly Xaa Thr Asp Lys Met Arg Ser
165 170 175
Arg Asp His Thr Val Ser Xaa Xaa Ser Trp Arg His Gly Pro Lys His
180 185 190
Gln Arg His His His Glu Arg Val Gln Val Xaa Ala Arg Leu Val Phe
195 200 205

(2) INFORMATION FOR SEQ ID NO:1188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..342
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:

atgaagtttg acatcagaga agcttcaggg aatcaacaa caggagttca gaacatnaat 60
attgatgaag nngcagaagc tggaacccca ccaagagtta actatacttc tcaacttagc 120
aagctgaaga ggacttttga ccacaagaag agagcaacag aaaggctagc tcagactgga 180
gatcctacaa aagatgactg ctctgtaaga gtcaagctta gtgaattaaa acaagctcac 240
ttgggaggaa gtcccatgtc tatccaggnt tgtctcattg atcattataa agtcaatggt 300
cgagtnaact caaaccaagt caagaaagat ctcagccggt ga

(2) INFORMATION FOR SEQ ID NO:1189:

03639930-10300

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:

Met Lys Phe Asp Ile Arg Glu Ala Ser Gly Lys Ser Thr Thr Gly Val
1 5 10 15
Gln Asn Xaa Asn Ile Asp Glu Xaa Ala Glu Ala Gly Thr Pro Pro Arg
20 25 30
Val Asn Tyr Thr Ser Gln Leu Ser Lys Leu Lys Arg Thr Phe Asp His
35 40 45
Lys Lys Arg Ala Thr Glu Arg Val Lys Leu Ala Gln Thr Gly Asp Pro Thr Lys
50 55 60
Asp Asp Cys Ser Val Arg Val Lys Leu Ser Glu Leu Lys Gln Ala His
65 70 75 80
Leu Gly Gly Ser Pro Met Ser Ile Gln Xaa Cys Leu Ile Asp His Tyr
85 90 95
Lys Val Asn Gly Arg Xaa Asn Ser Asn Gln Val Lys Lys Asp Leu Ser
100 105 110
Arg

(2) INFORMATION FOR SEQ ID NO:1190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1032 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1032
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:

atngcntgtn atcattnctg cttngtcatn cactngcctg ctatngccat ttctgctttt 60
agtttccattt catttcggtt attgcatact aggactgtta gaaccaacca acttttctact 120
tggcttgact tagagctttc tgatcatatc tcatctgttt gcgtcacact gaattggatt 180
gacatcctaa aatactacaa cgacaggata gtaccttgca acctgcttta cagacgcac 240
tctgattcgt ctgttatagc ccnggctgct atctgttgca tgcatacacg gtcagaagga 300
aatcagaacc tcctattcaa cgataacatc gaccgtattg ctcgccaact aagagaacag 360
acagaaaccg acacaatggc tgacgttgta gatgagcaag agcaacctac caacattggt 420
gctggtgact tccctcacia ccacaaccag cgtcatggaa ttgttccacc tccagtacag 480
aacaacaact ttgagatcaa aagcgggtctc attgctatgg ttcaaggga caagtttcat 540
ggcctgccaa tggaggatcc gctagatcat ctngacgagt tngaaagnct ctgtgncctn 600
actaaaatca atggagttag tgaagatggg tttnnnanttc gcttgtttcc attctcactt 660
ggagataaag cccatctgtg ggaaaagacg ctaccccaga attcaatcac aacctgggat 720
gactgcaaaa aggccttctt ggcaaaattc ttttccaact ccagaactgc aagactccgg 780
aatgagatat ccggaattac tcagaagcaa aatgaaagct tctgtgaagc ttgggagcgc 840
tttaagggtt atcaaacc aa atgccctcat caccgattta agcangctnc tctnctcagc 900
acactctata gagncgtctn gcctaagata aggatactgc ttgacaccgc ttcaaattggg 960
aattttttga agaaggatgt tgaagaagga tggagctag tngaaaanct ttgctcagtc 1020
gnatggcaat na

(2) INFORMATION FOR SEQ ID NO:1191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 amino acids
- (B) TYPE: amino acid

005501-005505

(B) LOCATION: 1..250

(D) OTHER INFORMATION: / Ceres Seq. ID 1597259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192:

Met His Thr Arg Ser Glu Gly Asn Gln Asn Leu Leu Phe Asn Asp Asn
1 5 10 15
Ile Asp Arg Ile Ala Arg Gln Leu Arg Glu Gln Thr Glu Thr Asp Thr
20 25 30
Met Ala Asp Val Val Asp Glu Gln Gln Pro Thr Asn Ile Gly Ala
35 40 45
Gly Asp Phe Pro His Asn His Asn Gln Arg His Gly Ile Val Pro Pro
50 55 60
Pro Val Gln Asn Asn Asn Phe Glu Ile Lys Ser Gly Leu Ile Ala Met
65 70 75 80
Val Gln Gly Asn Lys Phe His Gly Leu Pro Met Glu Asp Pro Leu Asp
85 90 95
His Xaa Asp Glu Xaa Glu Xaa Leu Cys Xaa Xaa Thr Lys Ile Asn Gly
100 105 110
Val Ser Glu Asp Gly Xaa Xaa Xaa Arg Leu Phe Pro Phe Ser Leu Gly
115 120 125
Asp Lys Ala His Leu Trp Glu Lys Thr Leu Pro Gln Asn Ser Ile Thr
130 135 140
Thr Trp Asp Asp Cys Lys Lys Ala Phe Leu Ala Lys Phe Phe Ser Asn
145 150 155 160
Ser Arg Thr Ala Arg Leu Arg Asn Glu Ile Ser Gly Phe Thr Gln Lys
165 170 175
Gln Asn Glu Ser Phe Cys Glu Ala Trp Glu Arg Phe Lys Gly Tyr Gln
180 185 190
Thr Lys Cys Pro His His Gly Phe Lys Xaa Ala Xaa Xaa Leu Ser Thr
195 200 205
Leu Tyr Arg Xaa Val Xaa Pro Lys Ile Arg Ile Leu Leu Asp Thr Ala
210 215 220
Ser Asn Gly Asn Phe Leu Lys Lys Asp Val Glu Glu Gly Trp Xaa Leu
225 230 235 240
Xaa Glu Xaa Leu Cys Ser Val Xaa Trp Gln
245 250

(2) INFORMATION FOR SEQ ID NO:1193:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..218

(D) OTHER INFORMATION: / Ceres Seq. ID 1597260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193:

Met Ala Asp Val Val Asp Glu Gln Glu Gln Pro Thr Asn Ile Gly Ala
1 5 10 15
Gly Asp Phe Pro His Asn His Asn Gln Arg His Gly Ile Val Pro Pro
20 25 30
Pro Val Gln Asn Asn Asn Phe Glu Ile Lys Ser Gly Leu Ile Ala Met
35 40 45
Val Gln Gly Asn Lys Phe His Gly Leu Pro Met Glu Asp Pro Leu Asp
50 55 60
His Xaa Asp Glu Xaa Glu Xaa Leu Cys Xaa Xaa Thr Lys Ile Asn Gly
65 70 75 80
Val Ser Glu Asp Gly Xaa Xaa Xaa Arg Leu Phe Pro Phe Ser Leu Gly
85 90 95
Asp Lys Ala His Leu Trp Glu Lys Thr Leu Pro Gln Asn Ser Ile Thr
100 105 110

09589980-101300


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                100                105                110
Ala Trp Arg Thr Asp Pro Ser Glu Lys Ala Ala Lys Pro Gly Leu Val
                115                120                125
Tyr Asp Met Gly Val Asn Asp Tyr Val Xaa Tyr Leu Cys Ser Val Gly
                130                135                140
Tyr Thr Asp Ser Ser Ile Thr Arg Leu Val Arg Lys Lys Thr Val Cys
                145                150                155                160
Ala Asn Pro Lys Pro Ser Val Leu Asp Leu Lys Leu Pro Ser Ile Thr
                165                170                175
Ile Pro Asn Leu Ala Lys Xaa Lys Leu Leu Ser Leu Glu Pro Leu Pro
                180                185                190
Thr Leu Asp Gln
                195

```

(2) INFORMATION FOR SEQ ID NO:1196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:

```

Met Lys Ser Gly Thr Ser Met Ser Thr Pro Phe Val Ala Gly Ile Val
1      5      10      15
Ala Leu Leu Lys Ser Leu His Pro His Trp Ser Pro Ala Ala Ile Arg
20     25     30
Ser Ala Ile Val Thr Thr Ala Trp Arg Thr Asp Pro Ser Glu Lys Ala
35     40     45
Ala Lys Pro Gly Leu Val Tyr Asp Met Gly Val Asn Asp Tyr Val Xaa
50     55     60
Tyr Leu Cys Ser Val Gly Tyr Thr Asp Ser Ser Ile Thr Arg Leu Val
65     70     75     80
Arg Lys Lys Thr Val Cys Ala Asn Pro Lys Pro Ser Val Leu Asp Leu
85     90     95
Lys Leu Pro Ser Ile Thr Ile Pro Asn Leu Ala Lys Xaa Lys Leu Leu
100    105    110
Ser Leu Glu Pro Leu Pro Thr Leu Asp Gln
115    120

```

(2) INFORMATION FOR SEQ ID NO:1197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..714
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:

```

tctgtctgtc tgcgcactca ggatcagatc ttagctaaat tgagacaagc tcaaaatgag      60
taagcttcag agtgaggccg ttcgtgaagc catcactact atcacaggga aatccgaggc      120
aaagaaaacgt aactttgtcg agactattga gctccagatc ggtctgaaga actatgaccc      180
tcaaaaaggac aagcgtttca gtggatctgt caagttacca catatcccc gtcctaaaat      240
gaagatctgc atgctcggag atgccagca tgttgaagag gaaaattccc aactcttgtg      300
agccaccagg aatccttggg gtcaaagggtg aatgaaacaa aggcaacagt gaagttccag      360
ctgaagaagg ttctgtgcat gggagttgca gtttgtaacc tttcaatgga agagaagcag      420
atctttcaga atgtgcagat gagcgtcaac ttctctgtct cgctattgaa gaagaactgg      480

```

DOCKET "08668960"

Ile	Glu	Ser	Leu	Gly	Ser	Leu	Cys	Val	Cys	Lys	Ser	Asp	Ala	Glu	Tyr
1				5					10					15	
Phe	Ala	Lys	Ala	Ala	Ala	Ser	Arg	Asp	Ser	Glu	Met	Ala	Thr	Glu	Asp
			20					25					30		
Val	Gln	Asp	Pro	Arg	Ile	Ala	Lys	Ile	Ala	Ser	Ser	Ile	Arg	Val	Ile
		35					40					45			
Pro	Asp	Phe	Pro	Lys	Pro	Gly	Ile	Met	Phe	Gln	Asp	Ile	Thr	Thr	Leu
	50					55					60				
Leu	Leu	Asp	Thr	Glu	Ala	Phe	Lys	Asp	Thr	Ile	Ala	Leu	Phe	Val	Asp
65				70						75					80
Arg	Tyr	Lys	Asp	Lys	Gly	Ile	Ser	Val	Val	Ala	Gly	Val	Glu	Ala	Arg
				85					90					95	
Gly	Phe	Ile	Phe	Gly	Pro	Pro	Ile	Ala	Leu	Ala	Ile	Gly	Ala	Lys	Phe
			100					105					110		
Val	Pro	Met	Arg	Thr	Pro	Lys	Lys	Leu	Pro	Gly	Lys	Val	Ile	Ser	Glu
		115					120					125			
Glu	Tyr	Ser	Leu	Glu	Tyr	Gly	Pro	Asp	Thr	Ile	Glu	Met	His	Val	Gly
	130					135					140				

Ala Val Glu Pro Gly Glu Arg Ala Ile Ile Ile Asp Xaa Leu Ile Ala
145 150 155 160
Thr Gly Gly Thr Leu Ala Ala Ala Ile Arg Leu Leu Glu Arg Val Gly
165 170 175
Val Xaa Ile Val Glu Cys Ala Cys Val Ile Glu Leu Pro Glu Leu Lys
180 185 190
Gly Lys Glu Lys Leu Gly Glu Thr Ser Leu Phe Val Leu Val Lys Ser
195 200 205
Ala Ala
210

(2) INFORMATION FOR SEQ ID NO:1203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203:

Met Ala Thr Glu Asp Val Gln Asp Pro Arg Ile Ala Lys Ile Ala Ser
1 5 10 15
Ser Ile Arg Val Ile Pro Asp Phe Pro Lys Pro Gly Ile Met Phe Gln
20 25 30
Asp Ile Thr Thr Leu Leu Leu Asp Thr Glu Ala Phe Lys Asp Thr Ile
35 40 45
Ala Leu Phe Val Asp Arg Tyr Lys Asp Lys Gly Ile Ser Val Val Ala
50 55 60
Gly Val Glu Ala Arg Gly Phe Ile Phe Gly Pro Pro Ile Ala Leu Ala
65 70 75 80
Ile Gly Ala Lys Phe Val Pro Met Arg Thr Pro Lys Lys Leu Pro Gly
85 90 95
Lys Val Ile Ser Glu Glu Tyr Ser Leu Glu Tyr Gly Pro Asp Thr Ile
100 105 110
Glu Met His Val Gly Ala Val Glu Pro Gly Glu Arg Ala Ile Ile Ile
115 120 125
Asp Xaa Leu Ile Ala Thr Gly Gly Thr Leu Ala Ala Ala Ile Arg Leu
130 135 140
Leu Glu Arg Val Gly Val Xaa Ile Val Glu Cys Ala Cys Val Ile Glu
145 150 155 160
Leu Pro Glu Leu Lys Gly Lys Glu Lys Leu Gly Glu Thr Ser Leu Phe
165 170 175
Val Leu Val Lys Ser Ala Ala
180

(2) INFORMATION FOR SEQ ID NO:1204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:

Met Phe Gln Asp Ile Thr Thr Leu Leu Asp Thr Glu Ala Phe Lys
1 5 10 15
Asp Thr Ile Ala Leu Phe Val Asp Arg Tyr Lys Asp Lys Gly Ile Ser

09689980-10300

Met	Ala	Thr	Glu	Asp	Val	Gln	Asp	Pro	Arg	Ile	Ala	Lys	Ile	Ala	Ser
1				5					10					15	
Ser	Ile	Arg	Val	Ile	Pro	Asp	Phe	Pro	Lys	Pro	Gly	Ile	Met	Phe	Gln
			20					25					30		
Asp	Ile	Thr	Thr	Leu	Leu	Leu	Asp	Thr	Glu	Ala	Phe	Lys	Asp	Thr	Ile
			35				40					45			
Ala	Leu	Phe	Val	Asp	Arg	Tyr	Lys	Asp	Lys	Gly	Ile	Ser	Val	Val	Ala
	50					55					60				
Gly	Val	Glu	Ala	Arg	Gly	Phe	Ile	Phe	Gly	Pro	Pro	Ile	Ala	Leu	Ala
65					70					75				80	
Ile	Gly	Ala	Lys	Phe	Val	Pro	Met	Arg	Thr	Pro	Lys	Lys	Leu	Pro	Gly
				85					90					95	
Lys	Val	Ile	Ser	Glu	Glu	Tyr	Ser	Leu	Glu	Tyr	Gly	Pro	Asp	Thr	Ile

Parameter	Value	Unit
Initial temperature	25.0	°C
Final temperature	25.0	°C
Initial pressure	1.0	atm
Final pressure	1.0	atm
Initial volume	1.0	L
Final volume	1.0	L
Initial concentration	1.0	M
Final concentration	1.0	M
Initial pH	7.0	
Final pH	7.0	
Initial ionic strength	0.1	M
Final ionic strength	0.1	M
Initial solvent	Water	
Final solvent	Water	
Initial gas	Nitrogen	
Final gas	Nitrogen	
Initial catalyst	Pt	
Final catalyst	Pt	
Initial ligand	None	
Final ligand	None	
Initial substrate	None	
Final substrate	None	
Initial product	None	
Final product	None	
Initial reagent	None	
Final reagent	None	
Initial solvent	Water	
Final solvent	Water	
Initial gas	Nitrogen	
Final gas	Nitrogen	
Initial catalyst	Pt	
Final catalyst	Pt	
Initial ligand	None	
Final ligand	None	
Initial substrate	None	
Final substrate	None	
Initial product	None	
Final product	None	
Initial reagent	None	
Final reagent	None	
Initial solvent	Water	
Final solvent	Water	
Initial gas	Nitrogen	
Final gas	Nitrogen	
Initial catalyst	Pt	
Final catalyst	Pt	
Initial ligand	None	
Final ligand	None	
Initial substrate	None	
Final substrate	None	
Initial product	None	
Final product	None	
Initial reagent	None	
Final reagent	None	
Initial solvent	Water	
Final solvent	Water	
Initial gas	Nitrogen	
Final gas	Nitrogen	
Initial catalyst	Pt	
Final catalyst	Pt	
Initial ligand	None	
Final ligand	None	
Initial substrate	None	
Final substrate	None	
Initial product	None	
Final product	None	
Initial reagent	None	
Final reagent	None	
Initial solvent	Water	
Final solvent	Water	
Initial gas	Nitrogen	
Final gas	Nitrogen	
Initial catalyst	Pt	
Final catalyst	Pt	
Initial ligand	None	
Final ligand	None	
Initial substrate	None	
Final substrate	None	
Initial product	None	
Final product	None	
Initial reagent	None	
Final reagent	None	
Initial solvent	Water	
Final solvent	Water	
Initial gas	Nitrogen	
Final gas	Nitrogen	
Initial catalyst	Pt	
Final catalyst	Pt	
Initial ligand	None	
Final ligand	None	
Initial substrate	None	
Final substrate	None	
Initial product	None	
Final product	None	
Initial reagent	None	
Final reagent	None	
Initial solvent	Water	
Final solvent	Water	
Initial gas	Nitrogen	
Final gas	Nitrogen	
Initial catalyst	Pt	
Final catalyst	Pt	
Initial ligand	None	
Final ligand	None	
Initial substrate	None	
Final substrate	None	
Initial product	None	
Final product	None	
Initial reagent	None	
Final reagent	None	
Initial solvent	Water	
Final solvent	Water	
Initial gas	Nitrogen	
Final gas	Nitrogen	
Initial catalyst	Pt	
Final catalyst	Pt	
Initial ligand	None	
Final ligand	None	
Initial substrate	None	
Final substrate	None	
Initial product	None	
Final product	None	
Initial reagent	None	
Final reagent	None	
Initial solvent	Water	
Final solvent	Water	
Initial gas	Nitrogen	
Final gas	Nitrogen	
Initial catalyst	Pt	
Final catalyst	Pt	
Initial ligand	None	
Final ligand	None	
Initial substrate	None	
Final substrate	None	
Initial product	None	
Final product	None	
Initial reagent	None	
Final reagent	None	
Initial solvent	Water	
Final solvent	Water	
Initial gas	Nitrogen	
Final gas	Nitrogen	
Initial catalyst	Pt	
Final catalyst	Pt	
Initial ligand	None	
Final ligand	None	

(2) INFORMATION FOR SEQ ID NO:1211:

(A) LENGTH: 154 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1597319

[illegible]

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 1097 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1097

(D) OTHER INFORMATION: / Ceres Seq. ID 1597344

(X1) SEQUENCE DESCRIPTION: SEQ ID: 1								
cacaatttga	tacggtcag	tttgaccaga	ggctgaatga	agttctcgat	ggacaggatg		60	
agttcttcac	ctcatatgat	gagggtccatg	agagctttga	tgccatgggt	ttgcaagaga		120	
atcttcttag	gggtatctat	gcttacggtt	tcgaaaagcc	ttctgctatt	cagcaaaagag		180	
gaattgtacc	ctttttgcaag	gggtcttgatg	tgatccagca	ggcacagctct	ggtactggaa		240	
aaaccgccac	tttctgctct	gggtcttttgc	agcagcttga	ctatgcccctt	ctccagtgcc		300	
aggctctcgt	tttggtctccc	accagagagc	ttgctcagca	gattgagaag	gtcatgcgtg		360	

(2) INFORMATION FOR SEQ ID NO:1213:

(A) LENGTH: 205 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..205

(D) OTHER INFORMATION: / Ceres Seq. ID 1597345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:

(2) INFORMATION FOR SEQ ID NO:1214:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1597346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:

Met Gly Leu Gln Glu Asn Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe
1 5 10 15
Glu Lys Pro Ser Ala Ile Gln Gln Arg Gly Ile Val Pro Phe Cys Lys
20 25 30
Gly Leu Asp Val Ile Gln Gln Ala Gln Ser Gly Thr Gly Lys Thr Ala
35 40 45
Thr Phe Cys Ser Gly Val Leu Gln Gln Leu Asp Tyr Ala Leu Leu Gln
50 55 60
Cys Gln Ala Leu Val Leu Ala Pro Thr Arg Glu Leu Ala Gln Gln Ile
65 70 75 80
Glu Lys Val Met Arg Ala Leu Gly Asp Tyr Gln Gly Val Lys Val His
85 90 95
Ala Cys Val Gly Gly Thr Ser Val Arg Xaa Asp Gln Arg Ile Leu Gln
100 105 110
Ala Gly Val His Val Val Val Gly Thr Pro Gly Arg Val Phe Asp Met
115 120 125
Leu Arg Arg Gln Ser Leu Arg Pro Asp Cys Ile Lys Met Phe Val Leu
130 135 140
Asp Glu Ala Asp Glu Met Leu Ser Arg Gly Phe Lys Asp Gln Leu Met
145 150 155 160
Glu Thr Trp Thr Lys Thr Pro Glu Thr Ser Ser
165 170

(2) INFORMATION FOR SEQ ID NO:1215:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1597347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:

Met Pro Phe Ser Ser Ala Arg Leu Ser Phe Trp Leu Pro Pro Glu Ser
1 5 10 15
Leu Leu Ser Arg Leu Arg Arg Ser Cys Val Pro Leu Val Thr Thr Lys
20 25 30
Val Ser Arg Phe Met Pro Val Leu Val Glu Pro Val Ser Xaa Arg Ile
35 40 45
Ser Ala Phe Ser Arg Leu Val Phe Met Leu Ser Leu Glu Leu Leu Val
50 55 60
Val Phe Leu Thr Cys Leu Glu Asp Asn Leu Ser Ala Leu Thr Ala Ser
65 70 75 80
Arg Cys Leu Ser Leu Met Lys Leu Met Lys Cys Ser Pro Val Val Ser
85 90 95
Arg Ile Ser Ser Trp Arg His Gly Pro Lys His Gln Arg His His His
100 105 110
Glu Arg Val Gln Val Xaa Ala Arg Leu Val Phe
115 120

(2) INFORMATION FOR SEQ ID NO:1216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1156 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

00609900-10100

(B) LOCATION: 1..1156

(D) OTHER INFORMATION: / Ceres Seq. ID 1597360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216:

tggtcggtctc	gaagaaggaa	cggtgaagtc	tttaatagaa	gaaaaaggag	tgatcaaagg	60
agtgacatac	aaaaataaag	caggcgaaga	aacaacagcc	ttggcacctc	tcactgtagt	120
atgcgacggt	tgctactcaa	accttcgtcg	gtctctaaac	gataacaatg	ctgaggttct	180
gtcttaccaa	gttgcttaca	tctcgaagaa	ttgtcggctt	gatgatccca	aaaaccttca	240
tttgataatg	tccaaaccct	cctacatcat	gttgtagcaa	ttaagcagca	ctgatgttcg	300
ttgtggtttt	gaacttttct	cgcgaatttt	tccttccatt	gcaaaagggtg	aaatggctac	360
ttttgcgaag	aacactctag	ctcctcaggt	acctccaaaa	cttcgcaaaa	tattcttgaa	420
aggtctagat	gaaggagcac	acataaaagc	gggtgccagca	aagcgcagta	cagcttcttt	480
aaccaagaaa	aatggagtga	ttgtgttggg	agatgcattc	aacatgcgtc	atcnttcggt	540
cgcggtcgtg	atgatggttt	tattgtctga	cattctcatt	ctacgtcgtc	ttctccagcc	600
actaagcaac	cttgggtgatg	caaacaaagt	ctcagaagtc	attaagtcct	ttaatattat	660
ccgcaagcca	atgtcagcga	cgggtgaacac	attaggaaat	gcattttctc	aagttctaata	720
tgcatacaact	gacgaagcaa	aagaggcaat	gagacaaggt	tgctatgatt	acctctctag	780
tggtggtttt	tgcacgtcgg	ggatgatggc	tctactaggt	ggcatgaatc	ctcgtccgct	840
ctctctcata	tatcatctat	gtgctatcac	tttacattca	attggccatc	ttctatctcc	900
atttccttcc	ccccttagca	tttggcatag	cctcaggctt	tttggtttgg	ctttgaaaat	960
gttggttccc	catctcaagg	ctgagggagt	tagcgaaatg	ttttttccag	caaacgcagc	1020
cgcatacgcg	aaaagctata	tggccgcac	tggtctttta	acattgatgc	tctaaacagc	1080
aacatacgtg	agcttgtaaa	ctcgttgaaa	tgttattgta	atgcttagct	tacataatat	1140
tacttaatga	gtttct					

(2) INFORMATION FOR SEQ ID NO:1217:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..352

(D) OTHER INFORMATION: / Ceres Seq. ID 1597361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217:

Val	Arg	Leu	Glu	Gly	Thr	Val	Lys	Ser	Leu	Ile	Glu	Glu	Lys	Gly
1			5				10						15	
Val	Ile	Lys	Gly	Val	Thr	Tyr	Lys	Asn	Lys	Ala	Gly	Glu	Glu	Thr
			20				25					30		Thr
Ala	Leu	Ala	Pro	Leu	Thr	Val	Val	Cys	Asp	Gly	Cys	Tyr	Ser	Asn
			35				40					45		Leu
Arg	Arg	Ser	Leu	Asn	Asp	Asn	Asn	Ala	Glu	Val	Leu	Ser	Tyr	Gln
			50				55				60			Val
Ala	Tyr	Ile	Ser	Lys	Asn	Cys	Arg	Leu	Asp	Asp	Pro	Lys	Asn	Leu
			65			70				75				80
Leu	Ile	Met	Ser	Lys	Pro	Ser	Tyr	Ile	Met	Leu	Tyr	Gln	Leu	Ser
			85						90				95	Ser
Thr	Asp	Val	Arg	Cys	Gly	Phe	Glu	Leu	Phe	Ser	Ala	Asn	Phe	Pro
			100					105					110	Ser
Ile	Ala	Lys	Gly	Glu	Met	Ala	Thr	Phe	Ala	Lys	Asn	Thr	Leu	Ala
			115				120					125		Pro
Gln	Val	Pro	Pro	Lys	Leu	Arg	Lys	Ile	Phe	Leu	Lys	Gly	Leu	Asp
			130				135				140			Glu
Gly	Ala	His	Ile	Lys	Ala	Val	Pro	Ala	Lys	Arg	Met	Thr	Ala	Ser
			145			150				155				160
Thr	Lys	Lys	Asn	Gly	Val	Ile	Val	Leu	Gly	Asp	Ala	Phe	Asn	Met
			165						170				175	Arg
His	Xaa	Ser	Val	Ala	Ala	Gly	Met	Met	Val	Leu	Leu	Ser	Asp	Ile
			180				185					190		Leu
Ile	Leu	Arg	Arg	Leu	Leu	Gln	Pro	Leu	Ser	Asn	Leu	Gly	Asp	Ala
			195				200					205		Asn

0366990 08669960

(2) INFORMATION FOR SEQ ID NO:1218:

(A) LENGTH: 270 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

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(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..270

(D) OTHER INFORMATION: / Ceres Seq. ID 1597362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218:

Descriptive Statistics					
Mean	100.00				
Standard Deviation	15.00				
Minimum	50.00				
Maximum	150.00				
Range	100.00				
Frequency Distribution					
Bin Width	10.00				
Bin 1 (50-60)	5				
Bin 2 (60-70)	10				
Bin 3 (70-80)	15				
Bin 4 (80-90)	20				
Bin 5 (90-100)	25				
Bin 6 (100-110)	30				
Bin 7 (110-120)	25				
Bin 8 (120-130)	15				
Bin 9 (130-140)	10				
Bin 10 (140-150)	5				
Skewness and Kurtosis					
Skewness	0.50				
Kurtosis	1.00				
Correlation Matrix					
Variable 1	Variable 2				
1.00	0.80				
0.80	1.00				
Regression Analysis					
Dependent Variable	Independent Variable				
100.00	50.00				
Regression Coefficient	2.00				
Intercept	50.00				
Adjusted R-Square	0.64				
F-Statistic	16.00				
p-Value	0.0001				
ANOVA Table					
Source	Sum of Squares	df	Mean Square	F	Significance
Regression	1200.00	1	1200.00	16.00	0.0001
Residual	800.00	9	88.89		
Total	2000.00	10			
Diagnostic Statistics					
Mean	100.00				
Standard Deviation	15.00				
Minimum	50.00				
Maximum	150.00				
Range	100.00				
Normality Test					
Statistic	0.50				
p-Value	0.50				
Linearity Test					
Statistic	0.50				
p-Value	0.50				
Heteroscedasticity Test					
Statistic	0.50				
p-Value	0.50				
Autocorrelation Test					
Statistic	0.50				
p-Value	0.50				

(B) LOCATION: 1..504

[illegible]

(D) OTHER INFORMATION: / Ceres Seq. ID 1597376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:

aatcacggcg gcggcgggcg aagagtagca gcagcaggcg gcgccgagta gcgtctcccc	60
acctcgagct tgccaccatg gctagaggat tgaagaagca tttgaagagg ctcaatgcgc	120
ccaagcattg gatgctggac aagcttggcg gasttttgct cccaaaccat cttctggacc	180
tcacaagtct agggagtgcc tgccactgat cctcatcatc aggaacaggc tcaagtatgc	240
tcttacatac cgtgagtcac ttccatcctg atgcaacgcc atgtacttgt tgatggcaag	300
gtcaggacag acaagaccta cctgctggg ttcatggatg tcatttccat cccaagacc	360
aacgagaact acaggctgct gtatgacact aaggggccgct tccgccttca cccaatcagg	420
gatgaggatg ctaagttaa gctttgcaag gttaggtctg ttcagtttg gcagaagggc	480
atcccgtaac tgaacacgta tgac	

(2) INFORMATION FOR SEQ ID NO:1221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1597377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:

Ser Arg Arg Arg Arg Arg Lys Ser Ser Ser Ser Arg Arg Arg Arg Val	
1 5 10 15	
Ala Ser Pro His Leu Glu Leu Ala Thr Met Ala Arg Gly Leu Lys Lys	
20 25 30	
His Leu Lys Arg Leu Asn Ala Pro Lys His Trp Met Leu Asp Lys Leu	
35 40 45	
Gly Gly Xaa Leu Leu Pro Asn His Leu Leu Asp Leu Thr Ser Leu Gly	
50 55 60	
Ser Ala Cys His	
65	

(2) INFORMATION FOR SEQ ID NO:1222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1597378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:

Met Gln Arg His Val Leu Val Asp Gly Lys Val Arg Thr Asp Lys Thr	
1 5 10 15	
Tyr Pro Ala Gly Phe Met Asp Val Ile Ser Ile Pro Lys Thr Asn Glu	
20 25 30	
Asn Tyr Arg Leu Leu Tyr Asp Thr Lys Gly Arg Phe Arg Leu His Pro	
35 40 45	
Ile Arg Asp Glu Asp Ala Lys Phe Lys Leu Cys Lys Val Arg Ser Val	
50 55 60	
Gln Phe Gly Gln Lys Gly Ile Pro Tyr Leu Asn Thr Tyr Asp	
65 70 75	

(2) INFORMATION FOR SEQ ID NO:1223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

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[illegible]

Lys Ser Pro
50

(2) INFORMATION FOR SEQ ID NO:1234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..57
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597415

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:

Met Asp Val Val Tyr Ala Leu Lys Xaa Arg Ala Glu Pro Ser Thr Ala
1 5 10 15
Ser Glu Ala Arg Leu Asp Ala Ser Ser Pro Cys Cys Arg Gly Cys Leu
20 25 30
Phe Val Val Arg Val Thr Ser Phe Ser Ser Leu Ser Val Thr Cys Trp
35 40 45
Thr Ile Val Ser Ser Ile Leu Glu Val
50 55

(2) INFORMATION FOR SEQ ID NO:1235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..509
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:

tngtctctcaa atatctctca ccacctctss sctcagcttn tcsscacctt tggtcaggca 60
ggctcaggca aagggggcgg msaacaagga cgagsgatgg sgaccaaggt catctgcttc 120
cttggtgctcg catccctgct cctcgccgct gcctttcccg tgtctgctct gcgncagcrg 180
ttcgaagaag ggccggcggcg gcgggtggtgg cggaggcagt gttagcggaa sgcaggcgcc 240
aacctgaatc cctgggagtg ctgcaccaag tgcgggtcgc ggtgctcaa gacgcagtac 300
aggaaggcct gcctcacctt atgcaacaag tgctgcgcca agtgcctctg cgtgccaccg 360
gggttctacg gcaacaaggg cgccctgccct gctacaacaa ctggaaaacc aaggaaggag 420
ggcccaagtg cccctagaat aagatccacc gcagctcccg tccgccattg tcscmccttc 480
tccgaatctg ggaacgtgtt gttcatctt

(2) INFORMATION FOR SEQ ID NO:1236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:

Xaa Leu Ser Asn Ile Ser His His Leu Xaa Xaa Gln Leu Xaa Xaa Thr
1 5 10 15
Phe Gly Gln Ala Gly Ser Gly Lys Gly Gly Xaa Xaa Gln Gly Arg Xaa
20 25 30
Met Xaa Thr Lys Val Ile Cys Phe Leu Val Leu Ala Ser Leu Leu Leu
35 40 45

00659960-10130

35 40 45
Phe Trp Thr Phe Asp Arg Phe Asn Ser Gln Leu Ser Trp Asp Pro Gln
50 55 60
Ile Ser Gln Ala Ala Gly Xaa Arg Asp Pro Tyr Asp Asp Leu Ile Ala
65 70 75 80
Arg His Ser Gly Ser Pro Pro Ser Ser
85

(2) INFORMATION FOR SEQ ID NO:1242:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1597429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:

Met Glu Asp Pro Asp Lys Arg Asp Gln Val Arg Arg Glu His Val Tyr
1 5 10 15
Lys Met Lys Glu Arg Cys Glu Arg Thr Lys Ala Ala Trp Ser Leu Pro
20 25 30
Leu Arg Pro Tyr Gly Phe Trp Thr Phe Asp Arg Phe Asn Ser Gln Leu
35 40 45
Ser Trp Asp Pro Gln Ile Ser Gln Ala Ala Gly Xaa Arg Asp Pro Tyr
50 55 60
Asp Asp Leu Ile Ala Arg His Ser Gly Ser Pro Pro Ser Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:1243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 868 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..868

(D) OTHER INFORMATION: / Ceres Seq. ID 1597430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:

agaagcttat cgcttatcat ccgcgcctct acattttcttc tctctctgct cctccgcctc 60
cgctccgcsc tggwtccsat ccaagacagg gatcgccatg tcggactcgg aggagcacca 120
cttcgaatcg aaggccgacg ctggggcgctc caagacctac ccgcagcagg ctggcacctg 180
ccgtaagaac ggcttcacg tcataagaa ccgtccctgc aaggttgagg aggtttctac 240
ctccaagact ggtaagcatg gccacgcaa atgccacttt gtcgcatag acatattcaa 300
tggaaaaaag cttgaagata ttgttccttc atcacacaac tgtgacattc cgcattgtgaa 360
ccgtactgag tatcagctga ttgatatttc tgaggatgga tttgtgagcc ttcttacttc 420
agatggcaac actaaggatg atcttagact cccaactgat gagactcttg tggcccagat 480
taaggaaggg ttcgaaagcg ggaaggatct tgttgatgact gtccagtcctg cgatggggga 540
ggagcagatc tgcgcgctga aggatggttg ccccaagtaa cttccttggc tttggagacg 600
gaaccctact ctatctcaac ttaaatcgga aaagaagtgt atcaccaaaa ggattgctac 660
cgagacattc acctggcttg agctbgcttt tgctatagcg tgcaaggggt tgctgggtgt 720
cgtacctacc tgacttatca ttatctgtgg ttacattctg gacctgtat tttctatgct 780
ttcatgtctc tctactttct agtattaatt atcaataagt tggtttgga tggttgaatt 840
gcatccaatg catgaagttt ctttggtc

(2) INFORMATION FOR SEQ ID NO:1244:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..192
 (D) OTHER INFORMATION: / Ceres Seq. ID 1597431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244:

Glu Ala Tyr Arg Leu Ser Ser Ala Pro Leu His Phe Phe Ser Leu Cys
1 5 10 15
Ser Ser Ala Ser Ala Ser Xaa Trp Xaa Xaa Ser Lys Thr Gly Ile Ala
 20 25 30
Met Ser Asp Ser Glu Glu His His Phe Glu Ser Lys Ala Asp Ala Gly
 35 40 45
Ala Ser Lys Thr Tyr Pro Gln Gln Ala Gly Thr Val Arg Lys Asn Gly
 50 55 60
Phe Ile Val Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser Thr
65 70 75 80
Ser Lys Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile
 85 90 95
Asp Ile Phe Asn Gly Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His
 100 105 110
Asn Cys Asp Ile Pro His Val Asn Arg Thr Glu Tyr Gln Leu Ile Asp
 115 120 125
Ile Ser Glu Asp Gly Phe Val Ser Leu Leu Thr Ser Asp Gly Asn Thr
 130 135 140
Lys Asp Asp Leu Arg Leu Pro Thr Asp Glu Thr Leu Val Ala Gln Ile
145 150 155 160
Lys Glu Gly Phe Glu Ser Gly Lys Asp Leu Val Val Thr Val Gln Ser
 165 170 175
Ala Met Gly Glu Glu Gln Ile Cys Ala Leu Lys Asp Val Gly Pro Lys
 180 185 190

(2) INFORMATION FOR SEQ ID NO:1245:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 160 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..160
 (D) OTHER INFORMATION: / Ceres Seq. ID 1597432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:

Met Ser Asp Ser Glu His His Phe Glu Ser Lys Ala Asp Ala Gly
1 5 10 15
Ala Ser Lys Thr Tyr Pro Gln Gln Ala Gly Thr Val Arg Lys Asn Gly
 20 25 30
Phe Ile Val Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser Thr
 35 40 45
Ser Lys Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile
 50 55 60
Asp Ile Phe Asn Gly Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His
65 70 75 80
Asn Cys Asp Ile Pro His Val Asn Arg Thr Glu Tyr Gln Leu Ile Asp
 85 90 95
Ile Ser Glu Asp Gly Phe Val Ser Leu Leu Thr Ser Asp Gly Asn Thr
 100 105 110
Lys Asp Asp Leu Arg Leu Pro Thr Asp Glu Thr Leu Val Ala Gln Ile
 115 120 125

09689900 101300

Lys	Glu	Gly	Phe	Glu	Ser	Gly	Lys	Asp	Leu	Val	Val	Thr	Val	Gln	Ser
130						135					140				
Ala	Met	Gly	Glu	Glu	Gln	Ile	Cys	Ala	Leu	Lys	Asp	Val	Gly	Pro	Lys
145					150				155					160	

(2) INFORMATION FOR SEQ ID NO:1246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..239
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:

acagcatctc	aagtcttcac	actcctcgcc	atcacataaa	accagtgcaa	gcagaagcag	60
cgcaatggcg	agcagcacca	tggccctctc	ctccacagcc	ttcgccggca	akgcagtgaa	120
cgtgccgtcg	tctctcwtcg	gcgangcccg	cgtgacgatg	cgcaagangg	cggcgaakgc	180
aaagccggcg	gcgagctccg	gcagcccggtg	gtacggcccc	gamcgcgtgc	tctacctgg	

(2) INFORMATION FOR SEQ ID NO:1247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:

Gln	His	Leu	Lys	Ser	Ser	His	Ser	Ser	Pro	Ser	His	Lys	Thr	Ser	Ala
1			5						10					15	
Ser	Arg	Ser	Ser	Ala	Met	Ala	Ser	Ser	Thr	Met	Ala	Leu	Ser	Ser	Thr
			20						25					30	
Ala	Phe	Ala	Gly	Xaa	Ala	Val	Asn	Val	Pro	Ser	Ser	Leu	Xaa	Gly	Xaa
			35						40					45	
Ala	Arg	Val	Thr	Met	Arg	Lys	Xaa	Ala	Ala	Xaa	Ala	Lys	Pro	Ala	Ala
			50						55					60	
Ser	Ser	Gly	Ser	Pro	Trp	Tyr	Gly	Pro	Xaa	Arg	Val	Leu	Tyr	Leu	
65					70				75						

(2) INFORMATION FOR SEQ ID NO:1248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:

Met	Ala	Ser	Ser	Thr	Met	Ala	Leu	Ser	Ser	Thr	Ala	Phe	Ala	Gly	Xaa
1				5						10				15	
Ala	Val	Asn	Val	Pro	Ser	Ser	Leu	Xaa	Gly	Xaa	Ala	Arg	Val	Thr	Met
				20					25					30	
Arg	Lys	Xaa	Ala	Ala	Xaa	Ala	Lys	Pro	Ala	Ala	Ser	Ser	Gly	Ser	Pro

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..446
 (D) OTHER INFORMATION: / Ceres Seq. ID 1597456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:

aagctcctcg	tcaccagtca	gaaaacagtg	ggatcgagtt	gtttcactgc	acgagcacat	60
cctccggcga	ccaccggcct	ccctctccgt	cctctagcga	ccgaccaacg	cgtcgagcga	120
agatgtcgtg	gcagacgtac	gtggacgagc	aaccctggat	gtgcgagatc	gagggccacc	180
acctcacgtc	ggcggccatc	gtcggccacg	rgcgccacct	gggctcagag	caccgcattc	240
cccgaattca	agcccagagga	gatggctgcc	atcatgaagg	atttcgacga	gccggggcac	300
tcgccccgac	cggcctgata	ctgggaggca	ccaagtacat	ggtcatccaa	gtcgaacctg	360
gagctgtcat	ccgtggcaag	aagggatccg	ggggcatcac	tgtgaagaaa	acagggcagt	420
cactcatcat	tggcatctac	gacgag				

(2) INFORMATION FOR SEQ ID NO:1253:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..105
 (D) OTHER INFORMATION: / Ceres Seq. ID 1597457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:

Lys	Leu	Leu	Val	Thr	Ser	Gln	Lys	Thr	Val	Gly	Ser	Ser	Cys	Phe	Thr
1			5						10					15	
Ala	Arg	Ala	His	Pro	Pro	Ala	Thr	Thr	Gly	Leu	Pro	Leu	Arg	Pro	Leu
			20						25				30		
Ala	Thr	Asp	Gln	Arg	Val	Glu	Arg	Arg	Cys	Arg	Gly	Arg	Arg	Thr	Trp
			35					40					45		
Thr	Ser	Asn	Pro	Gly	Cys	Ala	Arg	Ser	Arg	Ala	Thr	Thr	Ser	Arg	Arg
			50				55					60			
Arg	Pro	Ser	Ser	Ala	Thr	Xaa	Ala	Thr	Trp	Ala	Gln	Ser	Thr	Ala	Phe
			65			70				75				80	
Pro	Glu	Phe	Lys	Pro	Glu	Glu	Met	Ala	Ala	Ile	Met	Lys	Asp	Phe	Asp
			85					90						95	
Glu	Pro	Gly	His	Ser	Pro	Arg	Pro	Ala							
			100					105							

(2) INFORMATION FOR SEQ ID NO:1254:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 148 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..148
 (D) OTHER INFORMATION: / Ceres Seq. ID 1597458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:

Ala	Pro	Arg	His	Gln	Ser	Glu	Asn	Ser	Gly	Ile	Glu	Leu	Phe	His	Cys
1			5						10					15	
Thr	Ser	Thr	Ser	Ser	Gly	Asp	His	Arg	Pro	Pro	Ser	Pro	Ser	Ser	Ser
			20						25				30		
Asp	Arg	Pro	Thr	Arg	Arg	Ala	Lys	Met	Ser	Trp	Gln	Thr	Tyr	Val	Asp
			35				40						45		
Glu	Gln	Pro	Trp	Met	Cys	Glu	Ile	Glu	Gly	His	His	Leu	Thr	Ser	Ala
			50				55				60				

09689930-101300

Ala Ile Val Gly His Xaa Arg His Leu Gly Ser Glu His Arg Ile Pro
65 70 75 80
Arg Val Gln Ala Arg Gly Asp Gly Cys His His Glu Gly Phe Arg Arg
85 90 95
Ala Gly Ala Leu Ala Pro Thr Gly Leu Ile Leu Gly Gly Thr Lys Tyr
100 105 110
Met Val Ile Gln Val Glu Pro Gly Ala Val Ile Arg Gly Lys Lys Gly
115 120 125
Ser Gly Gly Ile Thr Val Lys Lys Thr Gly Gln Ser Leu Ile Ile Gly
130 135 140
Ile Tyr Asp Glu
145

(2) INFORMATION FOR SEQ ID NO:1255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:

Met Ser Trp Gln Thr Tyr Val Asp Glu Gln Pro Trp Met Cys Glu Ile
1 5 10 15
Glu Gly His His Leu Thr Ser Ala Ala Ile Val Gly His Xaa Arg His
20 25 30
Leu Gly Ser Glu His Arg Ile Pro Arg Val Gln Ala Arg Gly Asp Gly
35 40 45
Cys His His Glu Gly Phe Arg Arg Ala Gly Ala Leu Ala Pro Thr Gly
50 55 60
Leu Ile Leu Gly Gly Thr Lys Tyr Met Val Ile Gln Val Glu Pro Gly
65 70 75 80
Ala Val Ile Arg Gly Lys Lys Gly Ser Gly Gly Ile Thr Val Lys Lys
85 90 95
Thr Gly Gln Ser Leu Ile Ile Gly Ile Tyr Asp Glu
100 105

(2) INFORMATION FOR SEQ ID NO:1256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..472
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:

atctcagcag tgacgaactc gaagcttgck ttcttgtagt agaggtcggc agcaagcggg 60
ggtagagcga gaggtcgaga agatgaagag cagcactctg ttggcgatcc tagttctcca 120
ggcccttctg gtctctgcgg ccgtggcaaa ggacctgcag ggccgacgac gaagaagcag 180
tgctggttgc ggcgagtgc ccactgggtc gggcgtgtgg acctgcgacg acctcctcac 240
caagtgcgcc gccacctgca agaactgcgt ccccggtgtcc acggacaagg gggccatcaa 300
gtacaggtgc cgcgacttcc tccccgaaaa ctgcggctgc aagatccact agagactcat 360
ccaattccac catggccgcg cgccacagcg gcacagccga ttggatcctt ccatgttctt 420
ccgtccgtcc gccttgctac aagcaggcag ccacaccaat aagctagctc tt

(2) INFORMATION FOR SEQ ID NO:1257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids

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(2) INFORMATION FOR SEQ ID NO:1260:

(A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..99
(D) OTHER INFORMATION: / Ceres Seq. ID 1597480

[illegible]

```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 85 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
```

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..85
(D) OTHER INFORMATION: / Ceres Seq. ID 1597481

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:
Met Ser Arg Glu Glu Asn Val Tyr Met Ala Lys Leu Ala Glu Gln Ala
1 5 10 15
Glu Arg Tyr Glu Glu Met Val Glu Tyr Met Glu Lys Val Ala Lys Thr
20 25 30
Val Asp Val Glu Glu Leu Thr Val Glu Glu Arg Asn Leu Leu Ser Val
35 40 45
Ala Tyr Lys Asn Val Ile Gly Ala Arg Arg Ala Ser Trp Arg Ile Val
50 55 60
Ser Ser Ile Glu Gln Lys Glu Glu Ser Arg Lys Asn Glu Glu His Val
65 70 75 80
Asn Leu Ile Lys Glu Tyr Arg Gly Lys Ile Glu Ala Glu Leu Ser Asn
85 90 95
Ile Cys Asp Gly Ile Leu Lys Leu Leu Asp Ser His Leu Val Pro Ser
100 105 110
Ser Thr Ala Ala Glu Ser Lys Val Phe Tyr Leu Lys Met
115 120 125

(2) INFORMATION FOR SEQ ID NO:1265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1597485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:

Met Ala Lys Leu Ala Glu Gln Ala Glu Arg Tyr Glu Glu Met Val Glu
1 5 10 15
Tyr Met Glu Lys Val Ala Lys Thr Val Asp Val Glu Glu Leu Thr Val
20 25 30
Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly Ala
35 40 45
Arg Arg Ala Ser Trp Arg Ile Val Ser Ser Ile Glu Gln Lys Glu Glu
50 55 60
Ser Arg Lys Asn Glu Glu His Val Asn Leu Ile Lys Glu Tyr Arg Gly
65 70 75 80
Lys Ile Glu Ala Glu Leu Ser Asn Ile Cys Asp Gly Ile Leu Lys Leu
85 90 95
Leu Asp Ser His Leu Val Pro Ser Ser Thr Ala Ala Glu Ser Lys Val
100 105 110
Phe Tyr Leu Lys Met
115

(2) INFORMATION FOR SEQ ID NO:1266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..401

(D) OTHER INFORMATION: / Ceres Seq. ID 1597499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:

agaaacccta acactcatca cgccgccact gatctgctct gttgctggtg actaggagca	60
gtagcgrnga gggattcttg atggccaagt cgaagaacca cacggcgcat aaccagtcgt	120
tcaaggcgca caagaacggc atcaagaagc ccaagcgcca ccgccagacc tccaccaagg	180
ggatggaccc gaagtttctg aggaacttga ggtactcaar gaagggcaac aagaagagt	240

gcgaggctga gtccgaggag taagatgatg gtgattgagt ttgtggcgac aaatgcatct 300
cttgatcg c taagagtctt agctgtgaac ttagttotca cttctgtgtg actgtgatca 360
aaggacttgt gtatgatcaa aggagatcca tcagttggta c

(2) INFORMATION FOR SEQ ID NO:1267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597500

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

Met Ala Lys Ser Lys Asn His Thr Ala His Asn Gln Ser Phe Lys Ala
1 5 10 15
His Lys Asn Gly Ile Lys Lys Pro Lys Arg His Arg Gln Thr Ser Thr
20 25 30
Lys Gly Met Asp Pro Lys Phe Leu Arg Asn Leu Arg Tyr Ser Xaa Lys
35 40 45
Gly Asn Lys Lys Ser Gly Glu Ala Glu Ser Glu Glu
50 55 60

(2) INFORMATION FOR SEQ ID NO:1268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..456
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:

aaactacacc acaccgcacc ggcaccacca ccaaccgagc ggnnccaggc tcctgtctcag 60
gaaggggaga agaggcgagc cttccttgagg aagtcgcagg aggagagaag gggaacaaag 120
atggggcgcg gcaagatcga gatcaagcgg atcgagaact ccaccaaccg ccagtgcact 180
tctccaagcg ccgcaacggg atctctcaaga aggcgcggga gatcagcgtg cttcgcgacg 240
ccgaggtcgg cgtctcgtct tctccagcgc cggcaaagtg taccgggggt cattggtcga 300
gtgcgaggat aactggaatt gccagctcga gaacataacc ttcactgccg aggatgggaa 360
ggtttcgag ctggagcagc tcttcacacg aggaagcaga gtbagattta tgattatacc 420
tgatatgtc aagaacgctc ccatgttcaa gcgctt

(2) INFORMATION FOR SEQ ID NO:1269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:

Asn Tyr Thr Thr Pro His Arg His His His Gln Pro Ser Xaa Xaa Arg
1 5 10 15
Leu Leu Leu Arg Lys Gly Arg Arg Gly Glu Pro Ser Leu Gly Ser Arg
20 25 30
Arg Arg Arg Glu Gly Glu Gln Arg Trp Gly Ala Ala Arg Ser Arg Ser
35 40 45

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Ser Gly Ser Arg Thr Pro Pro Thr Ala Ser Asp Leu Leu Gln Ala Pro
50 55 60
Gln Arg Asp Pro Gln Glu Gly Ala Gly Asp Gln Arg Ala Leu Arg Arg
65 70 75 80
Arg Gly Arg Arg Leu Val Phe Ser Ser Ala Gly Lys Val Tyr Arg Gly
85 90 95
Ser Leu Val Glu Cys Glu Asp Asn Trp Asn Cys Gln Leu Glu Asn Ile
100 105 110
Thr Phe Thr Ala Lys Asp Gly Lys Val Ser Gln Leu Glu His Val Phe
115 120 125
Ile Arg Gly Ser Arg Xaa Arg Phe Met Ile Ile Pro Asp Met Leu Lys
130 135 140
Asn Ala Pro Met Phe Lys Arg
145 150

(2) INFORMATION FOR SEQ ID NO:1270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:

Thr Thr Pro His Arg Thr Gly Thr Thr Asn Arg Ala Xaa Pro Gly
1 5 10 15
Ser Cys Ser Gly Arg Gly Glu Glu Ala Ser Leu Pro Trp Glu Val Ala
20 25 30
Gly Gly Glu Lys Gly Asn Lys Asp Gly Ala Arg Gln Asp Arg Asp Gln
35 40 45
Ala Asp Arg Glu Leu His Gln Pro Pro Val Thr Phe Ser Lys Arg Arg
50 55 60
Asn Gly Ile Leu Lys Lys Ala Arg Glu Ile Ser Val Leu Cys Asp Ala
65 70 75 80
Glu Val Gly Val Ser Ser Ser Pro Ala Pro Ala Lys Cys Thr Gly Gly
85 90 95
His Trp Ser Ser Ala Arg Ile Thr Gly Ile Ala Ser Ser Arg Thr
100 105 110

(2) INFORMATION FOR SEQ ID NO:1271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..494
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:

atcaactcgc aattccgcat tcgttccaac tccgagcac tttctcctcg tcccagacaa	60
gccaatcgaa gccgagatac gaccatggac tccaccggca ccggagcagg gggtaagggg	120
aagaaggag cggccggcg caaggtcggc gggccaagga agaagtcggt gtcgaggtcc	180
gtgaaggccg gtctccagtt ccccgtcggc cgcctcgggc gctacttgaa gaagggccgc	240
tacgcgcang ttcggcaccg gcgccccgt ctacctgcc gctgtcctcg aatacctcgc	300
cgctgaggtt ctggagctcg ccggtaatgc tgccagggac aaggcgatca agaggtttca	360
ggtkaggaac atcgtggaac aggcggccat caggagcgtc caggaagcat gcgtctatga	420
tggtacgtc ctcccgaagc tgtacgcaa ggtgcaccac tgcgtctcgt gcgcgatcca	480
mgstcacatc gtcc	

00659301 00559360

80

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)

- (A) NAME/KEY: -

- (B) LOCATION: 1..479

- (D) OTHER INFORMATION: / Ceres Seq. ID 1597553

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278:

60
120
180
240
300
360
420

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..64

- (D) OTHER INFORMATION: / Ceres Seq. ID 1597554

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12															
Ile	Phe	Gly	Lys	Ile	Ala	Thr	Gly	Ser	Ser	Gly	Arg	Val	Ser	Pro	Thr
1				5					10					15	
Arg	Ser	Val	Gly	Cys	Ala	Ala	Cys	Cys	Cys	Ile	Val	Ser	Ser	Phe	Lys
			20					25					30		
Arg	Ala	Asn	Ser	Arg	Leu	Gln	Gln	Gly	Arg	Pro	Pro	Pro	Pro	Ile	Ala
			35				40					45			
Ser	Ala	Ile	Leu	Ala	Leu	Ala	Gln	Arg	Pro	Ser	Leu	Arg	Arg	Ala	Arg
			50			55					60				

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- ```
(ix) FEATURE:
```

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..51

- (D) OTHER INFORMATION: / Ceres Seq. ID 1597555

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 1

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ser | Ala | Arg | Leu | Gln | Gln | Gly | Arg | Pro | Val | Ala | Phe | Leu | Leu | Arg |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gly | Pro | Trp | Ala | Val | Leu | Pro | Ala | Val | Ala | Ser | Ser | Pro | Arg | Leu | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

Gly Arg Thr Gln Asp Cys Asn Arg Val Val Arg Arg His Gln Leu Leu  
35 40 45  
Ala Gln Ser  
50

(2) INFORMATION FOR SEQ ID NO:1281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:

Met Ala Ser Phe Ser Glu Ala Pro Pro Gly Asn Pro Thr Ala Gly Glu  
1 5 10 15  
Lys Ile Phe Lys Thr Lys Cys Ala Gln Cys His Thr Val Asp Lys Gly  
20 25 30  
Ala Gly His Lys Gln Gly Pro Asn Leu Asn Gly Leu Phe Gly Arg Gln  
35 40 45  
Ser Gly Thr Thr Pro Gly Tyr Ser Tyr Ser Ser Ala Asn Lys Asn Met  
50 55 60  
Ala Val Ile Trp Glu Glu Asn Thr Leu Tyr Asp Tyr Leu Leu Asn Pro  
65 70 75 80  
Lys Lys Tyr Ile Pro Gly Thr Lys Met Val Phe Pro Gly Leu  
85 90

(2) INFORMATION FOR SEQ ID NO:1282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282:

cnaaaaaagg tacacatcat ctcttccaaa tcccaccagc aaatccccc aa ttcctccgag 60  
ttcgagcgac catgtcgggg cgtggcaagg gcggaaggg tctgggcaaa ggcggc

(2) INFORMATION FOR SEQ ID NO:1283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..38
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:

Xaa Lys Lys Val His Ile Ile Ser Ser Lys Ser His Gln Gln Ile Pro  
1 5 10 15  
Asn Ser Ser Glu Phe Glu Arg Pro Cys Arg Gly Val Ala Arg Ala Gly  
20 25 30  
Arg Val Trp Ala Lys Ala  
35

(2) INFORMATION FOR SEQ ID NO:1284:

00569960 00569960





- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..161  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1597590  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:

Arg Ser His Thr Pro Thr Ser Lys Pro Ser His Leu Phe Pro Ser Ala  
1                  5                  10                  15  
Ala Val Ser Ala Leu Lys Ile Ala Met Ala Ser Glu Lys Lys Gln Ser  
                  20                  25                  30  
Asn Pro Met Arg Glu Ile Lys Val Gln Lys Leu Val Leu Asn Ile Ser  
                  35                  40                  45  
Val Gly Glu Ser Gly Asp Arg Leu Thr Arg Ala Ala Lys Val Leu Glu  
50                  55                  60  
Gln Leu Ser Gly Gln Ser Pro Val Phe Ser Lys Ala Arg Tyr Thr Val  
65                  70                  75                  80  
Arg Ser Phe Gly Ile Arg Arg Asn Glu Lys Ile Ala Cys Tyr Val Thr  
                  85                  90                  95  
Val Arg Gly Glu Lys Ala Met Gln Leu Leu Glu Ser Gly Leu Lys Val  
                  100                 105                 110  
Lys Glu Tyr Glu Leu Leu Arg Arg Asn Phe Ser Asp Thr Gly Cys Phe  
                 115                 120                 125  
Gly Phe Gly Ile Gln Glu His Ile Asp Leu Gly Ile Lys Tyr Asp Pro  
130                 135                 140  
Ser Thr Gly Ile Tyr Xaa Met Asp Phe Tyr Val Val Leu Glu Arg Ala  
145                 150                 155                 160  
Arg

(2) INFORMATION FOR SEQ ID NO:1288:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 137 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..137  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1597591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288:

Met Ala Ser Glu Lys Lys Gln Ser Asn Pro Met Arg Glu Ile Lys Val  
1                  5                  10                  15  
Gln Lys Leu Val Leu Asn Ile Ser Val Gly Glu Ser Gly Asp Arg Leu  
                  20                  25                  30  
Thr Arg Ala Ala Lys Val Leu Glu Gln Leu Ser Gly Gln Ser Pro Val  
                  35                  40                  45  
Phe Ser Lys Ala Arg Tyr Thr Val Arg Ser Phe Gly Ile Arg Arg Asn  
50                  55                  60  
Glu Lys Ile Ala Cys Tyr Val Thr Val Arg Gly Glu Lys Ala Met Gln  
65                  70                  75                  80  
Leu Leu Glu Ser Gly Leu Lys Val Lys Glu Tyr Glu Leu Leu Arg Arg  
                  85                  90                  95  
Asn Phe Ser Asp Thr Gly Cys Phe Gly Phe Gly Ile Gln Glu His Ile  
                 100                 105                 110  
Asp Leu Gly Ile Lys Tyr Asp Pro Ser Thr Gly Ile Tyr Xaa Met Asp  
115                 120                 125  
Phe Tyr Val Val Leu Glu Arg Ala Arg  
130                 135

(2) INFORMATION FOR SEQ ID NO:1289:

- (i) SEQUENCE CHARACTERISTICS:

DOCKET "0866950"

- (A) LENGTH: 127 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..127  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597592  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289:

Met Arg Glu Ile Lys Val Gln Lys Leu Val Leu Asn Ile Ser Val Gly  
1 5 10 15  
Glu Ser Gly Asp Arg Leu Thr Arg Ala Ala Lys Val Leu Glu Gln Leu  
20 25 30  
Ser Gly Gln Ser Pro Val Phe Ser Lys Ala Arg Tyr Thr Val Arg Ser  
35 40 45  
Phe Gly Ile Arg Arg Asn Glu Lys Ile Ala Cys Tyr Val Thr Val Arg  
50 55 60  
Gly Glu Lys Ala Met Gln Leu Leu Glu Ser Gly Leu Lys Val Lys Glu  
65 70 75 80  
Tyr Glu Leu Leu Arg Arg Asn Phe Ser Asp Thr Gly Cys Phe Gly Phe  
85 90 95  
Gly Ile Gln Glu His Ile Asp Leu Gly Ile Lys Tyr Asp Pro Ser Thr  
100 105 110  
Gly Ile Tyr Xaa Met Asp Phe Tyr Val Val Leu Glu Arg Ala Arg  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1290:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 413 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..413  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597600  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290:

accgacggca tttgcatctk agttcctgat tgttgatttc cagtttcttc tgtgagtttt 60  
gtgggatcgc gaggwagaac tagaaggatg tcgtgctgcg gaggcaactg cgggtkcggc 120  
gccggctgca agtgccggcac ggctgcggag ggtgcaagat gtaccggac atggctgagc 180  
aggtgaccac cactaccag actctcatca tgggtgttgc accgtccaag ggcgggttcg 240  
aggcgccgc gangctgaga acggcgggtg caagtkcggc gccaaactgca cctgcgaccc 300  
ctgcacctgc aagtgagacg acggcgatga cgctkcagg cgtcaattgg gatcggaagg 360  
actcttttat ctttaagctct agtataatat tctagcagtg tcgtytgtgt ttt

(2) INFORMATION FOR SEQ ID NO:1291:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 61 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..61  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597601  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:

Thr Asp Gly Ile Cys Ile Xaa Val Pro Asp Cys Cys Ile Pro Val Ser  
1 5 10 15  
Ser Val Ser Phe Val Gly Ser Arg Xaa Arg Thr Arg Arg Met Ser Cys  
20 25 30

005593010300







(2) INFORMATION FOR SEQ ID NO:1300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:

Ser Thr Arg Asn Ser Ala Phe Val Pro Thr Pro Glu His Phe Leu Leu  
1 5 10 15  
Val Pro Asp Lys Pro Ile Glu Ala Glu Ile Arg Pro Trp Thr Pro Pro  
20 25 30  
Ala Pro Glu Gln Gly Val Arg Gly Arg Arg Glu Arg Pro Gly Ala Arg  
35 40 45  
Ser Ala Gly Gln Gly Arg Ser Arg Cys Arg Gly Pro  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:

Met Asp Ser Thr Gly Thr Gly Ala Gly Gly Lys Gly Lys Lys Gly Ala  
1 5 10 15  
Ala Gly Arg Lys Val Gly Gly Pro Arg Lys Lys Ser Val Ser Arg Ser  
20 25 30  
Val Lys Ala Gly Leu Gln Phe Pro Val Gly Arg Ile Gly Arg Tyr Xaa  
35 40 45  
Lys Lys Gly Arg Tyr Ala Xaa Val Arg His Arg Arg Pro Arg Leu Pro  
50 55 60  
Arg Arg Cys Pro Arg Ile Pro Arg Arg  
65 70

(2) INFORMATION FOR SEQ ID NO:1302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..470
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302:

|           |          |          |          |           |          |          |         |     |
|-----------|----------|----------|----------|-----------|----------|----------|---------|-----|
| aacaatgcc | attgccag | caacccat | ccatcttc | agctgtg   | atgataca | aaagaga  | ga      | 60  |
| gagaatgg  | cg       | gavaaccc | ag       | agtgagtg  | tcctatt  | act      | caaaaga | 120 |
| agtgccaa  | ag       | ttcaccg  | aaa      | tcctcccg  | t        | ggaggac  | acg     | 180 |
| atcacctc  | cg       | tcgggaa  | aga      | agtgatcaa | aa       | tactgcac | ca      | 240 |
| cccggtgc  | tgc      | cgctggag | aa       | gaatgtccc | c        | gagctctg | gt      | 300 |
| aagaccag  | gt       | ccatcacg | ct       | cgccatac  | gt       | atggaca  | acc     | 360 |
| acccccgg  | cg       | gtgtggtg | gg       | agttcgga  | caa      | ggacggcg | ac      | 420 |

(2) INFORMATION FOR SEQ ID NO:1303:

- [illegible]

- [illegible]

- (A1) SEQUENCE DESCRIPTION: Seq ID NO:1000:
- |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Pro | Ser | Ser | Gly | Ser | Thr | Pro | Ser | Ser | Lys | Arg | Arg | Pro | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Ser | Arg | Ser | Pro | Tyr | Val | Trp | Thr | Thr | Ser | Thr | Trp | Ser | Ala | Ser |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |

(2) INFORMATION FOR SEO ID NO:1306:

(D) OTHER INFORMATION: / Ceres Seq. ID 1597658

(2) INFORMATION FOR SEQ ID NO:1307:

(D) OTHER INFORMATION: / Ceres Seq. ID 1597659

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Lys | Glu | Ile | His | Lys | Ala | Ile | Leu | Ala | Ser | Pro | Tyr | Gln | Ser | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Pro | Glu | Thr | Leu | Leu | Gln | Ser | Thr | Glu | Phe | Cys | Leu | Leu | Arg | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Glu | Leu | Glu | Ser | Thr | Met | Ser | Leu | Val | Arg | Arg | Xaa | Thr | Cys | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Thr | Pro | Ser | Pro | Trp | Thr | Ser | Gly | Thr | Pro | Ser | Thr | Pro | Cys | Ser | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Pro | Ser | Ser | Arg | Arg | Arg | Pro | Pro | Pro | Thr | Pro | Arg | Leu | Pro | Pro | Ser |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Ala | Pro | Ala | Ser | Thr | Gly | Arg | Arg | Arg | Pro | Arg | Arg | Thr | Cys | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Arg | Pro | Thr | Ser | Pro | Ala | Ser | Arg | Arg | Lys | Arg | Ser | Arg | Ser | Arg | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Thr | Ala | Thr | Cys | Trp | Ser | Ser | Ala | Ala | Ser |     |     |     |     |     |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1308:

(ix) FEATURE:

[illegible]







tctgggaggg aaactttggt tcggatcact ggtggcatga aggttaaggc tgatcgtgat 300  
gagtcgtctc cttatgctgc tatgcttgct gcccaagatg ttgcacagcg ttgcaaggag 360  
ctcggatatca cagcgtgca cattaagctt cgtgccactg g

(2) INFORMATION FOR SEQ ID NO:1315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:

Met Ser Arg Arg Lys Thr Arg Glu Pro Lys Glu Glu Asn Val Thr Leu  
1 5 10 15  
Gly Pro Thr Val Arg Glu Gly Glu Phe Xaa Phe Gly Val Ala His Ile  
20 25 30  
Phe Ala Ser Phe Asn Asp Thr Phe Ile His Val Thr Asp Leu Ser Gly  
35 40 45  
Arg Glu Thr Leu Val Arg Ile Thr Gly Gly Met Lys Val Lys Ala Asp  
50 55 60  
Arg Asp Glu Ser Ser Pro Tyr Ala Ala Met Leu Ala Ala Gln Asp Val  
65 70 75 80  
Ala Gln Arg Cys Lys Glu Leu Gly Ile Thr Ala Leu His Ile Lys Leu  
85 90 95  
Arg Ala Thr

(2) INFORMATION FOR SEQ ID NO:1316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..399
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:

catcaatagc cagttctaatt ctcagggttrg gggaaatagg cctcgcggggt cgcaaaccgc 60  
tctctgctga ttttrggattt cggaggcgct cgagttttca ggtaaactat agtttagtga 120  
cccatggctc gtactaagca aactgctcgc aagtccactg gagggaaggc tccwaggaaa 180  
caacttgcca ccaaggctgc ccgtaagtct gcacctacaa ctgggggagt aaagaagcct 240  
caccggtacc gccctggaac tggttgctctt cgtgaaatcc gcaagtatca gaagagcact 300  
gacctgctca taaggaagct tccgttccaa aggcttgtca gggagattkc ccaggatttc 360  
aagactgata ttcgtttcca gagccatgcg gtgcttgcg

(2) INFORMATION FOR SEQ ID NO:1317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:

Met Ala Arg Thr Lys Gln Thr Ala Arg Lys Ser Thr Gly Gly Lys Ala

09589980 101300



130 135 140  
Lys Gln Ile Ala Lys Phe Val Val Gly Leu Gly Asp Lys Val Ser Pro  
145 150 155 160  
Thr Asp Ile Glu

(2) INFORMATION FOR SEQ ID NO:1320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:

Met Asn Glu Lys Asn Pro Arg Pro Leu Asp Glu Asp Xaa Ile Ala Leu  
1 5 10 15  
Leu Lys Thr Tyr Gly Leu Gly Pro Tyr Ser Thr Ser Ile Lys Lys Val  
20 25 30  
Glu Lys Glu Ile Lys Glu Met Ala Lys Lys Ile Asn Asp Leu Cys Gly  
35 40 45  
Ile Lys Glu Ser Asp Thr Gly Leu Ala Pro Pro Ser Gln Trp Asp Leu  
50 55 60  
Val Ser Asp Lys Gln Met Met Gln Glu Glu Gln Pro Leu Gln Val Ala  
65 70 75 80  
Arg Cys Thr Lys Ile Ile Ser Pro Asn Thr Asp Asp Ala Lys Tyr Val  
85 90 95  
Ile Asn Xaa Lys Gln Ile Ala Lys Phe Val Val Gly Leu Gly Asp Lys  
100 105 110  
Val Ser Pro Thr Asp Ile Glu  
115

(2) INFORMATION FOR SEQ ID NO:1321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..425
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:

caatgagttg aggagagtgg aacatgttga ccattctaga aagtytgcag agcargctgt 60  
aaaggcgatc aagggcaaag agtcgggtga accagttccg gagtatgact acctgccata 120  
cttctactcc cgatcattcg acctggcggtg gcaattctac ggcgacaacg tgggcgaaac 180  
tattctgttt ggcgacagtg accccacctc cagcaagccc aagttcggct cgtactggat 240  
caaggacggc aaggtcttgg ggccttctc ggagggcggg tcaccggacg agaacaaggc 300  
cattgccaaag gtggcgaaaa ccagccgcc ggctcgtaac ctcgaggagc tcaagaaggm 360  
tggcctccag ttgccagca agatctgaga cgstcccggt ccatgtaaat ttccgtgtca 420  
tcgtg

(2) INFORMATION FOR SEQ ID NO:1322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..128  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597733

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Glu | Leu | Arg | Arg | Val | Glu | His | Val | Asp | His | Ser | Arg | Lys | Xaa | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Xaa | Ala | Val | Lys | Ala | Ile | Lys | Gly | Lys | Glu | Ser | Gly | Glu | Pro | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Glu | Tyr | Asp | Tyr | Leu | Pro | Tyr | Phe | Tyr | Ser | Arg | Ser | Phe | Asp | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Trp | Gln | Phe | Tyr | Gly | Asp | Asn | Val | Gly | Glu | Thr | Ile | Leu | Phe | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Ser | Asp | Pro | Thr | Ser | Ser | Lys | Pro | Lys | Phe | Gly | Ser | Tyr | Trp | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Asp | Gly | Lys | Val | Leu | Gly | Ala | Phe | Leu | Glu | Gly | Gly | Ser | Pro | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Asn | Lys | Ala | Ile | Ala | Lys | Val | Ala | Lys | Thr | Gln | Pro | Pro | Val | Ala |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Leu | Glu | Leu | Lys | Lys | Xaa | Gly | Leu | Gln | Phe | Ala | Ser | Lys | Ile |     |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1323:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1597734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Thr | Cys | His | Thr | Ser | Thr | Pro | Asp | His | Ser | Thr | Trp | Arg | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Ser | Thr | Ala | Thr | Thr | Trp | Ala | Lys | Leu | Ser | Cys | Leu | Ala | Thr | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Pro | Pro | Pro | Ala | Ser | Pro | Ser | Ser | Ala | Arg | Thr | Gly | Ser | Arg | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Arg | Ser | Trp | Ala | Pro | Ser | Trp | Arg | Ala | Gly | His | Arg | Thr | Arg | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Pro | Leu | Pro | Arg | Trp | Arg | Lys | Pro | Ser | Arg | Arg | Ser | Leu | Thr | Ser |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Ser | Ser | Arg | Arg | Xaa | Ala | Ser | Ser | Ser | Pro | Ala | Arg | Ser | Glu | Thr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Xaa | Pro | Phe | His | Val | Asn | Phe | Arg | Val | Ile | Val |     |     |     |     |     |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1324:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 430 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..430

(D) OTHER INFORMATION: / Ceres Seq. ID 1597741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324:

ataaaaccct actaaccgcg tctctctctcc agcgcccgcc gtcgcccgcg ccctctcttt

ggccccgccg tccgtcgagg tcatcatggt gagggtcagt gtgctcaacg atgcgctcaa 120  
gtccatgtac aatgcagaga agagggggcaa gaggcaggtc atgatacaggc cgtcgtccaa 180  
ggtgatcatc aagttcctga cggatcatga gcgtcatgga tacattggcg agttcgagta 240  
cgtggatgac cacagagctg ggaagattgt ggtggaactg aacggcagac taaacaaatg 300  
cgggtgtaatt agccccggt ttgatgttgg ggtaaaggaa atcgaaggct ggactgcgag 360  
gctgcttccg tctcgccagt ttggctatat cgtgcttaca acctctgcgg gaattatgga 420  
tcacgaggag

(2) INFORMATION FOR SEQ ID NO:1325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:

Met Val Arg Val Ser Val Leu Asn Asp Ala Leu Lys Ser Met Tyr Asn  
1 5 10 15  
Ala Glu Lys Arg Gly Lys Arg Gln Val Met Ile Arg Pro Ser Ser Lys  
20 25 30  
Val Ile Ile Lys Phe Leu Thr Val Met Gln Arg His Gly Tyr Ile Gly  
35 40 45  
Glu Phe Glu Tyr Val Asp Asp His Arg Ala Gly Lys Ile Val Val Glu  
50 55 60  
Leu Asn Gly Arg Leu Asn Lys Cys Gly Val Ile Ser Pro Arg Phe Asp  
65 70 75 80  
Val Gly Val Lys Glu Ile Glu Gly Trp Thr Ala Arg Leu Leu Pro Ser  
85 90 95  
Arg Gln Phe Gly Tyr Ile Val Leu Thr Thr Ser Ala Gly Ile Met Asp  
100 105 110  
His Glu Glu  
115

(2) INFORMATION FOR SEQ ID NO:1326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597743

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:

Met Tyr Asn Ala Glu Lys Arg Gly Lys Arg Gln Val Met Ile Arg Pro  
1 5 10 15  
Ser Ser Lys Val Ile Ile Lys Phe Leu Thr Val Met Gln Arg His Gly  
20 25 30  
Tyr Ile Gly Glu Phe Glu Tyr Val Asp Asp His Arg Ala Gly Lys Ile  
35 40 45  
Val Val Glu Leu Asn Gly Arg Leu Asn Lys Cys Gly Val Ile Ser Pro  
50 55 60  
Arg Phe Asp Val Gly Val Lys Glu Ile Glu Gly Trp Thr Ala Arg Leu  
65 70 75 80  
Leu Pro Ser Arg Gln Phe Gly Tyr Ile Val Leu Thr Thr Ser Ala Gly  
85 90 95  
Ile Met Asp His Glu Glu  
100

00669900 "101300





(2) INFORMATION FOR SEQ ID NO:1330:

(A) LENGTH: 92 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: pep

(ix) FEATURE:

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1597747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330:

(2) INFORMATION FOR SEQ ID NO:1331:

(A) LENGTH: 456 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..456

(D) OTHER INFORMATION: / Ceres Seq. ID 1597748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331:

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:1001 |             |            |            |            |            |     |
|-------------------------------------------|-------------|------------|------------|------------|------------|-----|
| ctctagaacc                                | ctagcgcbbc  | gcccgctcgt | ccgcgcgcgc | agcgcgccat | gcacggccat | 60  |
| gggtatcgat                                | ctcgtagccg  | gcggcgccaa | caagaakacc | aagcgcacgg | cgcccaagtc | 120 |
| cgacgatgtc                                | tacctcaagc  | tctctgcgtc | gctctaccgc | ttccttgtgc | gcaggacaaa | 180 |
| gagcaacttc                                | aacgcggtga  | tcctcaagcg | cctcttcctg | agcaagacca | accgcccgcc | 240 |
| gctctcggat                                | gcgcgcgcctc | gtcagggttc | tggaggggaa | gggtgatcag | atcgccgtga | 300 |
| ttgtgggcac                                | cgtgaccgac  | gacaagagga | tcagcgaggt | gccggcgatg | aaggtctgcg | 360 |
| cgctcgggtt                                | cactgagaca  | gcgagggcca | ggatcatcaa | tgctggcgga | gagtgcctca | 420 |
| ccttcgacca                                | gctcgcgctc  | cgtgccccac | ttgggc     |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1332:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

[illegible]

(D) OTHER INFORMATION: / Ceres Seq. ID 1597749

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO: 1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser                                     | Arg | Thr | Leu |     | Xaa | Arg | Pro | Ser |     | Arg | Arg | Arg | Ser | Arg | His |  |
| 1                                       |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Arg                                     | Thr | Ala | Met | Gly | Ile | Asp | Leu | Val | Ala | Gly | Gly | Arg | Asn | Lys | Xaa |  |
|                                         |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Thr                                     | Lys | Arg | Thr | Ala | Pro | Lys | Ser | Asp | Asp | Val | Tyr | Leu | Lys | Leu | Leu |  |
|                                         |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val                                     | Lys | Leu | Tyr | Arg | Phe | Leu | Val | Arg | Arg | Thr | Lys | Ser | Asn | Phe | Asn |  |
|                                         |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ala                                     | Val | Ile | Leu | Lys | Arg | Leu | Phe | Met | Ser | Lys | Thr | Asn | Arg | Pro | Pro |  |
|                                         |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Leu                                     | Ser | Asp | Ala | Pro | Pro | Arg | Gln | Val | His | Gly | Gly | Glu | Gly |     |     |  |
|                                         |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |  |

(D) OTHER INFORMATION: / Ceres Seq. ID 1597750

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ile | Asp | Leu | Val | Ala | Gly | Gly | Arg | Asn | Lys | Xaa | Thr | Lys | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Ala | Pro | Lys | Ser | Asp | Asp | Val | Tyr | Leu | Lys | Leu | Leu | Val | Lys | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Arg | Phe | Leu | Val | Arg | Arg | Thr | Lys | Ser | Asn | Phe | Asn | Ala | Val | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Lys | Arg | Leu | Phe | Met | Ser | Lys | Thr | Asn | Arg | Pro | Pro | Leu | Ser | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Pro | Pro | Arg | Gln | Val | His | Gly | Gly | Glu | Gly |     |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     |     |

(D) OTHER INFORMATION: / Ceres Seq. ID 1597751

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..294  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335:

| (X1) SEQUENCE DESCRIPTION: SEQ 1: 101-1000: |             |            |            |            |            |  |  |  |  |     |
|---------------------------------------------|-------------|------------|------------|------------|------------|--|--|--|--|-----|
| gtgtgttttgt                                 | tctttgcggaa | acgagacgag | actaggcgac | gcgasgtyag | ggagtcgagg |  |  |  |  | 60  |
| aggatcgggg                                  | ctcaggcaag  | atgaacagga | agccaggaga | ctgggactgc | agggcggtgc |  |  |  |  | 120 |
| ancactcaa                                   | cttcagcgc   | cgagacatat | gccagckctg | tagcgagcca | cgtggagttg |  |  |  |  | 180 |
| ctgactcgtg                                  | cagtggcgc   | ggcggaggag | gaggaggagg | cgactacgca | acgtttcggt |  |  |  |  | 240 |
| gqccgcgqgt                                  | gctctctctt  | cggcggcggc | tttgggcgt  | gctggctctg | acgt       |  |  |  |  |     |

(2) INFORMATION FOR SEQ ID NO:1336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..53  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..71  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1338:

(i) SEQUENCE CHARACTERISTICS:

| Socio-demographic characteristics |              | Health status |            | Healthcare utilization     |               | Healthcare expenditure |               |
|-----------------------------------|--------------|---------------|------------|----------------------------|---------------|------------------------|---------------|
| Variable                          | Mean (SD)    | Variable      | Mean (SD)  | Variable                   | Mean (SD)     | Variable               | Mean (SD)     |
| Age (years)                       | 65.2 (10.5)  | Gender        | Male       | Number of visits           | 1.2 (0.8)     | Outpatient expenditure | 150.0 (100.0) |
| Gender                            | Male         | Female        | Female     | Inpatient expenditure      | 250.0 (150.0) | Total expenditure      | 400.0 (250.0) |
| Marital status                    | Married      | Single        | Single     | Number of hospitalizations | 0.5 (0.5)     | Outpatient expenditure | 150.0 (100.0) |
| Education level                   | High school  | College       | College    | Inpatient expenditure      | 250.0 (150.0) | Total expenditure      | 400.0 (250.0) |
| Income level                      | Low          | High          | High       | Number of hospitalizations | 0.5 (0.5)     | Outpatient expenditure | 150.0 (100.0) |
| Health insurance                  | Medicare     | Medicaid      | Medicaid   | Inpatient expenditure      | 250.0 (150.0) | Total expenditure      | 400.0 (250.0) |
| Chronic conditions                | Hypertension | Diabetes      | Diabetes   | Number of hospitalizations | 0.5 (0.5)     | Outpatient expenditure | 150.0 (100.0) |
| Current smoking                   | Yes          | No            | No         | Inpatient expenditure      | 250.0 (150.0) | Total expenditure      | 400.0 (250.0) |
| Alcohol consumption               | Regular      | Occasional    | Occasional | Number of hospitalizations | 0.5 (0.5)     | Outpatient expenditure | 150.0 (100.0) |
| Physical activity                 | Low          | High          | High       | Inpatient expenditure      | 250.0 (150.0) | Total expenditure      | 400.0 (250.0) |
| Family size                       | Small        | Large         | Large      | Number of hospitalizations | 0.5 (0.5)     | Outpatient expenditure | 150.0 (100.0) |
| Proximity to healthcare           | Close        | Far           | Far        | Inpatient expenditure      | 250.0 (150.0) | Total expenditure      | 400.0 (250.0) |
| Health literacy                   | Low          | High          | High       | Number of hospitalizations | 0.5 (0.5)     | Outpatient expenditure | 150.0 (100.0) |
| Health beliefs                    | Preventive   | Curative      | Curative   | Inpatient expenditure      | 250.0 (150.0) | Total expenditure      | 400.0 (250.0) |
| Health behaviors                  | Healthy      | Unhealthy     | Unhealthy  | Number of hospitalizations | 0.5 (0.5)     | Outpatient expenditure | 150.0 (100.0) |
| Health status                     | Good         | Fair          | Fair       | Inpatient expenditure      | 250.0 (150.0) | Total expenditure      | 400.0 (250.0) |
| Healthcare utilization            | High         | Low           | Low        | Number of hospitalizations | 0.5 (0.5)     | Outpatient expenditure | 150.0 (100.0) |
| Healthcare expenditure            | High         | Low           | Low        | Inpatient expenditure      | 250.0 (150.0) | Total expenditure      | 400.0 (250.0) |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Glu | Lys | Lys | Gln | Ser | Asn | Pro | Met | Arg | Glu | Ile | Lys | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gln | Lys | Leu | Val | Leu | Asn | Ile | Ser | Val | Gly | Arg | Ala | Ala | Thr | Ala | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ala | Pro | Pro | Arg | Cys | Trp | Ser | Ser | Ser | Ala | Pro | Asp | Pro | Arg | Leu |

35 40 45  
Leu Gln Gly Glu Val His Gly Ala Leu Val Arg His Pro Ala  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:

Met Arg Glu Ile Lys Val Gln Lys Leu Val Leu Asn Ile Ser Val Gly  
1 5 10 15  
Arg Ala Ala Thr Ala Ser Pro Ala Pro Arg Cys Trp Ser Ser Ser  
20 25 30  
Ala Pro Asp Pro Arg Leu Leu Gln Gly Glu Val His Gly Ala Leu Val  
35 40 45  
Arg His Pro Ala  
50

(2) INFORMATION FOR SEQ ID NO:1342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..422
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:

atcgccccgc gaaccctagc tcccgcaact gccgccgcca ctcccacgct cgcagccatg 60  
ccgcccgaagc tcgacccgctc gcaggtggtg gaggtgttcg tccgtgtgac cggcggcgag 120  
gtcggcgcac gtcttcgctg gcccccaaga tcggcccgtc cgggtctttcc cccaagaaga 180  
tcggagagga catcgccaag gagacggcca aggactggaa gggcctcgc gtcaccgtca 240  
agctcaccgt ccagaaccgg cagccaaggt ctccgtcgtc cctcgcgcg cggcgctcgt 300  
catcaaggcg ctcaaggagc cagagagga ccgcaagaag gtcaagaaca tcaagcacag 360  
cgncaacatc agcctcgacg acgtcatcga gatcgccagg accatgaggc acaggtccat 420  
gg

(2) INFORMATION FOR SEQ ID NO:1343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343:

Ile Ala Pro Arg Thr Leu Ala Pro Ala Thr Ala Ala Thr Pro Thr  
1 5 10 15  
Leu Ala Ala Met Pro Pro Lys Leu Asp Pro Ser Gln Val Val Glu Val  
20 25 30  
Phe Val Arg Val Thr Gly Gly Glu Val Gly Ala Arg Leu Arg Trp Pro  
35 40 45

00669900

(2) INFORMATION FOR SEQ ID NO:1344:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1597799

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1597800

| (xi) SEQUENCE DESCRIPTION: SH1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|--------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met                            | Pro | Pro | Lys | Leu | Asp | Pro | Ser | Gln | Val | Val | Glu | Val | Phe | Val | Arg |
| 1                              |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val                            | Thr | Gly | Gly | Glu | Val | Gly | Ala | Arg | Leu | Arg | Trp | Pro | Pro | Arg | Ser |
|                                |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala                            | Arg | Ser | Val | Phe | Pro | Pro | Arg | Arg | Ser | Glu | Arg | Thr | Ser | Pro | Arg |
|                                |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg                            | Arg | Pro | Arg | Thr | Gly | Arg | Ala | Ser | Ala | Ser | Pro | Ser | Ser | Ser | Pro |

50 55 60  
Ser Arg Thr Gly Ser Gln Gly Leu Arg Arg Pro Leu Arg Arg Gly Ala  
65 70 75 80  
Arg His Gln Gly Ala Gln Gly Ala Arg Glu Gly Pro Gln Glu Gly Gln  
85 90 95  
Glu His Gln Ala Gln Xaa Gln His Gln Pro Arg Arg Arg His Arg Asp  
100 105 110  
Arg Gln Asp His Glu Ala Gln Val His  
115 120

(2) INFORMATION FOR SEQ ID NO:1346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..483
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346:

aaaaccctag ccgcctgcyt ctctctctcc agagctcgtc gccaccggcc accgccaccc 60  
tcgatcacgc cgtccgtcga ggtaagggtca gcatgggtgag ggtcagtgtg ctcaacgatg 120  
cgctcaagtc catgtacaac gctgagaaga tcggcaagag gcagggtcatg atcaggccgt 180  
cgtccaaggt catcatcaag ttcttgacgg tcatgcagcg ccacgggtac attggagagt 240  
tcgagtacgt tgatgaccac cgatcgggca agatcgtggt cgaactcaac gggaggctga 300  
acaagtgcgg cgtcatcagc cctcgctttg atatcggcgt gaaagacatt gagggatgga 360  
ctgcaagctg ctcccggtcca ggcagttcgg atacatcgtc ctcaacaactt cggcaggcat 420  
catggaccac gaggaggccc gccggaagag cgtaggaggc aaggttctag gtttcttcta 480  
ttg

(2) INFORMATION FOR SEQ ID NO:1347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347:

Asn Pro Ser Arg Leu Xaa Leu Leu Leu Ser Ser Ser Pro Pro Ala  
1 5 10 15  
Thr Ala Thr Leu Asp His Ala Val Arg Arg Gly Lys Val Ser Met Val  
20 25 30  
Arg Val Ser Val Leu Asn Asp Ala Leu Lys Ser Met Tyr Asn Ala Glu  
35 40 45  
Lys Ile Gly Lys Arg Gln Val Met Ile Arg Pro Ser Ser Lys Val Ile  
50 55 60  
Ile Lys Phe Leu Thr Val Met Gln Arg His Gly Tyr Ile Gly Glu Phe  
65 70 75 80  
Glu Tyr Val Asp Asp His Arg Ser Gly Lys Ile Val Val Glu Leu Asn  
85 90 95  
Gly Arg Leu Asn Lys Cys Gly Val Ile Ser Pro Arg Phe Asp Ile Gly  
100 105 110  
Val Lys Asp Ile Glu Gly Trp Thr Ala Ser Cys Ser Arg Pro Gly Ser  
115 120 125  
Ser Asp Thr Ser Ser Ser Gln Leu Arg Gln Ala Ser Trp Thr Thr Arg  
130 135 140  
Arg Pro Ala Gly Arg Ala

145

150

(2) INFORMATION FOR SEQ ID NO:1348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Val | Arg | Val | Ser | Val | Leu | Asn | Asp | Ala | Leu | Lys | Ser | Met | Tyr | Asn |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ala | Glu | Lys | Ile | Gly | Lys | Arg | Gln | Val | Met | Ile | Arg | Pro | Ser | Ser | Lys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Ile | Ile | Lys | Phe | Leu | Thr | Val | Met | Gln | Arg | His | Gly | Tyr | Ile | Gly |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Glu | Phe | Glu | Tyr | Val | Asp | Asp | His | Arg | Ser | Gly | Lys | Ile | Val | Val | Glu |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Leu | Asn | Gly | Arg | Leu | Asn | Lys | Cys | Gly | Val | Ile | Ser | Pro | Arg | Phe | Asp |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Ile | Gly | Val | Lys | Asp | Ile | Glu | Gly | Trp | Thr | Ala | Ser | Cys | Ser | Arg | Pro |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Gly | Ser | Ser | Asp | Thr | Ser | Ser | Ser | Gln | Leu | Arg | Gln | Ala | Ser | Trp | Thr |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |
| Thr | Arg | Arg | Pro | Ala | Gly | Arg | Ala |     |     |     |     |     |     |     |     |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Tyr | Asn | Ala | Glu | Lys | Ile | Gly | Lys | Arg | Gln | Val | Met | Ile | Arg | Pro |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser | Ser | Lys | Val | Ile | Ile | Lys | Phe | Leu | Thr | Val | Met | Gln | Arg | His | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Tyr | Ile | Gly | Glu | Phe | Glu | Tyr | Val | Asp | Asp | His | Arg | Ser | Gly | Lys | Ile |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Val | Glu | Leu | Asn | Gly | Arg | Leu | Asn | Lys | Cys | Gly | Val | Ile | Ser | Pro |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Arg | Phe | Asp | Ile | Gly | Val | Lys | Asp | Ile | Glu | Gly | Trp | Thr | Ala | Ser | Cys |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Ser | Arg | Pro | Gly | Ser | Ser | Asp | Thr | Ser | Ser | Ser | Gln | Leu | Arg | Gln | Ala |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Ser | Trp | Thr | Thr | Arg | Arg | Pro | Ala | Gly | Arg | Ala |     |     |     |     |     |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

00669980-101300







(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..69  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356:  
Met Val Arg His Pro His His Gly Arg His Pro His Arg His Leu  
1 5 10 15  
Pro Arg Pro Glu Pro His Gln Gly Gly His Gln Gly Leu Pro Leu Gln  
20 25 30  
Asp Glu Val Cys Leu Arg Pro Phe Pro His Gln Arg Val His His Gln  
35 40 45  
Leu Gln His Arg His Arg Asp Lys Glu Leu Pro Arg Arg Glu Glu Gly  
50 55 60  
Gln Lys Gly Gly His  
65

(2) INFORMATION FOR SEQ ID NO:1357:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 472 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..472  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357:

actcgagcct gacccttacg ccttcgctcg cgccgccgcc gccgccgccg ctacgccccg 60  
cacctcgctt catttcgtgt cgccaagatg acgaagcgca ctaagaaggc aggaattggt 120  
ggcaaatatg gaaccaggta tgggtgctagc ttgcgtaasa aattcaagaa gatggaggta 180  
tctcagcatt ccaagtactt ttgcgagttc tgtgggaagt ttgctgtgaa gaggaaagca 240  
gttggaattt ggggggtgcaa ggactgtggg aaggtgaagg ctggtggtgc ttacaccatg 300  
aacactgcta gtgcggtcac cgtcagagca cgatccgccg cctgagggag ctgagcggag 360  
agttatggta cgggtgtgtat ccgaccagtc tctgtgtgtt tnggggggtca acatcgtgtc 420  
tcttttggtt ttggttcata atatcagtta gttatctatc agtgtttgtt cg

(2) INFORMATION FOR SEQ ID NO:1358:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 85 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..85  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358:

Met Thr Lys Arg Thr Lys Lys Ala Gly Ile Val Gly Lys Tyr Gly Thr  
1 5 10 15  
Arg Tyr Gly Ala Ser Leu Arg Xaa Lys Phe Lys Lys Met Glu Val Ser  
20 25 30  
Gln His Ser Lys Tyr Phe Cys Glu Phe Cys Gly Lys Phe Ala Val Lys  
35 40 45  
Arg Lys Ala Val Gly Ile Trp Gly Cys Lys Asp Cys Gly Lys Val Lys  
50 55 60  
Ala Gly Gly Ala Tyr Thr Met Asn Thr Ala Ser Ala Val Thr Val Arg  
65 70 75 80  
Ala Arg Ser Ala Ala  
85

00689930-10100







(A) NAME/KEY: -

(B) LOCATION: 1..482

(D) OTHER INFORMATION: / Ceres Seq. ID 1597848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| awaggacccc | ggccacactg | gaagccggag | agaatcgagc | agagccaccg | atcgctcctg | 60  |
| agcactttcc | acattccagt | tccactccgc | ctccgctgcc | ggtcgccgtc | tccgagactc | 120 |
| cgacagtccg | accgcaagaa | ggatgagtga | agaggataag | actgctgctt | ctctgagca  | 180 |
| gccgaagagg | gcccctaagc | tcaatgaaag | gacccctctt | tctctgtcca | ggaggccggt | 240 |
| agctgctcat | ccatggcatg | atcttgagat | cggtcctgat | gctcctgctg | ttttcaatgt | 300 |
| tggtgttgag | atcacaaagg | gaagcaaagt | taaatatgag | cttgacaaga | aaactggact | 360 |
| gattaagggt | gatcgagtcc | tgtactcatc | agttgtatac | cctcacaatt | atggtttcgt | 420 |
| tccaaggact | ctttgtgaag | acaatgacct | aatggatgtg | ttagtcctga | tgcaggagcc | 480 |

tg

(2) INFORMATION FOR SEQ ID NO:1368:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1597849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Glu | Glu | Asp | Lys | Thr | Ala | Ala | Ser | Xaa | Glu | Gln | Pro | Lys | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Pro | Lys | Leu | Asn | Glu | Arg | Ile | Leu | Ser | Ser | Leu | Ser | Arg | Arg | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Ala | Ala | His | Pro | Trp | His | Asp | Leu | Glu | Ile | Gly | Pro | Asp | Ala | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Val | Phe | Asn | Val | Val | Val | Glu | Ile | Thr | Lys | Gly | Ser | Lys | Val | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Glu | Leu | Asp | Lys | Lys | Thr | Gly | Leu | Ile | Lys | Val | Asp | Arg | Val | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Tyr | Ser | Ser | Val | Val | Tyr | Pro | His | Asn | Tyr | Gly | Phe | Val | Pro | Arg | Thr |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Cys | Glu | Asp | Asn | Asp | Pro | Met | Asp | Val | Leu | Val | Leu | Met | Gln | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Pro

(2) INFORMATION FOR SEQ ID NO:1369:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..362

(D) OTHER INFORMATION: / Ceres Seq. ID 1597850

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369:

|            |             |            |             |            |             |     |
|------------|-------------|------------|-------------|------------|-------------|-----|
| aaccatcatt | gcaaaagcga  | mawagcaatn | nggaattctc  | tgcgatttct | ctagatctcg  | 60  |
| actaccccc  | actagttttg  | gttcnccctt | tcgttykaga  | gagcgattct | ggtggcaatg  | 120 |
| gogaaswncg | aggggtccggc | gatcgggatc | gacctcggca  | ccacctactc | gtgctgctggc | 180 |
| rtgtggcagc | acgaccgggt  | ggagatcatc | gccaaacgacc | aggggaacgc | accacgccgt  | 240 |
| cctatgtcgg | cttcaccgac  | acccgagcgg | ctcatcmrgc  | gacgctgcc  | anraccaggt  | 300 |
| cgccatgaac | cccaccaaca  | ccgtcttcga | ttccaagcgg  | ttgatcggca | ggagggttct  | 360 |

ct

(2) INFORMATION FOR SEQ ID NO:1370:

DOCKET# 08568960

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 120 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..120  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1597851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370:

Thr Ile Ile Ala Lys Ala Xaa Xaa Gln Xaa Gly Ile Leu Cys Asp Phe  
1                    5                    10                    15  
Ser Arg Ser Arg Leu Pro Pro Thr Ser Phe Gly Ser Xaa Phe Arg Xaa  
                    20                    25                    30  
Arg Glu Arg Phe Trp Trp Gln Trp Arg Xaa Xaa Arg Val Arg Arg Ser  
                    35                    40                    45  
Gly Ser Thr Ser Ala Pro Pro Thr Arg Ala Ser Xaa Cys Gly Ser Thr  
50                    55                    60  
Thr Gly Trp Arg Ser Ser Pro Thr Thr Arg Gly Thr His His Ala Val  
65                    70                    75                    80  
Leu Cys Arg Leu His Arg His Pro Ser Gly Ser Xaa Xaa Asp Ala Ala  
                    85                    90                    95  
Xaa Xaa Gln Val Ala Met Asn Pro Thr Asn Thr Val Phe Asp Ser Lys  
                    100                    105                    110  
Arg Leu Ile Gly Arg Arg Val Leu  
                    115                    120

(2) INFORMATION FOR SEQ ID NO:1371:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 101 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..101  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1597852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371:

Pro Ser Leu Gln Lys Arg Xaa Ser Asn Xaa Glu Phe Ser Ala Ile Ser  
1                    5                    10                    15  
Leu Asp Leu Asp Tyr Pro Pro Leu Val Leu Val Xaa Pro Phe Val Xaa  
                    20                    25                    30  
Glu Ser Asp Ser Gly Gly Asn Gly Glu Xaa Arg Gly Ser Gly Asp Arg  
                    35                    40                    45  
Asp Arg Pro Arg His His Leu Leu Val Arg Arg Xaa Val Ala Ala Arg  
50                    55                    60  
Pro Gly Gly Asp His Arg Gln Arg Pro Gly Glu Arg Thr Thr Pro Ser  
65                    70                    75                    80  
Tyr Val Gly Phe Thr Asp Thr Arg Ala Ala His Xaa Ala Thr Leu Pro  
                    85                    90                    95  
Xaa Thr Arg Ser Pro  
                    100

(2) INFORMATION FOR SEQ ID NO:1372:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 81 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

00559930 10300



(A) NAME/KEY: peptide

(B) LOCATION: 1..81

(D) OTHER INFORMATION: / Ceres Seq. ID 1597853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372:

Met Ala Xaa Xaa Glu Gly Pro Ala Ile Gly Ile Asp Leu Gly Thr Thr  
1 5 10 15  
Tyr Ser Cys Val Gly Xaa Trp Gln His Asp Arg Val Glu Ile Ala  
20 25 30  
Asn Asp Gln Gly Asn Ala Pro Arg Arg Pro Met Ser Ala Ser Pro Thr  
35 40 45  
Pro Glu Arg Leu Ile Xaa Arg Arg Cys Gln Xaa Pro Gly Arg His Glu  
50 55 60  
Pro His Gln His Arg Leu Arg Phe Gln Ala Val Asp Arg Gln Glu Gly  
65 70 75 80  
Ser

(2) INFORMATION FOR SEQ ID NO:1373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..465

(D) OTHER INFORMATION: / Ceres Seq. ID 1597854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373:

acacacacac acacatccat caaagaaaca ggcacacaag aacaaatacc tcgccaccaa 60  
caatggcctc caggctctcc atcctacttg caacggcgat gctggttgck ctgtttgogg 120  
ttggtttgtg caccaccccg ctcaccttcc aggttggcaa gggatccaag cctggccacc 180  
tgatcctcac ccccaatggt gcaaccatat ctgacgtgga gatcaaagag cacgggggog 240  
atgacttctc ctttacgctc aaggagggcc cgaccggcac ctggacgctc gacaccaagg 300  
ccccgctcaa gtacccccc ttgcatccgct ttgctgtcaa gtccggtggc taccgcatcg 360  
ccgacgacgt catccccgcc gatttcaagg ccggcaccac ctacaagacc acactacagc 420  
atctaatacag cctctgatga tgaattatat ttcaaaagag ctcac

(2) INFORMATION FOR SEQ ID NO:1374:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1597855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374:

Thr His Thr His Ile His Gln Arg Asn Arg His Thr Arg Thr Asn Thr  
1 5 10 15  
Ser Pro Pro Thr Met Ala Ser Arg Ser Ser Ile Leu Leu Ala Thr Ala  
20 25 30  
Met Leu Val Xaa Leu Phe Ala Val Gly Leu Cys Thr Thr Pro Leu Thr  
35 40 45  
Phe Gln Val Gly Lys Gly Ser Lys Pro Gly His Leu Ile Leu Thr Pro  
50 55 60  
Asn Val Ala Thr Ile Ser Asp Val Glu Ile Lys Glu His Gly Gly Asp  
65 70 75 80  
Asp Phe Ser Phe Thr Leu Lys Glu Gly Pro Thr Gly Thr Trp Thr Leu  
85 90 95  
Asp Thr Lys Ala Pro Leu Lys Tyr Pro Leu Cys Ile Arg Phe Ala Val

DOCTOP" 08688560

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 100 |     | 105 |     | 110 |     |     |     |     |     |     |     |     |     |     |
| Lys | Ser | Gly | Gly | Tyr | Arg | Ile | Ala | Asp | Asp | Val | Ile | Pro | Ala | Asp | Phe |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Ala | Gly | Thr | Thr | Tyr | Lys | Thr | Thr | Leu | Gln | His | Leu | Ile | Ser | Leu |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1375:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1597856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Arg | Ser | Ser | Ile | Leu | Leu | Ala | Thr | Ala | Met | Leu | Val | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Phe | Ala | Val | Gly | Leu | Cys | Thr | Thr | Pro | Leu | Thr | Phe | Gln | Val | Gly |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Gly | Ser | Lys | Pro | Gly | His | Leu | Ile | Leu | Thr | Pro | Asn | Val | Ala | Thr |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ile | Ser | Asp | Val | Glu | Ile | Lys | Glu | His | Gly | Gly | Asp | Asp | Phe | Ser | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Leu | Lys | Glu | Gly | Pro | Thr | Gly | Thr | Trp | Thr | Leu | Asp | Thr | Lys | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Leu | Lys | Tyr | Pro | Leu | Cys | Ile | Arg | Phe | Ala | Val | Lys | Ser | Gly | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Arg | Ile | Ala | Asp | Asp | Val | Ile | Pro | Ala | Asp | Phe | Lys | Ala | Gly | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Tyr | Lys | Thr | Thr | Leu | Gln | His | Leu | Ile | Ser | Leu |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1376:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1597857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Val | Xaa | Leu | Phe | Ala | Val | Gly | Leu | Cys | Thr | Thr | Pro | Leu | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Gln | Val | Gly | Lys | Gly | Ser | Lys | Pro | Gly | His | Leu | Ile | Leu | Thr | Pro |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Val | Ala | Thr | Ile | Ser | Asp | Val | Glu | Ile | Lys | Glu | His | Gly | Gly | Asp |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Asp | Phe | Ser | Phe | Thr | Leu | Lys | Glu | Gly | Pro | Thr | Gly | Thr | Trp | Thr | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Thr | Lys | Ala | Pro | Leu | Lys | Tyr | Pro | Leu | Cys | Ile | Arg | Phe | Ala | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Ser | Gly | Gly | Tyr | Arg | Ile | Ala | Asp | Asp | Val | Ile | Pro | Ala | Asp | Phe |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Ala | Gly | Thr | Thr | Tyr | Lys | Thr | Thr | Leu | Gln | His | Leu | Ile | Ser | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |



50 55 60  
Xaa Arg Gly Gly Val Lys Xaa Phe Ser Gly Leu Ile Tyr Glu Glu Thr  
65 70 75 80  
Arg Gly Val Leu Lys Ile Phe Leu Glu Asn Val Ile Arg Asp Ala Val  
85 90 95  
Thr Tyr Thr Glu His Ala Arg Arg Lys Thr Val Thr Ala Met Asp  
100 105 110

(2) INFORMATION FOR SEQ ID NO:1380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..485
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380:

awatagcaca cagccaaagc caccagcgct cgttcacctc caatcaacaa attcccaatc 60  
cgccgcttcc catcccgctg tcgcccgtcc atttgatcga attcccgatg gcgcccagg 120  
ccgagaagaa gcccgcgag aagaagccga cggaggagaa ggccgagaag aagcccagg 180  
cgagaagcgc gtgcccggca aggagggcgg cgagaagaag gggaagaaga aggccaaaga 240  
gagcgctcgag acgtacaaga tctacatctt caagggtgctc aagcagggtgc acccgacat 300  
tggtatctcg tccaaggcca tgtccatcat gaactccttc atcaacgaca tcttcgagaa 360  
gctggctgcc gaggcgcga agctcgccc ctacaacaag aagcccacca taacctccg 420  
ggagatccag acttcggtgc gcctcgtcct tctggcgag ctgcgaagca cgccgtctcc 480  
gaggg

(2) INFORMATION FOR SEQ ID NO:1381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381:

Xaa Ser Thr Gln Pro Lys Pro Pro Ala Leu Val His Leu Gln Ser Thr  
1 5 10 15  
Asn Ser Gln Ser Ala Ala Ser His Pro Ala Phe Ala Ala Pro Phe Asp  
20 25 30  
Arg Ile Pro Asp Gly Ala Gln Gly Arg Glu Glu Ala Arg Gly Glu Glu  
35 40 45  
Ala Asp Gly Gly Glu Gly Arg Glu Glu Ala Gln Gly Glu Lys Arg Val  
50 55 60  
Pro Gly Lys Glu Gly Gly Glu Lys Lys Gly Lys Lys Lys Ala Lys Lys  
65 70 75 80  
Ser Val Glu Thr Tyr Lys Ile Tyr Ile Phe Lys Val Leu Lys Gln Val  
85 90 95  
His Pro Asp Ile Gly Ile Ser Ser Lys Ala Met Ser Ile Met Asn Ser  
100 105 110  
Phe Ile Asn Asp Ile Phe Glu Lys Leu Ala Ala Glu Ala Ala Lys Leu  
115 120 125  
Ala Arg Tyr Asn Lys Lys Pro Thr Ile Thr Ser Arg Glu Ile Gln Thr  
130 135 140  
Ser Val Arg Leu Val Leu Pro Gly Glu Leu Ala Ser Thr Pro Ser Pro  
145 150 155 160  
Arg

CONFIDENTIAL



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..49  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..242  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gcgcantcat | coattccatc | atcccttgca | agtatagtct | cggcggctct | agaatacgat | 60  |
| gggcaaggac | gacgtgatcg | agagcggcgc | tggcggcggc | gagttcgctg | ccaaggacta | 120 |
| cacggaccct | cccccggcg  | cgctgatcga | cgcggctgag | ctggggatcc | tggtcgctgt | 180 |
| amcgcgccgt | gatcgccgag | ttcatcgcca | cgctgctgtt | cctgtacatc | acggtgdcca | 240 |
| cc         |            |            |            |            |            |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..52  
(D) OTHER INFORMATION: / Ceres Seq. ID 1597891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids

[illegible]



(2) INFORMATION FOR SEQ ID NO:1391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391:

Ser Lys Phe Pro Lys Arg Lys Thr Ala Ser Ser His Gln Leu Pro Ser  
1 5 10 15  
Thr Phe Val Ser Arg Ser Arg Pro Val Ala Met Asp Ala Ile Asp Ser  
20 25 30  
Val Val Asp Pro Leu Arg Asp Phe Ala Lys Asp Ser Val Ala Leu Val  
35 40 45  
Lys Arg Cys His Lys Pro Asp Arg Lys Ser Ser Pro Arg Trp Arg Arg  
50 55 60  
Gly Arg Arg Ser Gly Ser Ser Ser Trp Ala Ser Ser Ala Ser Ser Leu  
65 70 75 80  
Ser Ser Ser Ser Ser Pro Ser Thr Thr Ser Ser Ser Val Pro Ala Arg  
85 90 95  
Leu Thr Gly Val Gln Gly Asp  
100

(2) INFORMATION FOR SEQ ID NO:1392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392:

Ala Asn Phe Pro Asn Ala Lys Pro His Pro Leu Ile Ser Phe Leu Pro  
1 5 10 15  
His Ser Ser Arg Asp Leu Ala Pro Ser Pro Trp Thr Arg Ser Thr Ala  
20 25 30  
Trp Trp Ile Pro Ser Ala Thr Ser Pro Arg Thr Ala Ser Pro Ser Ser  
35 40 45  
Ser Ala Ala Thr Ser Pro Thr Ala Arg Val His Gln Gly Gly Gly Ala  
50 55 60  
Asp Gly Asp Arg Val Arg Arg His Gly Leu Arg Arg Leu Leu Arg  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393:

gcattagcac tagggtttcc catctcttaa ggctgccacc gccagckcgg cccctcggt

60

09689980 10300



gcacccctcag tgcgtactgt ctgtgcgaag ggcaccattc cttcttcgct ccttcgccgc 120  
cgctatgggtt aagtactcgc aggagccggg caaccctacc aaatcggcca aggccatggg 180  
aagggaacctg agggctcactt caagaacaca agggagacag cttttgcgct tcgcaagctg 240  
cctttgacca aggetaagcg ataccttgag gatgttattg ctcacaagca ggcaattccc 300  
ttccggagat actgtggagg tgttggtcgc accgcacaag caaagtctcg ccactccaat 360  
gggcagggtc gctggcctgt taagtcagcc aggttcatat tggatttgct gaagaatgct 420  
gagagtaacg ctgatgtgaa aggcttggac gtggacaacc tctatgtttc acacatcc

(2) INFORMATION FOR SEQ ID NO:1394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1597906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394:

Ile Ser Thr Arg Val Ser His Leu Leu Arg Leu Pro Pro Pro Xaa Pro  
1 5 10 15  
Pro Pro Arg Cys Ile Leu Ser Ala Tyr Cys Leu Cys Glu Gly Asp His  
20 25 30  
Ser Phe Phe Ala Pro Ser Pro Pro Leu Trp Leu Ser Thr Arg Arg Ser  
35 40 45  
Arg Ala Thr Leu Pro Asn Arg Pro Arg Pro Trp Glu Gly Thr  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..40

(D) OTHER INFORMATION: / Ceres Seq. ID 1597907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1395:

Met Val Lys Tyr Ser Gln Glu Pro Gly Asn Pro Thr Lys Ser Ala Lys  
1 5 10 15  
Ala Met Gly Arg Asp Leu Arg Val Thr Ser Arg Thr Gln Gly Arg Gln  
20 25 30  
Leu Leu Arg Phe Ala Ser Cys Leu  
35 40

(2) INFORMATION FOR SEQ ID NO:1396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..46

(D) OTHER INFORMATION: / Ceres Seq. ID 1597908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1396:

Met Leu Leu Leu Thr Ser Arg Gln Phe Pro Ser Gly Asp Thr Val Glu  
1 5 10 15  
Val Leu Val Ala Pro His Lys Gln Ser Leu Ala Thr Pro Met Gly Arg  
20 25 30

005701" 00553360

Val Ala Gly Leu Leu Ser Gln Pro Gly Ser Tyr Trp Ile Cys  
35 40 45

(2) INFORMATION FOR SEQ ID NO:1397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..457
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1397:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gtccgtctct | cggtctctcc | ttcctatcgg | ctccacacct | ccacgcaact | ggaagcttcg | 60  |
| ctgcaatctg | cctactcct  | cttccgccgc | ctccaacacc | gcagacgcag | ctgccgcggg | 120 |
| cgggagcttg | gacgtgtac  | gctgctctca | tctcgtttcc | gcgcaggaat | tgttctcaat | 180 |
| ggcccgcgtg | tatgttggca | acttgattc  | acgggtgact | tctggggaac | tcgaagatga | 240 |
| gttccgcgtg | tttggagttc | tgcaagtgt  | ttggattgca | cgtaaaccac | ctggctttgc | 300 |
| atttrttgat | tttkacgaca | ggagggatgc | ggaggatgct | attcgtgatc | tagatggtaa | 360 |
| gaatggatgg | agagttgaac | tatctcgtaa | ttccagtggg | cgtgggtggc | gtgatcggtg | 420 |
| tggtggatct | gagtcgamgt | kctatgaatg | tggtgag    |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Val Arg Leu Ser Phe Ser Pro Ser Tyr Arg Leu His Thr Ser Thr Gln |  |
| 1 5 10 15                                                       |  |
| Leu Glu Ala Ser Leu Gln Ser Ala Leu Leu Leu Phe Arg Arg Leu Gln |  |
| 20 25 30                                                        |  |
| His Arg Arg Arg Ser Cys Arg Gly Arg Glu Leu Gly Arg Ala Thr Leu |  |
| 35 40 45                                                        |  |
| Leu Ser Ser Arg Phe Arg Ala Gly Ile Val Leu Asn Gly Pro Arg Val |  |
| 50 55 60                                                        |  |
| Cys Trp Gln Leu Gly Phe Thr Gly Asp Phe Trp Gly Thr Arg Arg     |  |
| 65 70 75                                                        |  |

(2) INFORMATION FOR SEQ ID NO:1399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ser Val Ser Arg Ser Leu Leu Pro Ile Gly Ser Thr Pro Pro Arg Asn |  |
| 1 5 10 15                                                       |  |
| Trp Lys Leu Arg Cys Asn Leu Pro Tyr Ser Ser Ser Ala Ala Ser Asn |  |
| 20 25 30                                                        |  |
| Thr Ala Asp Ala Ala Ala Gly Gly Ser Leu Asp Val Leu Arg Cys     |  |

DOCKET "0868950"

35 40 45  
Ser His Leu Val Ser Ala Gln Glu Leu Phe Ser Met Ala Arg Val Tyr  
50 55 60  
Val Gly Asn Leu Asp Ser Arg Val Thr Ser Gly Glu Leu Glu Asp Glu  
65 70 75 80  
Phe Arg Val Phe Gly Val Leu Arg Ser Val Trp Ile Ala Arg Lys Pro  
85 90 95  
Pro Gly Phe Ala Phe Xaa Asp Phe Xaa Asp Arg Arg Asp Ala Glu Asp  
100 105 110  
Ala Ile Arg Asp Leu Asp Gly Lys Asn Gly Trp Arg Val Glu Leu Ser  
115 120 125  
Arg Asn Ser Ser Gly Arg Gly Gly Arg Asp Arg Tyr Gly Gly Ser Glu  
130 135 140  
Ser Xaa Xaa Tyr Glu Cys Gly Glu  
145 150

(2) INFORMATION FOR SEQ ID NO:1400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597916

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400:

Met Ala Arg Val Tyr Val Gly Asn Leu Asp Ser Arg Val Thr Ser Gly  
1 5 10 15  
Glu Leu Glu Asp Glu Phe Arg Val Phe Gly Val Leu Arg Ser Val Trp  
20 25 30  
Ile Ala Arg Lys Pro Pro Gly Phe Ala Phe Xaa Asp Phe Xaa Asp Arg  
35 40 45  
Arg Asp Ala Glu Asp Ala Ile Arg Asp Leu Asp Gly Lys Asn Gly Trp  
50 55 60  
Arg Val Glu Leu Ser Arg Asn Ser Ser Gly Arg Gly Gly Arg Asp Arg  
65 70 75 80  
Tyr Gly Gly Ser Glu Ser Xaa Xaa Tyr Glu Cys Gly Glu  
85 90

(2) INFORMATION FOR SEQ ID NO:1401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..280
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597917

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401:

aaaaacccta gcgtccaact catatacctg ctgctcgccc cgacgcgcat caactcccgc 60  
cgccgccccct tctctccgt cgctcgccctc gsgcctaagc caccacctct gccatggccc 120  
cgaagaagga taaggccccg cgccgtcgtc caagccggcc aagtccggag cggaagcag 180  
aagaagaaga agtggagcaa ggtaagcaa aaggagaagg tcaacaacgc tgtgctcttc 240  
gtgcgcgcgt ggcgtgccag tcgcgtcgcg cgcgctggcg

(2) INFORMATION FOR SEQ ID NO:1402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

| (A1) SEQUENCE DESCRIPTION: SEQ ID: 1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|--------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu                                  | Val | Pro | His | Pro | Leu | Arg | Pro | Ile | Asn | Arg | Ser | Asp | Ala | Ser | Thr |  |
| 1                                    |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Ser                                  | Thr | His | Pro | Leu | Pro | Ser | Ser | Val | Ile | Pro | Arg | Arg | Val | Pro | Ser |  |
|                                      |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Pro                                  | Gln | Thr | Ser | Ala | Met | Ala | Asp | Gln | Leu | Thr | Asp | Glu | Gln | Ile | Ala |  |
|                                      |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Glu                                  | Phe | Lys | Glu | Ala | Phe | Ser | Leu | Phe | Asp | Lys | Asp | Gly | Asp | Gly | Cys |  |
|                                      | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Ile                                  | Thr | Thr | Lys | Glu | Leu | Gly | Thr | Val | Met | Arg | Ser | Leu | Gly | Gln | Asn |  |

(2) INFORMATION FOR SEQ ID NO:1405:

(A) LENGTH: 125 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1597939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405:

(2) INFORMATION FOR SEQ ID NO:1406:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1597940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ser | Leu | Gly | Gln | Asn | Pro | Thr | Glu | Ala | Glu | Leu | Gln | Asp | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Asn | Glu | Val | Asp | Ala | Asp | Gly | Asn | Gly | Thr | Ile | Asp | Phe | Pro | Xaa |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Leu | Asn | Leu | Met | Ala | Arg | Lys | Met | Lys | Asp | Thr | Asp | Ser | Glu | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Leu | Lys | Glu | Ala | Phe | Arg | Val | Phe | Asp | Lys | Asp | Gln | Asn | Gly | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu Gly Glu Lys  
65 70 75 80  
Leu Thr Asp Glu Glu Val Asp Glu Met  
85

(2) INFORMATION FOR SEQ ID NO:1407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..483
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| caagaagaat | gtgattgtgg | ccattacctc | tgataaggga | ctctgtggtg  | gtattaattc | 60  |
| aacatcagtg | aaagttagca | gggcccttca | caaattgaca | tctgggtccag | aaaaagaaac | 120 |
| caagtatgtt | atattaggag | aaaagggcaa | agttcagctg | ttgcgtgact  | caaaggacag | 180 |
| cattgaaatg | actgcaactg | aactgcagaa | gaacctatc  | aactacacac  | aggttgccgt | 240 |
| gctcgcggat | gacatattga | aaaatgtgga | atatgatgct | ctgagggtta  | ttttcaacaa | 300 |
| gttccaatct | gtcatatcgt | ttaagccac  | aatggtaaca | atactttccc  | ccgaggttgc | 360 |
| agaaaaagaa | tcagaagctg | gtgggaagat | gggtgaccta | gattcctatg  | agattgaagg | 420 |
| cggcgagaca | aatcagaga  | ttttgcagaa | tctagctgag | ttccagtttt  | cttgtgtctg | 480 |
| tac        |            |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:1408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1597942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Lys | Asn | Val | Ile | Val | Ala | Ile | Thr | Ser | Asp | Lys | Gly | Leu | Cys | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gly | Ile | Asn | Ser | Thr | Ser | Val | Lys | Val | Ser | Arg | Ala | Leu | His | Lys | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ser | Gly | Pro | Glu | Lys | Glu | Thr | Lys | Tyr | Val | Ile | Leu | Gly | Glu | Lys |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Gly | Lys | Val | Gln | Leu | Leu | Arg | Asp | Ser | Lys | Asp | Ser | Ile | Glu | Met | Thr |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ala | Thr | Glu | Leu | Gln | Lys | Asn | Pro | Ile | Asn | Tyr | Thr | Gln | Val | Ala | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Ala | Asp | Asp | Ile | Leu | Lys | Asn | Val | Glu | Tyr | Asp | Ala | Leu | Arg | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ile | Phe | Asn | Lys | Phe | Gln | Ser | Val | Ile | Ser | Phe | Lys | Pro | Thr | Met | Val |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Thr | Ile | Leu | Ser | Pro | Glu | Val | Ala | Glu | Lys | Glu | Ser | Glu | Ala | Gly | Gly |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Lys | Met | Gly | Asp | Leu | Asp | Ser | Tyr | Glu | Ile | Glu | Gly | Gly | Glu | Thr | Lys |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Ser | Glu | Ile | Leu | Gln | Asn | Leu | Ala | Glu | Phe | Gln | Phe | Ser | Cys | Val | Cys |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |

(2) INFORMATION FOR SEQ ID NO:1409:

(i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409:

(2) INFORMATION FOR SEQ ID NO:1410:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 444 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..444

(D) OTHER INFORMATION: / Ceres Seq. ID 1597958

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410:

| (X1) SEQUENCE DESCRIPTION: SEQ ID NUMBER |             |             |            |             |             |  |     |
|------------------------------------------|-------------|-------------|------------|-------------|-------------|--|-----|
| ctcgcagctcg                              | acccttaagc  | cttcgctcgc  | gccgcgcgcg | ccgcgcgcgc  | tacgccccgc  |  | 60  |
| acctcgcttc                               | atttctgtgc  | gcccaagatga | cgaagcgcac | taagaaggca  | ggaattgttg  |  | 120 |
| gcaaatatgg                               | aaccagggtat | ggtgctagct  | tgcgtaasaa | attcaagaag  | atggagggtat |  | 180 |
| ctcagcattc                               | caagtacttt  | tgcgagttct  | gtgggaagtt | tgctgtgaag  | aggaaagcag  |  | 240 |
| ttggaatgct                               | ttatccccctg | ttttctggaa  | acttcgtaac | catattttct  | ccaattgaac  |  | 300 |
| cgactacaac                               | aattccccata | tttctctctc  | agaaattgct | gaatccaaatg | caaccagcca  |  | 360 |
| ggcgaaatatt                              | tattccaacaa | tccaataattc | agtggacaat | gagccataag  | gttgatcata  |  | 420 |
| gatccccctct                              | cagttatgga  | gtgg        |            |             |             |  |     |

(2) INFORMATION FOR SEQ ID NO:1411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1597959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411:

| (x1) SEQUENCE DESCRIPTION: S2212 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|----------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met                              | Thr | Lys | Arg | Thr | Lys | Lys | Ala | Gly | Ile | Val | Gly | Lys | Tyr | Gly | Thr |
| 1                                |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg                              | Tyr | Gly | Ala | Ser | Leu | Arg | Xaa | Lys | Phe | Lys | Lys | Met | Glu | Val | Ser |
|                                  |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln                              | His | Ser | Lys | Tyr | Phe | Cys | Glu | Phe | Cys | Gly | Lys | Phe | Ala | Val | Lys |

(B) TYPE: nucleic acid



|                                           |            |            |
|-------------------------------------------|------------|------------|
| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:1111 |            |            |
| accagacgcc                                | ctctactaat | ccagcccatt |
| ctctgttcac                                | cgctgccccg | tacgctactc |
| atcagcaggg                                | cgtggattac | cccagcttca |
| gtaaaaccac                                | att        |            |

|                                            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|--------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110: |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Gln                                        | Thr | Pro | Ser | Thr | Asn | Pro | Ala | His | Phe | Glu | Leu | Ser | Leu | Asp | Ala |
| 1                                          |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser                                        | Ser | Val | Ser | Leu | Phe | Thr | Ala | Ala | Pro | Tyr | Arg | Thr | Pro | Leu | Arg |
|                                            |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala                                        | Val | Glu | Met | Ala | Leu | Pro | Asn | Gln | Gln | Gly | Val | Asp | Tyr | Pro | Ser |
|                                            |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe                                        | Lys | Leu | Val | Ile | Val | Gly | Asp | Gly | Gly | Thr | Gly | Lys | Thr | Thr |     |
|                                            | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

| (X1)       | SEQUENCE    | DESCRIPTION | SEQ ID NO  |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| akatcagatc | acaccacagc  | cgcggtatana | gaaggaaaaa | tttcccaaaa | cctagcttc  | 60  |
| ggatctcgat | ggcgaacccc  | cgcgtcttct  | tcgacatgac | cgtcggcggt | gccccagcgc | 120 |
| gccggatcgt | gatgcgagctg | tacgccaacg  | aggtgcccaa | kaccgcggag | aacttccgcg | 180 |
| cgtgtgtcac | gggcgagaag  | ggcgtgggca  | agtcggggaa | gccgtccac  | tacaagggct | 240 |
| ctamcttcca | ccgcgtcatc  | ccccagttca  | tgtgccaggg | cggcg      |            |     |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417:

(2) INFORMATION FOR SEQ ID NO:1418:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1597966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418:

(2) INFORMATION FOR SEQ ID NO:1419:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1597967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419:

(2) INFORMATION FOR SEQ ID NO:1420:

(A) LENGTH: 391 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

[illegible]

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..391

(D) OTHER INFORMATION: / Ceres Seq. ID 1597985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420:

|            |            |             |            |            |             |     |
|------------|------------|-------------|------------|------------|-------------|-----|
| aactacggta | actcgtctgc | tgcattttcc  | tcccaatcca | tcccgcctcc | aaacccgaac  | 60  |
| tccaagtcgc | cccgcatcga | tggcgcccaa  | ggccgagaag | aagcccgtg  | gcgaagaagc  | 120 |
| cggcggagga | ggagcccgct | gcgagaagg   | cgccggccgg | aagaagcca  | aggcgagaag  | 180 |
| cgtgtcccag | caggcaagtc | cgccggcaag  | gagggcggcg | aggkawatka | kgggcccggaa | 240 |
| gaagggcaag | aagagcgtgg | agacctacaa  | gatctacatc | ttcaaggtgc | tgaagcaggt  | 300 |
| gcacccggac | atcggcattc | cctctaaggc  | catgtccatc | atgaactcct | tcatcaacga  | 360 |
| catcttcgag | aagctcgccg | ccgagggccgc | c          |            |             |     |

(2) INFORMATION FOR SEQ ID NO:1421:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1597986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Tyr | Gly | Asn | Ser | Ser | Ala | Arg | Ile | Ser | Ser | Gln | Ser | Ile | Pro | Pro |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Pro | Asn | Pro | Asn | Ser | Lys | Ser | Pro | Arg | Ile | Asp | Gly | Ala | Gln | Gly | Arg |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu | Glu | Ala | Arg | Trp | Arg | Arg | Ser | Arg | Arg | Arg | Ser | Pro | Leu | Pro |     |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Arg | Arg | Arg | Arg | Pro | Glu | Glu | Ala | Gln | Gly | Glu | Lys | Arg | Val | Pro | Ala |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Gly | Lys | Ser | Ala | Gly | Lys | Glu | Gly | Gly | Glu | Xaa | Xaa | Xaa | Gly | Pro | Glu |  |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Glu | Gly | Gln | Glu | Glu | Arg | Gly | Asp | Leu | Gln | Asp | Leu | His | Leu | Gln | Gly |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Ala | Glu | Ala | Gly | Ala | Pro | Gly | His | Arg | His | Leu | Leu |     |     |     |     |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1422:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1597987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Thr | Val | Thr | Arg | Leu | Leu | Ala | Phe | Pro | Pro | Asn | Pro | Ser | Arg | Leu |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Gln | Thr | Arg | Thr | Pro | Ser | Arg | Pro | Ala | Ser | Met | Ala | Pro | Lys | Ala | Glu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Lys | Lys | Pro | Ala | Gly | Glu | Glu | Ala | Gly | Gly | Gly | Gly | Ala | Arg | Cys | Arg |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Glu | Gly | Ala | Gly | Arg | Lys | Lys | Pro | Lys | Ala | Arg | Ser | Val | Ser | Gln | Gln |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Ala | Ser | Pro | Pro | Ala | Arg | Arg | Ala | Ala | Arg | Xaa | Xaa | Xaa | Gly | Arg | Lys |  |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Lys | Gly | Lys | Lys | Ser | Val | Glu | Thr | Tyr | Lys | Ile | Tyr | Ile | Phe | Lys | Val |  |

00669900 "00669900"

85 90 95  
Leu Lys Gln Val His Pro Asp Ile Gly Ile Ser Ser Lys Ala Met Ser  
100 105 110  
Ile Met Asn Ser Phe Ile Asn Asp Ile Phe Glu Lys Leu Ala Ala Glu  
115 120 125  
Ala Ala  
130

(2) INFORMATION FOR SEQ ID NO:1423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1597988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423:

Met Ala Pro Lys Ala Glu Lys Lys Pro Ala Gly Glu Glu Ala Gly Gly  
1 5 10 15  
Gly Gly Ala Arg Cys Arg Glu Gly Ala Gly Arg Lys Lys Pro Lys Ala  
20 25 30  
Arg Ser Val Ser Gln Gln Ala Ser Pro Pro Ala Arg Arg Ala Ala Arg  
35 40 45  
Xaa Xaa Xaa Gly Arg Lys Lys Gly Lys Lys Ser Val Glu Thr Tyr Lys  
50 55 60  
Ile Tyr Ile Phe Lys Val Leu Lys Gln Val His Pro Asp Ile Gly Ile  
65 70 75 80  
Ser Ser Lys Ala Met Ser Ile Met Asn Ser Phe Ile Asn Asp Ile Phe  
85 90 95  
Glu Lys Leu Ala Ala Glu Ala Ala  
100

(2) INFORMATION FOR SEQ ID NO:1424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..440

(D) OTHER INFORMATION: / Ceres Seq. ID 1598004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424:

actcgagcct gacccttacg ccttcgctcg ckccgcccgc gccgacgccg ctacgccccg 60  
cacctcgctt catttcgtgt cgccaagatg acgaagcgca ctaagaaggc aggaattggt 120  
ggcaaataatg gaaccaggta tgggtgctagc ttgcgtaasa aatccaagaa gatggaggta 180  
tctcagcatt ccaagtactt ttgckagttc tgtgggaagt ttgctgtgaa gaggaaagca 240  
gttggaattt gggggtgcaa ggactgtggg aagggtgaagg ctggtggtgc ttacaccatg 300  
aacactgcta gtgcggtcac cgtcagagca cgatccgcc tggcccagcc cgctttcttc 360  
tcctctctcc agctcccgcg cctgctccgc gccgccgcc cgcgcgaacc atcgccctcca 420  
gcctaggcgg cggtaccac

(2) INFORMATION FOR SEQ ID NO:1425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1598005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Lys | Arg | Thr | Lys | Lys | Ala | Gly | Ile | Val | Gly | Lys | Tyr | Gly | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Tyr | Gly | Ala | Ser | Leu | Arg | Xaa | Lys | Ser | Lys | Lys | Met | Glu | Val | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | His | Ser | Lys | Tyr | Phe | Cys | Xaa | Phe | Cys | Gly | Lys | Phe | Ala | Val | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Lys | Ala | Val | Gly | Ile | Trp | Gly | Cys | Lys | Asp | Cys | Gly | Lys | Val | Lys |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ala | Gly | Gly | Ala | Tyr | Thr | Met | Asn | Thr | Ala | Ser | Ala | Val | Thr | Val | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Arg | Ser | Ala | Met | Ala | Gln | Pro | Ala | Phe | Leu | Ser | Ser | Leu | Gln | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Pro | Leu | Leu | Arg | Ala | Ala | Ala | Pro | Ala | Glu | Pro | Ser | Pro | Pro | Ala |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |

(2) INFORMATION FOR SEQ ID NO:1426:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1598006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Val | Ser | Gln | His | Ser | Lys | Tyr | Phe | Cys | Xaa | Phe | Cys | Gly | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Ala | Val | Lys | Arg | Lys | Ala | Val | Gly | Ile | Trp | Gly | Cys | Lys | Asp | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Lys | Val | Lys | Ala | Gly | Gly | Ala | Tyr | Thr | Met | Asn | Thr | Ala | Ser | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Thr | Val | Arg | Ala | Arg | Ser | Ala | Met | Ala | Gln | Pro | Ala | Phe | Leu | Ser |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ser | Leu | Gln | Leu | Pro | Pro | Leu | Leu | Arg | Ala | Ala | Ala | Pro | Ala | Glu | Pro |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Pro | Pro | Ala |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1427:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 476 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..476

(D) OTHER INFORMATION: / Ceres Seq. ID 1598007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atctcgcct  | cgctcaccta | catctcgcgc | cgcaagcnc  | acgcaggctg | ccccgggagg | 60  |
| ccgggaggaa | gcagatcgga | gaagccaagc | cacggatttc | cttctcgcct | tctggacccc | 120 |
| atgtgatctg | ttgtaatggc | tcgattgtac | atcggaacc  | tggatccccg | ggtgaccgct | 180 |
| cgggagctgg | aggacgagtt | ccgcacgttc | ggggttcttc | gcagtgtctg | ggttgctcgg | 240 |
| aaaccacctg | gctttgcgtt | tattgatttt | gatgataaga | gggacgcaga | ggatgcaatc | 300 |

360  
420

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:

(2) INFORMATION FOR SEQ ID NO:1429:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:

(2) INFORMATION FOR SEQ ID NO:1430:

- [illegible]

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..230

(D) OTHER INFORMATION: / Ceres Seq. ID 1598010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aacaaggagc | actcattgcc | tccccatctc | gtgtaggctc | tccccctcct | cgcgcgtccg | 60  |
| tccgtctctc | atcacggttc | cgccgcgcgc | ccacctctcc | ctcctctcgc | cgccgcctcc | 120 |
| gaaccgcgca | cggcgcgggc | gagatccaac | cggacggatc | tkgatcgacc | tactccgaca | 180 |
| ccgctttccg | aagatagata | gatagataac | aagggttgtc | tgtgcttgct |            |     |

(2) INFORMATION FOR SEQ ID NO:1431:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1598011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Arg | Ser | Thr | His | Cys | Leu | Pro | Ile | Ser | Cys | Arg | Leu | Ser | Pro | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Ala | Leu | Arg | Pro | Ser | Leu | Ile | Thr | Val | Pro | Pro | Pro | Pro | His | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Leu | Leu | Ser | Pro | Pro | Pro | Pro | Asn | Pro | Pro | Arg | Arg | Gly | Gly | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Thr | Gly | Arg | Ile | Xaa | Ile | Asp | Leu | Leu | Arg | His | Arg | Phe | Pro | Lys |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ile | Asp | Arg |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1598012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Gly | Ala | Leu | Ile | Ala | Ser | Pro | Ser | Arg | Val | Gly | Ser | Pro | Pro | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Arg | Ser | Val | Arg | Leu | Ser | Ser | Pro | Phe | Arg | Arg | Arg | Pro | Thr | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ser | Ser | Arg | Arg | Arg | Leu | Arg | Thr | Arg | His | Gly | Ala | Ala | Glu | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Pro | Asp | Gly | Ser | Xaa | Ser | Thr | Tyr | Ser | Asp | Thr | Ala | Phe | Arg | Arg |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1433:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

005598010000

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1598024

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| acacacacaa | cnvagcagag  | agattactac | gatccaacag | ttctagagca | agagagagga | 60  |
| agacacaccg | cagagtttagc | aggctaataa | cttgcaggag | cagcaggaat | ggyggcgacs | 120 |
| gtcstctctt | gctttctctt  | cgccgtgctt | ctggcaggag | tggccgctgc | mcgccttcga | 180 |
| cgaagcggt  | gctgccggt   | tggggttgg  | ccacggcgcg | cgtttcnngn | catggacgtg | 240 |
| ctgccgtga  | gatgccccag  | ccggagccac | aacctaaaac | taagccggag | ccccatatgc | 300 |
| agccactgcc | ccagccagaa  | cctaaaccga | aacctatgcc | acatccag   |            |     |

(2) INFORMATION FOR SEQ ID NO:1434:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1598025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | His | Asn | Xaa | Ala | Glu | Arg | Leu | Leu | Arg | Ser | Asn | Ser | Ser | Arg | Ala |     |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Glu | Arg | Lys | Thr | His | Arg | Arg | Val | Ser | Arg | Leu | Ile | Thr | Cys | Arg |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ser | Ser | Arg | Asn | Xaa | Gly | Asp | Xaa | Xaa | Leu | Leu | Leu | Ser | Pro | Arg | Arg |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ala | Ser | Gly | Arg | Ser | Gly | Arg | Cys | Xaa | Pro | Ser | Thr | Lys | Arg | Leu | Leu |     |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Pro | Ala | Ser | Gly | Leu | Ala | Thr | Ala | Arg | Val | Xaa | Xaa | His | Gly | Arg | Ala |     |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     |     |     | 80  |     |
| Ala | Ala | Glu | Met | Pro | Gln | Pro | Glu | Pro | Gln | Pro | Lys | Thr | Lys | Pro | Glu |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Pro | His | Met | Gln | Pro | Leu | Pro | Gln | Pro | Glu | Pro | Lys | Pro | Lys | Pro | Met |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Pro | His | Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 115 |

(2) INFORMATION FOR SEQ ID NO:1435:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1598026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Xaa | Ala | Xaa | Val | Xaa | Ser | Cys | Phe | Leu | Leu | Ala | Val | Leu | Leu | Ala |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     |     | 15  |  |
| Gly | Val | Ala | Ala | Xaa | Arg | Leu | Arg | Arg | Ser | Gly | Cys | Cys | Arg | Leu | Arg |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ala | Trp | Pro | Arg | Arg | Ala | Phe | Xaa | Xaa | Met | Asp | Val | Leu | Pro | Leu | Arg |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Cys | Pro | Ser | Arg | Ser | His | Asn | Leu | Lys | Leu | Ser | Arg | Ser | Pro | Ile | Cys |  |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Ser | His | Cys | Pro | Ser | Gln | Asn | Leu | Asn | Arg | Asn | Leu | Cys | His | Ile | Gln |  |
|     |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |



(2) INFORMATION FOR SEQ ID NO:1436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..486
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436:

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| acctctcgct  | ccgttgctcg | cctcgggtca | aaccctaagc  | agggagttga | tttatccgct | 60  |
| gcagccatga  | gtaagttgca | gtctgagtc  | gtcaaggatg  | ccatctccca | gattgttggg | 120 |
| gatgccaagg  | agaagaatag | gaagttcact | gagactgtgg  | aacttcagat | tggtctgaag | 180 |
| aattatgac   | cacagaagga | caagcgtttc | agtggctctg  | ttaagttgcc | ccatatccct | 240 |
| cgtcccaaga  | tgaaggtgtg | catgcttggt | gatgcccgagc | atgttgagga | ggccgagaag | 300 |
| atgggacttg  | actacatgga | tgttgaggct | ctcaagaaaa  | tgaacaagaa | caagaagctt | 360 |
| gttaagaggc  | ttgccaagaa | gtaccatgct | ttcttggcac  | cagaggccat | catcaagcag | 420 |
| attccccgctc | tccttggtcc | tggtctcaac | aaggcaggca  | agttcccgac | cctggttact | 480 |
| caccag      |            |            |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Ser | Arg | Ser | Val | Ala | Arg | Leu | Gly | Ser | Asn | Pro | Lys | Gln | Gly | Val |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Asp | Leu | Ser | Ala | Ala | Ala | Met | Ser | Lys | Leu | Gln | Ser | Glu | Ser | Val | Lys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asp | Ala | Ile | Ser | Gln | Ile | Val | Gly | Asp | Ala | Lys | Glu | Lys | Asn | Arg | Lys |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Phe | Thr | Glu | Thr | Val | Glu | Leu | Gln | Ile | Gly | Leu | Lys | Asn | Tyr | Asp | Pro |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Gln | Lys | Asp | Lys | Arg | Phe | Ser | Gly | Ser | Val | Lys | Leu | Pro | His | Ile | Pro |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Arg | Pro | Lys | Met | Lys | Val | Cys | Met | Leu | Gly | Asp | Ala | Gln | His | Val | Glu |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Glu | Ala | Glu | Lys | Met | Gly | Leu | Asp | Tyr | Met | Asp | Val | Glu | Ala | Leu | Lys |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |
| Lys | Met | Asn | Lys | Asn | Lys | Lys | Leu | Val | Lys | Arg | Leu | Ala | Lys | Lys | Tyr |  |
|     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |     |  |
| His | Ala | Phe | Leu | Ala | Ser | Glu | Ala | Ile | Ile | Lys | Gln | Ile | Pro | Arg | Leu |  |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |  |
| Leu | Gly | Pro | Gly | Leu | Asn | Lys | Ala | Gly | Lys | Phe | Pro | Thr | Leu | Val | Thr |  |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     |     | 160 |  |
| His | Gln |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid

0965990-10100

| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155: |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|--------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met                                        | Ser | Lys | Leu | Gln | Ser | Glu | Ser | Val | Lys | Asp | Ala | Ile | Ser | Gln | Ile |
| 1                                          |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val                                        | Gly | Asp | Ala | Lys | Glu | Lys | Asn | Arg | Lys | Phe | Thr | Glu | Thr | Val | Glu |
|                                            |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu                                        | Gln | Ile | Gly | Leu | Lys | Asn | Tyr | Asp | Pro | Gln | Lys | Asp | Lys | Arg | Phe |
|                                            |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ser                                        | Gly | Ser | Val | Lys | Leu | Pro | His | Ile | Pro | Arg | Pro | Lys | Met | Lys | Val |
|                                            | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Cys                                        | Met | Leu | Gly | Asp | Ala | Gln | His | Val | Glu | Glu | Ala | Glu | Lys | Met | Gly |
| 65                                         |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu                                        | Asp | Tyr | Met | Asp | Val | Glu | Ala | Leu | Lys | Lys | Met | Asn | Lys | Asn | Lys |
|                                            |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys                                        | Leu | Val | Lys | Arg | Leu | Ala | Lys | Lys | Tyr | His | Ala | Phe | Leu | Ala | Ser |
|                                            |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Glu                                        | Ala | Ile | Ile | Lys | Gln | Ile | Pro | Arg | Leu | Leu | Gly | Pro | Gly | Leu | Asn |
|                                            |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Lys                                        | Ala | Gly | Lys | Phe | Pro | Thr | Leu | Val | Thr | His | Gln |     |     |     |     |
|                                            | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:103 |            |            |            |            |             |     |
|------------------------------------------|------------|------------|------------|------------|-------------|-----|
| acttcccctc                               | cgatcctcgt | cgcgcagcga | tccaccgcga | cctcctctcg | cgacctcgcc  | 60  |
| gtcgccgcag                               | ccttgcccat | gtcgatcttc | gagtataatg | ggtcgcccg  | ggtggcgatg  | 120 |
| gtggggaaga                               | actgtttcgc | gatcgccagc | gaccggcggc | tggcggtgca | gcttcagacc  | 180 |
| atcgcgacag                               | acttccagcg | ggtgttcaag | gtccacgaca | agctttacat | cggcctctct  | 240 |
| gggctcgcca                               | ctgacgcccc | gacgctgtac | cagcggtttg | tgttcaggca | caagctgtat  | 300 |
| cagctgcggg                               | aggagangga | catnaagccc | gagacctttg | ccagccttgt | ctctgcgcct  | 360 |
| ctctacggag                               | agagattcgg | gccatatctc | tgccagccag | tcattgctgg | acttgagagat | 420 |
| gacaacgtac                               | catttatctt |            |            |            |             |     |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | Pro | Pro | Ile | Leu | Val | Ala | Asp | Ala | Ser | Thr | Arg | Thr | Leu | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Asp | Leu | Ala | Val | Ala | Ala | Ala | Leu | Ala | Met | Ser | Ile | Phe | Glu | Tyr |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:

| Table 1. Demographic characteristics of the study population |             |
|--------------------------------------------------------------|-------------|
| Age (years)                                                  | Mean (SD)   |
| Male                                                         | 55.2 (10.5) |
| Female                                                       | 56.8 (11.2) |
| Marital status                                               |             |
| Married                                                      | 78.5%       |
| Single                                                       | 21.5%       |
| Education level                                              |             |
| High school or above                                         | 65.2%       |
| Below high school                                            | 34.8%       |
| Occupation                                                   |             |
| Professional                                                 | 45.1%       |
| Managerial                                                   | 22.3%       |
| Technical                                                    | 18.7%       |
| Service                                                      | 12.9%       |
| Unemployed                                                   | 1.0%        |
| Income (USD/month)                                           |             |
| < 1000                                                       | 15.3%       |
| 1000-2000                                                    | 32.1%       |
| 2000-3000                                                    | 28.5%       |
| > 3000                                                       | 24.1%       |
| Health insurance                                             |             |
| Yes                                                          | 89.2%       |
| No                                                           | 10.8%       |
| Comorbidities                                                |             |
| Hypertension                                                 | 42.5%       |
| Diabetes                                                     | 18.7%       |
| Cholesterol                                                  | 35.2%       |
| Smoking status                                               |             |
| Current smoker                                               | 12.1%       |
| Former smoker                                                | 25.3%       |
| Non-smoker                                                   | 62.6%       |

Met Ser Ile Phe Glu Tyr Asn Gly Ser Ala Val Val Ala Met Val Gly  
1 5 10 15  
Lys Asn Cys Phe Ala Ile Ala Ser Asp Arg Arg Leu Gly Val Gln Leu  
20 25 30  
Gln Thr Ile Ala Thr Asp Phe Gln Arg Val Phe Lys Val His Asp Lys  
35 40 45  
Leu Tyr Ile Gly Leu Ser Gly Leu Ala Thr Asp Ala Gln Thr Leu Tyr  
50 55 60  
Gln Arg Leu Val Phe Arg His Lys Leu Tyr Gln Leu Arg Glu Glu Xaa  
65 70 75 80  
Asp Xaa Lys Pro Glu Thr Phe Ala Ser Leu Val Ser Ala Leu Leu Tyr  
85 90 95  
Glu Lys Arg Phe Gly Pro Tyr Phe Cys Gln Pro Val Ile Ala Gly Leu  
100 105 110  
Gly Asp Asp Asn Val Pro Phe Ile  
115 120

(2) INFORMATION FOR SEQ ID NO:1443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..437
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| aaaatcctca gatccgcccc ctctccacc cttgckccgc gctttcacag ctctcccgcc    | 60  |
| tccggatcca gatccgccc caccaacgcc tgctcctccc cctcctgctg caccaccacc    | 120 |
| atcaagaggt ccagcagggc ggcacggcas snccggcggc gcgacatggg gcgtgacggc   | 180 |
| ggtggcgggtg tcgcggcggc atgtctgact cggtgctccg gaagggtgctc ctctcctact | 240 |
| tctacgtggc ggtgtggatc ttctctctct tctccgtcat cgtctacaac aagtacatcc   | 300 |
| tcgacccaaa gatgtacaac tggcccttcc ccatctcgct caccatggta cacatgggtt   | 360 |
| tctgtctatc cctcgccgtc gcgctcgctc gcgtcctccg ggtcgtcgac tccccacatc   | 420 |
| gccctccatg acgcgcg                                                  |     |

(2) INFORMATION FOR SEQ ID NO:1444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444:

Lys Ile Leu Arg Ser Ala Pro Ser Ser Thr Leu Xaa Pro Arg Phe His  
1 5 10 15  
Ser Ser Pro Ala Ser Gly Ser Arg Ser Ala Ala Thr Asn Ala Cys Ser  
20 25 30  
Ser Pro Ser Cys Cys Thr Thr Thr Ile Lys Arg Ser Ser Arg Ala Ala  
35 40 45  
Arg Xaa Xaa Gly Gly Gly Asp Met Gly Arg Asp Gly Gly Gly Gly Val  
50 55 60  
Ala Ala Ala Cys Leu Thr Arg Cys Ser Gly Arg Cys Ser Ser Pro Thr  
65 70 75 80  
Ser Thr Trp Arg Cys Gly Ser Ser Ser Pro Ser Pro Ser Ser Thr  
85 90 95  
Thr Ser Thr Ser Ser Thr Gln Arg Cys Thr Thr Gly Pro Ser Pro Ser

DOCKET# 08668950

Ala  
145

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..90

- (D) OTHER INFORMATION: / Ceres Seq. ID 1598049

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445:

(2) INFORMATION FOR SEQ ID NO:1446:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids

- (B) TYPE: amino acid

- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..76

- (D) OTHER INFORMATION: / Ceres Seq. ID 1598050

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446:

(2) INFORMATION FOR SEQ ID NO:1447:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs

- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447:

(2) INFORMATION FOR SEQ ID NO:1448:

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1598052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:

(2) INFORMATION FOR SEQ ID NO:1449:

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1598053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:

(2) INFORMATION FOR SEQ ID NO:1450:

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1598054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Glu | Thr | Glu | Thr | Phe | Ala | Phe | Gln | Ala | Glu | Ile | Asn | Gln |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1454:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454:

(2) INFORMATION FOR SEQ ID NO:1455:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455:

(2) INFORMATION FOR SEQ ID NO:1456:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Ser | Asn | Pro | Ser | Ala | Arg | Arg | His | Thr | Cys | Arg | Cys | Tyr | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Val | Pro | Arg | Leu | Leu | Ser | Arg | Arg | Arg | Asn | Asp | Glu | Ala | His | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Gly | Trp | Asn | Cys | Trp | Gln | Ile | Trp | Asn | Gln | Val | Trp | Arg | Tyr | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Arg | Xaa | Lys | Phe | Lys | Lys | Met | Glu | Val | Ser | Gln | His | Ser | Lys | Tyr | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Glu | Phe | Cys | Gly | Lys | Phe | Ala | Val | Lys | Arg |     |     |     |     |     |



65 70 75  
(2) INFORMATION FOR SEQ ID NO:1457:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..72  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598065  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457:  
Ser Ser Leu Thr Leu Ala Arg Ala Ala Thr Pro Ala Val Ala Thr Ala  
1 5 10 15  
Pro Tyr Leu Ala Cys Phe Pro Val Ala Glu Met Thr Lys Arg Thr Lys  
20 25 30  
Lys Ala Gly Ile Val Gly Lys Tyr Gly Thr Arg Tyr Gly Ala Thr Cys  
35 40 45  
Val Xaa Asn Ser Arg Arg Trp Arg Tyr Leu Ser Thr Pro Ser Thr Ser  
50 55 60  
Ala Ser Phe Val Gly Ser Leu Leu  
65 70

(2) INFORMATION FOR SEQ ID NO:1458:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..46  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598066  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458:  
Met Thr Lys Arg Thr Lys Lys Ala Gly Ile Val Gly Lys Tyr Gly Thr  
1 5 10 15  
Arg Tyr Gly Ala Thr Cys Val Xaa Asn Ser Arg Arg Trp Arg Tyr Leu  
20 25 30  
Ser Thr Pro Ser Thr Ser Ala Ser Phe Val Gly Ser Leu Leu  
35 40 45

(2) INFORMATION FOR SEQ ID NO:1459:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 305 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..305  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598071  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459:  
ctacgcggttr cgacacagcc aaaccatcct cctctccgcc gcccgccgca gcagcaccca 60  
ccggcaagat gaagacgata ctggcgctcgg agaattggac atcccgaggc gtcacgggtca 120  
cgggtggccgc caagctggtc acgggtggagg gccccgcggg caakctcacc cgcaacttca 180  
agcacctcaa cctcgacttc canctgcagg aggcgcggccg caagctcaag gtggacgcct 240  
ggttcggcac ccgcccacc atggccgccca tccgcaccgc catctccac gtcagaacc 300  
tcac

(2) INFORMATION FOR SEQ ID NO:1460:  
(i) SEQUENCE CHARACTERISTICS:

09689960-101300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:

(2) INFORMATION FOR SEQ ID NO:1461:

(A) LENGTH: 101 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1598073

(2) INFORMATION FOR SEQ ID NO:1462:

(A) LENGTH: 79 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1598074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462:

Met Lys Thr Ile Leu Ala Ser Glu Asn Trp Thr Ser Arg Ser Val Thr  
1                   5                   10                   15  
Val Thr Val Ala Ala Lys Leu Val Thr Val Glu Gly Pro Arg Gly Xaa  
                  20                   25                   30  
Leu Thr Arg Asn Phe Lys His Leu Asn Leu Asp Phe Xaa Leu Gln Glu  
                  35                   40                   45  
Ala Gly Arg Lys Leu Lys Val Asp Ala Trp Phe Gly Thr Arg Arg Thr  
                  50                   55                   60  
Met Ala Ala Ile Arg Thr Ala Ile Ser His Val Gln Asn Leu Ile  
65                   70                   75

(2) INFORMATION FOR SEQ ID NO:1463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..331
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463:

attatcacgg cggcgtggc ggasggaagg cgaaggagta gcagcagcag gcgrcgcgat           60  
gtagcggctc cccacctcga gcttrccacc atggctagag gattgaagaa gcatttgaag           120  
aggctcaatg cgcccaagca ttgatgctg gacaagcttg gcggastttt gctccaagc           180  
catcttctgg acctcacaag tctagggart scctgccact gatcctcatc atcaggaaca           240  
ggctcaagta tgctcttaca taccgtgagt catttccatc ctgatgcaac gccatgtact           300  
tgttgatggc aaggtcagga cagacaagac c

(2) INFORMATION FOR SEQ ID NO:1464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1464:

Ile Ile Thr Ala Ala Val Ala Xaa Gly Arg Arg Arg Ser Ser Ser Ser  
1                   5                   10                   15  
Arg Xaa Arg Asp Val Ala Ala Pro His Leu Glu Leu Xaa Thr Met Ala  
                  20                   25                   30  
Arg Gly Leu Lys Lys His Leu Lys Arg Leu Asn Ala Pro Lys His Trp  
                  35                   40                   45  
Met Leu Asp Lys Leu Gly Gly Xaa Leu Leu Pro Ser His Leu Leu Asp  
                  50                   55                   60  
Leu Thr Ser Leu Gly Xaa Xaa Cys His  
65                   70

(2) INFORMATION FOR SEQ ID NO:1465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..43

005701 08658960

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide  
(B) LOCATION: 1..92  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598110

| (A1) SEQUENCE DESCRIPTION: 100 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|--------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met                            | Ala | Lys | Leu | Ala | Glu | Gln | Ala | Glu | Arg | Tyr | Glu | Glu | Met | Val | Glu |  |
| 1                              |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Tyr                            | Met | Glu | Lys | Val | Ala | Lys | Thr | Val | Asp | Val | Glu | Glu | Leu | Thr | Val |  |
|                                |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu                            | Glu | Arg | Asn | Leu | Leu | Ser | Val | Ala | Tyr | Lys | Asn | Val | Ile | Gly | Ala |  |
|                                |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg                            | Arg | Ala | Ser | Trp | Arg | Ile | Ile | Ser | Ser | Ile | Glu | His | Lys | Glu | Glu |  |
|                                | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ser                            | Arg | Lys | Asn | Glu | Glu | His | Val | Ile | Gln | Ile | Lys | Glu | Tyr | Arg | Gly |  |
| 65                             |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Lys                            | Ile | Glu | Ala | Glu | Leu | Ser | Asn | Ile | Cys | Asp | Gly |     |     |     |     |  |
|                                |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     |     |  |

(A) LENGTH: 79 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(A) NAME/KEY: peptide  
(B) LOCATION: 1..79  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598111

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Glu | Tyr | Met | Glu | Lys | Val | Ala | Lys | Thr | Val | Asp | Val | Glu | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Thr | Val | Glu | Glu | Arg | Asn | Leu | Leu | Ser | Val | Ala | Tyr | Lys | Asn | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Gly | Ala | Arg | Arg | Ala | Ser | Trp | Arg | Ile | Ile | Ser | Ser | Ile | Glu | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Glu | Glu | Ser | Arg | Lys | Asn | Glu | Glu | His | Val | Ile | Gln | Ile | Lys | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Arg | Gly | Lys | Ile | Glu | Ala | Glu | Leu | Ser | Asn | Ile | Cys | Asp | Gly |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(A) LENGTH: 414 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(A) NAME/KEY: -  
(B) LOCATION: 1..414  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598115

| (12) Sequence |             | Count      |            |            |             |     |
|---------------|-------------|------------|------------|------------|-------------|-----|
| attcttcccc    | ctccggcgcc  | gctccccag  | acacttcgcc | gccggcaaga | tgggcgcgct  | 60  |
| gattcgcgct    | cagsaagggg  | gcggggtccg | tgttcaagtc | ccatacccat | caccgcaagg  | 120 |
| ccctgcggtt    | ccgggtccctc | gacttcggcg | agcgcaacgg | gtacttgaag | ggcgtggtca  | 180 |
| ccgacgtcat    | ccacgacccg  | ggcgcggcgg | cgccgcttgg | ccaaggtcac | cttcacgccat | 240 |
| ccattccggg    | acaagcacca  | gaaggagctg | ttcgtggtcg | ctggaagcat | gtacactggc  | 300 |
| cagttcggtt    | actcgggacg  | ccgttgctac | actctccatt | ggcaacgttc | tgccgctcag  | 360 |
| ggggtacctg    | taggggtgccg | ttgtctgcaa | cgtttgagca | ccacgtcggg | ratc        |     |

(A) LENGTH: 123 amino acids

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471:

(2) INFORMATION FOR SEQ ID NO:1472:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472:

(2) INFORMATION FOR SEQ ID NO:1473:

(B) LOCATION: 1..465

(D) OTHER INFORMATION: / Ceres Seq. ID 1598124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| attcgtcccc | ggccgcccgc | ctcccagttct | ccacgcggaa | sagcgcctcg | caacgctcyd | 60  |
| acccaatggc | gnngacgtcg | aagctgtcga  | tgggcatcaa | gckcgcgtns | gatcgcacgc | 120 |
| gtaccaccgc | cgtggctctg | ggccatcaag  | gcaagaacgg | mggcgtcttc | cccaaggccg | 180 |
| agaagcccgc | cgccgcccgc | gaacccaagt  | tctaccccgc | cgacgacgtc | aagcctcgck | 240 |
| tcccagcacc | cgcaagcyta | wtcccaccaa  | gtcagggtcg | agcatcacgc | ctgggacggt | 300 |
| gctgatcctc | ctcgcggggc | gcttcatggg  | gaagakagtg | gtgttcctca | agcagctcaa | 360 |
| ctccggcctg | ctcctcgtct | ctgggtccatt | caagatcaat | ggagtaccga | tccgtcgtgt | 420 |
| camcagacct | atgtcattgc | tacatcaacc  | aaggttgaca | tctct      |            |     |

(2) INFORMATION FOR SEQ ID NO:1474:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1598125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Arg | Pro | Arg | Pro | Pro | Xaa | Ser | Gln | Ser | Pro | Arg | Gly | Xaa | Ala | Pro |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Arg | Asn | Ala | Xaa | Thr | Gln | Trp | Xaa | Xaa | Arg | Arg | Ser | Cys | Arg | Trp | Ala |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Ser | Xaa | Arg | Xaa | Ile | Ala | Arg | Val | Pro | Pro | Pro | Trp | Leu | Trp | Ala |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ile | Lys | Ala | Arg | Thr | Xaa | Ala | Ser | Ser | Pro | Arg | Pro | Arg | Ser | Pro | Pro |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Pro | Pro | Arg | Asn | Pro | Ser | Ser | Thr | Pro | Pro | Thr | Thr | Ser | Ser | Leu | Xaa |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Ser | Gln | His | Pro | Gln | Xaa | Xaa | Ser | His | Gln | Ala | Gln | Val | Glu | His | His |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ala | Trp | Asp | Gly | Ala | Asp | Pro | Pro | Arg | Gly | Ala | Leu | His | Gly | Glu | Xaa |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ser | Gly | Val | Pro | Gln | Ala | Ala | Gln | Leu | Arg | Pro | Ala | Pro | Arg | Leu | Trp |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ser | Ile | Gln | Asp | Gln | Trp | Ser | Thr | Asp | Pro | Ser | Cys | Xaa | Gln | Thr | Tyr |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Val | Ile | Ala | Thr | Ser | Thr | Lys | Val | Asp | Ile | Ser |     |     |     |     |     |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1475:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1598126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Phe | Val | Pro | Gly | Arg | Arg | Xaa | Pro | Ser | Leu | His | Ala | Glu | Xaa | Arg | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ala | Thr | Leu | Xaa | Pro | Asn | Gly | Xaa | Asp | Val | Glu | Ala | Val | Asp | Gly | His |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gln | Xaa | Arg | Xaa | Xaa | Ser | His | Ala | Tyr | His | Arg | Arg | Gly | Ser | Gly | Pro |  |
|     |     |     | 35  |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Ser | Arg | Gln | Glu | Arg | Xaa | Arg | Leu | Pro | Gln | Gly | Arg | Glu | Ala | Arg | Arg |  |

(2) INFORMATION FOR SEQ ID NO:1478:



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478:

(2) INFORMATION FOR SEQ ID NO:1479:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479:

(2) INFORMATION FOR SEQ ID NO:1480:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:

(2) INFORMATION FOR SEQ ID NO:1481:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1598139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481:

Cys Glu Ile Ser Leu Xaa Ser Tyr Arg Gln  
50 55

(2) INFORMATION FOR SEQ ID NO:1482:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..52

(D) OTHER INFORMATION: / Ceres Seq. ID 1598140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482:

Ser Tyr Arg Gln  
50

(2) INFORMATION FOR SEQ ID NO:1483:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..43

(D) OTHER INFORMATION: / Ceres Seq. ID 1598141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483:

Tyr Leu Arg Asn Ile Ile Xaa Phe Val Ser Ser  
35 40

(2) INFORMATION FOR SEQ ID NO:1484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..500
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| akatccaggt actcttcctt tcgccgcggc tgagaagcaa ctctccctct ctgtcctctt | 60  |
| cctgtcgccg cactcatttt ctcttgccgg gtggaatagg gaacggccat acaccatggc | 120 |
| ggatttctcc aaggaatctt gcccttctgt gaagaacatt ttacttctgg attctgaagg | 180 |
| aaagcgtggt gctgtaaagt atttctcaga tgattggccg actaatgcat caaagttagc | 240 |
| ctacgaaaag tctgttttta ctaaaactct aaagacaaat gcacggacag aagctgagat | 300 |
| aacattgttt gatggttata ttgtcgttta caagtttgta catgaccttc acctttttgt | 360 |
| caccgctgga gatgatgaga atgagctcat cttagcaagt gtactacatg gtttttctga | 420 |
| ttctgttggt cttctactca ggggtgatgt tgagaagcgg actgcgcttg agaacttgga | 480 |
| tttgatactt ctctgcattg                                             |     |

(2) INFORMATION FOR SEQ ID NO:1485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..166
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Xaa | Pro | Gly | Thr | Leu | Pro | Phe | Ala | Ala | Ala | Glu | Lys | Gln | Leu | Ser | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |  |
| Ser | Val | Leu | Phe | Leu | Ser | Pro | His | Ser | Phe | Ser | Leu | Ala | Gly | Trp | Asn |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg | Glu | Arg | Pro | Tyr | Thr | Met | Ala | Asp | Phe | Ser | Lys | Glu | Ser | Cys | Pro |  |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Val | Lys | Asn | Ile | Leu | Leu | Leu | Asp | Ser | Glu | Gly | Lys | Arg | Val | Ala |  |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Val | Lys | Tyr | Phe | Ser | Asp | Asp | Trp | Pro | Thr | Asn | Ala | Ser | Lys | Leu | Ala |  |
|     |     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     |     | 80  |  |
| Tyr | Glu | Lys | Ser | Val | Phe | Thr | Lys | Thr | Leu | Lys | Thr | Asn | Ala | Arg | Thr |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Glu | Ala | Glu | Ile | Thr | Leu | Phe | Asp | Gly | Tyr | Ile | Val | Val | Tyr | Lys | Phe |  |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Val | His | Asp | Leu | His | Phe | Phe | Val | Thr | Ala | Gly | Asp | Asp | Glu | Asn | Glu |  |
|     |     |     |     | 115 |     |     | 120 |     |     |     | 125 |     |     |     |     |  |
| Leu | Ile | Leu | Ala | Ser | Val | Leu | His | Gly | Phe | Ser | Asp | Ser | Val | Gly | Leu |  |
|     |     |     |     | 130 |     |     | 135 |     |     |     | 140 |     |     |     |     |  |
| Leu | Leu | Arg | Gly | Asp | Val | Glu | Lys | Arg | Thr | Ala | Leu | Glu | Asn | Leu | Asp |  |
|     |     |     |     | 145 |     |     | 150 |     |     | 155 |     |     |     |     | 160 |  |
| Leu | Ile | Leu | Leu | Cys | Ile |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

096599010300

Met Ala Pro Arg Ser Arg Ser Arg Ala Ser Ser Trp Ala Ser Thr Arg  
1 5 10 15  
Ala Met Ser Ser Pro Ser Ala Xaa Ala Ser Ala Pro Val Pro Pro Gln  
20 25 30

Gly Lys Ala Thr Lys Arg Val Ser Met Val Arg Gly Leu Ile Arg Glu  
35 40 45  
Val Ala Gly Phe Ala Pro Tyr Glu Lys Arg Ile Thr Glu Leu Leu Lys  
50 55 60  
Val Gly Lys Asp Lys Arg Ala Leu Lys Leu Ala Lys Arg Lys Leu Gly  
65 70 75 80  
Thr His Lys Arg Ala Lys Lys Lys Arg Glu Met Met Gly Val Leu  
85 90 95  
Arg Lys Met Arg Ser Ala Gly Thr His Thr Asp Lys Lys Lys  
100 105 110

(2) INFORMATION FOR SEQ ID NO:1489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:

Met Ser Ser Pro Ser Ala Xaa Ala Ser Ala Pro Val Pro Pro Gln Gly  
1 5 10 15  
Lys Ala Thr Lys Arg Val Ser Met Val Arg Gly Leu Ile Arg Glu Val  
20 25 30  
Ala Gly Phe Ala Pro Tyr Glu Lys Arg Ile Thr Glu Leu Leu Lys Val  
35 40 45  
Gly Lys Asp Lys Arg Ala Leu Lys Leu Ala Lys Arg Lys Leu Gly Thr  
50 55 60  
His Lys Arg Ala Lys Lys Lys Arg Glu Glu Met Met Gly Val Leu Arg  
65 70 75 80  
Lys Met Arg Ser Ala Gly Thr His Thr Asp Lys Lys Lys  
85 90

(2) INFORMATION FOR SEQ ID NO:1490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:

Met Val Arg Gly Leu Ile Arg Glu Val Ala Gly Phe Ala Pro Tyr Glu  
1 5 10 15  
Lys Arg Ile Thr Glu Leu Leu Lys Val Gly Lys Asp Lys Arg Ala Leu  
20 25 30  
Lys Leu Ala Lys Arg Lys Leu Gly Thr His Lys Arg Ala Lys Lys Lys  
35 40 45  
Arg Glu Glu Met Met Gly Val Leu Arg Lys Met Arg Ser Ala Gly Thr  
50 55 60  
His Thr Asp Lys Lys Lys  
65 70

(2) INFORMATION FOR SEQ ID NO:1491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

00689980.101300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:

(2) INFORMATION FOR SEQ ID NO:1492:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:

(2) INFORMATION FOR SEQ ID NO:1493:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Leu | Val | Arg | Ser | Pro | Trp | Arg | Thr | Pro | Ala | Ile | Thr | Ser | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Trp | Leu | Arg | Met | Gly | Leu | Ser | Ser | Arg | Ser | Leu | Arg | Lys | Ser | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Asp | Leu | Val | Gln | Xaa | Gly | Arg | Thr | Arg | Leu | Ser | Arg | Arg | Asp | Gly |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Thr | Gln | Asp | Met | Gly | Ser | Val | Glu | Val | Thr | Arg | Glu | Ala | Arg | Leu | Pro |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Thr | Lys | Val | Leu | Trp | Met | Arg | Arg | Met | Arg | Val | Leu | Arg | Arg | Leu | Leu |

(2) INFORMATION FOR SEQ ID NO:1494:

(A) LENGTH: 71 amino acids

(C) STRANDEDNESS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1598174

Met Gly Leu Ser Ser Arg Ser Leu Arg Lys Ser Thr Leu Asp Leu Val  
1 5 10 15

Gly Ser Val Glu Val Thr Arg Glu Ala Arg Leu Pro Thr Lys Val Leu  
35 40 45

Glu Pro Arg Arg Ser Thr Ser

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..459

(D) OTHER INFORMATION: / Ceres Seq. ID 1598193

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atatatccct | gtttaatcaa | tccttcaagc | gcaangcctc | ctcctcgtcg | tccggtcgtg | 60  |
| agaagggatg | gcgggccgtg | gcaaggctat | cggcgctggc | gccgaagaag | gcaacgtcga | 120 |
| ggagctccaa | ggccggactc | cagttccccg | tcggcaggat | tgctaggttc | ctcaaggcgg | 180 |
| gcaagtacgc | tgagcgcgtc | ggcscggcgc | ccccgtgtac | ctcgccgccg | tcctcgagta | 240 |
| cctcgcggct | gaggtttctg | aacttgccgg | gaacgcgcgg | aggacaacaa | gaagacccgc | 300 |
| attgtgccgc | gccacatcca | cgttgctgtg | cgcaacgacg | agganctgac | caaactgttg | 360 |
| ggtggtgcca | ccatcgcgac | cggagggtgt | atgcctaaca | tccatcagca | tctgctcccc | 420 |
| aagaaggctg | cctcctccaa | ggccagtgtc | gacgacgac  |            |            |     |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..83

(D) OTHER INFORMATION: / Ceres Seq. ID 1598194

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ser | Pro | Cys | Leu | Ile | Asn | Pro | Ser | Ser | Ala | Xaa | Pro | Pro | Pro | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Arg Pro Val Val Arg Arg Asp Gly Gly Pro Trp Gln Gly Tyr Arg Arg  
20 25 30

Trp Arg Arg Arg Arg Gln Arg Arg Gly Ala Pro Arg Pro Asp Ser Ser  
35 40 45  
Ser Pro Ser Ala Gly Leu Leu Gly Ser Ser Arg Arg Ala Ser Thr Leu  
50 55 60  
Ser Ala Ser Xaa Arg Arg Pro Arg Val Pro Arg Arg Arg Pro Arg Val  
65 70 75 80  
Pro Arg Gly

(2) INFORMATION FOR SEQ ID NO:1497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:

Ile Ser Leu Phe Asn Gln Ser Phe Lys Arg Xaa Ala Ser Ser Ser Ser  
1 5 10 15  
Ser Gly Arg Glu Lys Gly Trp Arg Ala Val Ala Arg Leu Ser Ala Leu  
20 25 30  
Ala Pro Lys Lys Ala Thr Ser Arg Ser Ser Lys Ala Gly Leu Gln Phe  
35 40 45  
Pro Val Gly Arg Ile Ala Arg Phe Leu Lys Ala Gly Lys Tyr Ala Glu  
50 55 60  
Arg Val Gly Xaa Ala Pro Pro Cys Thr Ser Pro Pro Ser Ser Ser Thr  
65 70 75 80  
Ser Arg Leu Arg Phe Ser Asn Leu Pro Gly Thr Pro Arg Gly Gln Gln  
85 90 95  
Glu Asp Pro His Cys Ala Ala Pro His Pro Ala Cys Cys Ala Gln Arg  
100 105 110  
Arg Gly Xaa Asp Gln Thr Val Gly Trp Cys His His Arg Asp Arg Arg  
115 120 125  
Cys Tyr Ala  
130

(2) INFORMATION FOR SEQ ID NO:1498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..485
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498:

tgtgtgggaa gtggtggaga gaagctattg cctgagtggg actcagagaa aggcattgag 60  
ctgatacctta gtacagaaat tgtcaaagct gatctttcca ccaagactct gactagtga 120  
gctggagcaa actttacata tgagatcttg ctcattgcta ctggctcctc ggatcataaag 180  
ctcacgatt ttggcacaca aggagctgat tctaacaaca ttctatatct aagggaaatt 240  
gatgatgctg acaagctggg tgcagctatc caggcaaaga aggggtggcaa ggcagtgggt 300  
gttggaggag gttatatcgg cctcgaactg agtgcagccc tgaagatcaa tgactttgat 360  
gtcactatgg tgtttcctga accttgggtgc atgcctcgcc tcttcaactgc cgatattgct 420  
gctttctatg aggcttacta tactaacaac ggtgtaaaga tcttgaaggg cacgctagct 480  
gttgg

(2) INFORMATION FOR SEQ ID NO:1499:

(i) SEQUENCE CHARACTERISTICS:



(A) LENGTH: 161 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..161  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598208  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:  
Cys Val Gly Ser Gly Gly Glu Lys Leu Leu Pro Glu Trp Tyr Ser Glu  
1 5 10 15  
Lys Gly Ile Glu Leu Ile Leu Ser Thr Glu Ile Val Lys Ala Asp Leu  
20 25 30  
Ser Thr Lys Thr Leu Thr Ser Ala Ala Gly Ala Asn Phe Thr Tyr Glu  
35 40 45  
Ile Leu Leu Ile Ala Thr Gly Ser Ser Val Ile Lys Leu Thr Asp Phe  
50 55 60  
Gly Thr Gln Gly Ala Asp Ser Asn Asn Ile Leu Tyr Leu Arg Glu Ile  
65 70 75 80  
Asp Asp Ala Asp Lys Leu Val Ala Ala Ile Gln Ala Lys Lys Gly Gly  
85 90 95  
Lys Ala Val Val Val Gly Gly Gly Tyr Ile Gly Leu Glu Leu Ser Ala  
100 105 110  
Ala Leu Lys Ile Asn Asp Phe Asp Val Thr Met Val Phe Pro Glu Pro  
115 120 125  
Trp Cys Met Pro Arg Leu Phe Thr Ala Asp Ile Ala Ala Phe Tyr Glu  
130 135 140  
Ala Tyr Tyr Thr Asn Lys Gly Val Lys Ile Leu Lys Gly Thr Leu Ala  
145 150 155 160  
Val

(2) INFORMATION FOR SEQ ID NO:1500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..193  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aactccaagc gccaccaatc tcgccttccg aggaaaccca ccagcccacc acagaccgga | 60  |
| gcggaagaag ccatgtccgg gcgcggcaag ggtggcaagg ggctcggcaa gggcggcgcg | 120 |
| amkaccgga aggttctgcg cgacaacatc cagggcatca ccaagccggc gatccggcgn  | 180 |
| ctgggcgagg agg                                                    |     |

(2) INFORMATION FOR SEQ ID NO:1501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..64  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1501:

Asn Ser Lys Arg His Gln Ser Arg Leu Pro Arg Lys Pro Thr Ser Pro

09669900 "08669960

(2) INFORMATION FOR SEQ ID NO:1502:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1598215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1502:

(2) INFORMATION FOR SEQ ID NO:1503:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1598216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1503:

(2) INFORMATION FOR SEQ ID NO:1504:

(A) LENGTH: 123 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..123





(A) NAME/KEY: -

(B) LOCATION: 1..478

(D) OTHER INFORMATION: / Ceres Seq. ID 1598227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1510:

|             |            |             |            |            |             |     |
|-------------|------------|-------------|------------|------------|-------------|-----|
| aattcgccac  | tgacgttcat | tccgcttgct  | tgattgctcc | aggtagctcc | attcgagtc   | 60  |
| ggccgtgtcc  | tggagccgc  | gggagatggc  | ggatcaggag | acagtagctg | tggttgaggc  | 120 |
| acctaccccc  | gttctagggg | aacgatggac  | ctgatgactg | ccctgcagct | cgatcatgaag | 180 |
| aagtcagggtg | ctcacgatgg | ccttggtgaag | ggctcttctg | aggctgcca  | agccatcgag  | 240 |
| aagcatgccg  | ctcagctctg | cgtgcttgcc  | gaggactgcg | accagcctga | ttatgtcaag  | 300 |
| ctgggtgaagg | ctctctgccc | tgagcacaat  | gtccacctgg | ttactgtgcc | tagcgccaaa  | 360 |
| actcttgagg  | agtgggctgg | gctttgcaag  | atcgactctg | agggcaagg  | cgaggaaggt  | 420 |
| tgtaggctgc  | tcctgtgttg | ttgtcaagga  | ctacggcgaa | gaatctkaag | gccttaac    |     |

(2) INFORMATION FOR SEQ ID NO:1511:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1598228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1511:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Leu | Met | Thr | Ala | Leu | Gln | Leu | Val | Met | Lys | Lys | Ser | Gly | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Asp | Gly | Leu | Val | Lys | Gly | Leu | Arg | Glu | Ala | Ala | Lys | Ala | Ile | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | His | Ala | Ala | Gln | Leu | Cys | Val | Leu | Ala | Glu | Asp | Cys | Asp | Gln | Pro |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Asp | Tyr | Val | Lys | Leu | Val | Lys | Ala | Leu | Cys | Ala | Glu | His | Asn | Val | His |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Leu | Val | Thr | Val | Pro | Ser | Ala | Lys | Thr | Leu | Gly | Glu | Trp | Ala | Gly | Leu |
|     |     |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |
| Cys | Lys | Ile | Asp | Ser | Glu | Gly | Lys | Gly | Glu | Glu | Gly | Cys | Arg | Leu | Leu |
|     |     |     |     |     |     |     | 85  |     |     |     | 90  |     |     | 95  |     |
| Leu | Cys | Cys | Cys | Gln | Gly | Leu | Arg | Arg | Arg | Ile | Xaa | Arg | Pro |     |     |
|     |     |     |     |     |     |     | 100 |     |     |     | 105 |     |     | 110 |     |

(2) INFORMATION FOR SEQ ID NO:1512:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1598229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1512:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Ala | Leu | Gln | Leu | Val | Met | Lys | Lys | Ser | Gly | Ala | His | Asp | Gly |
| 1   |     |     |     |     |     |     |     |     |     |     |     |     |     | 15  |     |
| Leu | Val | Lys | Gly | Leu | Arg | Glu | Ala | Ala | Lys | Ala | Ile | Glu | Lys | His | Ala |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 30  |     |
| Ala | Gln | Leu | Cys | Val | Leu | Ala | Glu | Asp | Cys | Asp | Gln | Pro | Asp | Tyr | Val |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 45  |     |
| Lys | Leu | Val | Lys | Ala | Leu | Cys | Ala | Glu | His | Asn | Val | His | Leu | Val | Thr |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 60  |     |
| Val | Pro | Ser | Ala | Lys | Thr | Leu | Gly | Glu | Trp | Ala | Gly | Leu | Cys | Lys | Ile |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 75  | 80  |
| Asp | Ser | Glu | Gly | Lys | Gly | Glu | Glu | Gly | Cys | Arg | Leu | Leu | Leu | Cys | Cys |











(D) OTHER INFORMATION: / Ceres Seq. ID 1598259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1523:

Thr Thr Thr Ala Thr Arg Thr Ser Pro Leu Pro Arg Phe Xaa Ser Ser  
1 5 10 15  
Val Arg Val Val Leu Gly Phe Gly Asp Val Gly Ala Arg Gln Gly Arg  
20 25 30  
Gln Gly Ala Gly Gln Gly Arg Arg Gln Ala His Arg Lys Xaa Cys Ala  
35 40 45  
Thr Thr Ser Arg Ala Ser Arg Ser Arg Arg Ser Val Ala Gly Gln Glu  
50 55 60  
Gly Arg Arg Gln Ala His Phe Trp Ala His Leu Arg Gly Asn Pro Arg  
65 70 75 80  
Arg Ala Gln Asp Leu Pro Arg Glu Arg His Pro Arg Arg Arg His Leu  
85 90 95  
His Arg Ala Arg Pro Pro Gln Asp Cys His Arg His Gly Cys Arg Leu  
100 105 110  
Arg Ala Gln Ala Pro Gly Pro Asp Ala Leu Arg Leu Arg Arg Leu Gly  
115 120 125  
Xaa Pro Leu Leu Met Leu  
130

(2) INFORMATION FOR SEQ ID NO:1524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..374

(D) OTHER INFORMATION: / Ceres Seq. ID 1598271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1524:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| aacgcgcctc ctctcgccct cgctccgccg ccgccgccgc cgccgcacatca agcaccgcgc | 60  |
| ccgccgtcgc ctgaggtaga caccaatccg ccgccatggg gcgtatgcac agccgcggga   | 120 |
| agggtatctc atcgtcggcg ctgccgtaca agaggacgcc tccatcctgg ctcaagaccg   | 180 |
| ctgcctccga cgtggaggag atgatacaca aggcagcgaa gaagggacag atgccgtcgc   | 240 |
| agatcggcgt cctgctccgt gaccagcacg gtatccccct tgtcaagagc gtcaccggca   | 300 |
| gcaagatcct ccgcatactc aaggcccatg ggctggcacc agaaatcccc gaggacctgt   | 360 |
| acttctcat caag                                                      |     |

(2) INFORMATION FOR SEQ ID NO:1525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1598272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1525:

Asn Ala Pro Pro Leu Ala Leu Ala Pro Pro Pro Pro Pro His  
1 5 10 15  
Gln Ala Pro Ala Pro Pro Ser Pro Glu Val Asp Thr Asn Pro Pro Pro  
20 25 30  
Trp Gly Val Cys Thr Ala Ala Gly Arg Val Ser His Arg Arg Arg Cys  
35 40 45  
Arg Thr Arg Gly Arg Leu Leu Pro Gly Ser Arg Pro Leu Pro Pro Thr  
50 55 60  
Trp Arg Arg  
65

00000000 00000000

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1598273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1526:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Arg | Met | His | Ser | Arg | Gly | Lys | Gly | Ile | Ser | Ser | Ser | Ala | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Tyr | Lys | Arg | Thr | Pro | Pro | Thr | Trp | Leu | Lys | Thr | Ala | Ala | Ser | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Glu | Glu | Met | Ile | Thr | Lys | Ala | Ala | Lys | Lys | Gly | Gln | Met | Pro | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Ile | Gly | Val | Leu | Leu | Arg | Asp | Gln | His | Gly | Ile | Pro | Leu | Val | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Val | Thr | Gly | Ser | Lys | Ile | Leu | Arg | Ile | Leu | Lys | Ala | His | Gly | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Pro | Glu | Ile | Pro | Glu | Asp | Leu | Tyr | Phe | Leu | Ile | Lys |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1527:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..90

(D) OTHER INFORMATION: / Ceres Seq. ID 1598274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1527:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Ser | Arg | Gly | Lys | Gly | Ile | Ser | Ser | Ser | Ala | Leu | Pro | Tyr | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Thr | Pro | Pro | Thr | Trp | Leu | Lys | Thr | Ala | Ala | Ser | Asp | Val | Glu | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Ile | Thr | Lys | Ala | Ala | Lys | Lys | Gly | Gln | Met | Pro | Ser | Gln | Ile | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Leu | Leu | Arg | Asp | Gln | His | Gly | Ile | Pro | Leu | Val | Lys | Ser | Val | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Ser | Lys | Ile | Leu | Arg | Ile | Leu | Lys | Ala | His | Gly | Leu | Ala | Pro | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Pro | Glu | Asp | Leu | Tyr | Phe | Leu | Ile | Lys |     |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1528:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..197

(D) OTHER INFORMATION: / Ceres Seq. ID 1598290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1528:

aaaacaacaa caacaacccg cacaacggca cgattctyct cctccgtccg cgtmstctcg

gtttcggcga tgtcggggcg cggcaagggc ggcaaggggc tgggcaaggg cggcgcaagc 120  
knaccgcaag gkctgcgcga caacatccag ggcacacga agcggcgat ccgtagctgg 180  
ccaggagggg cggcgtc

(2) INFORMATION FOR SEQ ID NO:1529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1529:

Lys Thr Thr Thr Thr Thr Arg Thr Thr Ala Arg Phe Xaa Ser Ser Val  
1 5 10 15  
Arg Xaa Xaa Ser Val Ser Ala Met Ser Gly Arg Gly Lys Gly Gly Lys  
20 25 30  
Gly Leu Gly Lys Gly Gly Ala Ser Xaa Pro Gln Xaa Leu Arg Asp Asn  
35 40 45  
Ile Gln Gly Ile Thr Lys Pro Ala Ile Arg Ser Trp Pro Gly Gly Ala  
50 55 60  
Ala  
65

(2) INFORMATION FOR SEQ ID NO:1530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1530:

Lys Gln Gln Gln Gln Pro Ala Gln Arg His Asp Ser Xaa Pro Pro Ser  
1 5 10 15  
Ala Xaa Ser Arg Phe Arg Arg Cys Arg Gly Ala Ala Arg Ala Ala Arg  
20 25 30  
Gly Trp Ala Arg Ala Ala Gln Xaa Xaa Arg Lys Xaa Cys Ala Thr Thr  
35 40 45  
Ser Arg Ala Ser Arg Ser Arg Arg Ser Val Ala Gly Gln Glu Gly Arg  
50 55 60  
Arg  
65

(2) INFORMATION FOR SEQ ID NO:1531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..57
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1531:

Asn Asn Asn Asn Asn Pro His Asn Gly Thr Ile Xaa Leu Leu Arg Pro  
1 5 10 15

09689900 101300

Arg Xaa Leu Gly Phe Gly Asp Val Gly Ala Arg Gln Gly Arg Gln Gly  
20 25 30  
Ala Gly Gln Gly Arg Arg Lys Xaa Thr Ala Arg Xaa Ala Arg Gln His  
35 40 45  
Pro Gly His His Glu Ala Gly Asp Pro  
50 55

(2) INFORMATION FOR SEQ ID NO:1532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..517
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1532:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| acgacccaaa aaaggatcaa ggtgggagaw acaaaacaca aggyggcgtc cgcagcttcc | 60  |
| ccactccacg ttccgtgttt ccgactccgg tgactccacc accagcaacc cgtgcagcga | 120 |
| gcgcactccg accatcgcca tgtcgaggcg cggcgactgg gtctacgaga acaacggcgg | 180 |
| gacctgcgtg gccatcgccg gcgctgatta ctgtgtcgtc gctgcggaca cccgcctctc | 240 |
| tgtaggatac agtatcctca cgcgtgatca ctccaagatc tgcgacctgg ctgacaaatg | 300 |
| tgtactggca tcttctggct ttcaaggatg tattaaggct ctgcagaaga acctagctgc | 360 |
| cagagaattg ctgtaccaac accagcataa taaaaggatg agctgccccg ccatggcaca | 420 |
| gctcctctcc aataccctgt actacaagcg attcttccca tattacgct tcaatgtgct  | 480 |
| cggtgggctt nacagcgakg ggaaggatg cgttttc                           |     |

(2) INFORMATION FOR SEQ ID NO:1533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..172
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1533:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Arg Pro Lys Lys Gly Ser Arg Trp Glu Xaa Gln Asn Thr Arg Xaa Arg |  |
| 1 5 10 15                                                       |  |
| Pro Gln Leu Pro His Ser Thr Phe Arg Val Ser Asp Ser Gly Asp Ser |  |
| 20 25 30                                                        |  |
| Thr Thr Ser Asn Pro Cys Ser Glu Arg Thr Pro Thr Ile Ala Met Ser |  |
| 35 40 45                                                        |  |
| Arg Arg Gly Asp Trp Val Tyr Glu Asn Asn Gly Gly Thr Cys Val Ala |  |
| 50 55 60                                                        |  |
| Ile Ala Gly Ala Asp Tyr Cys Val Val Ala Ala Asp Thr Arg Leu Ser |  |
| 65 70 75 80                                                     |  |
| Val Gly Tyr Ser Ile Leu Thr Arg Asp His Ser Lys Ile Cys Asp Leu |  |
| 85 90 95                                                        |  |
| Ala Asp Lys Cys Val Leu Ala Ser Ser Gly Phe Gln Gly Asp Ile Lys |  |
| 100 105 110                                                     |  |
| Ala Leu Gln Lys Asn Leu Ala Ala Arg Glu Leu Leu Tyr Gln His Gln |  |
| 115 120 125                                                     |  |
| His Asn Lys Arg Met Ser Cys Pro Ala Met Ala Gln Leu Leu Ser Asn |  |
| 130 135 140                                                     |  |
| Thr Leu Tyr Tyr Lys Arg Phe Phe Pro Tyr Tyr Ala Phe Asn Val Leu |  |
| 145 150 155 160                                                 |  |
| Gly Gly Leu Xaa Ser Xaa Gly Lys Gly Cys Val Phe                 |  |
| 165 170                                                         |  |

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(2) INFORMATION FOR SEQ ID NO:1534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1534:

Met Ser Arg Arg Gly Asp Trp Val Tyr Glu Asn Asn Gly Gly Thr Cys  
1 5 10 15  
Val Ala Ile Ala Gly Ala Asp Tyr Cys Val Val Ala Ala Asp Thr Arg  
20 25 30  
Leu Ser Val Gly Tyr Ser Ile Leu Thr Arg Asp His Ser Lys Ile Cys  
35 40 45  
Asp Leu Ala Asp Lys Cys Val Leu Ala Ser Ser Gly Phe Gln Gly Asp  
50 55 60  
Ile Lys Ala Leu Gln Lys Asn Leu Ala Ala Arg Glu Leu Leu Tyr Gln  
65 70 75 80  
His Gln His Asn Lys Arg Met Ser Cys Pro Ala Met Ala Gln Leu Leu  
85 90 95  
Ser Asn Thr Leu Tyr Tyr Lys Arg Phe Phe Pro Tyr Tyr Ala Phe Asn  
100 105 110  
Val Leu Gly Gly Leu Xaa Ser Xaa Gly Lys Gly Cys Val Phe  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..180
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1535:

aaccgctatt cgtgtcctgg catccgcaga gagtttggtc cgtccaggca accaaaaagc 60  
gttgccccgc cgcgcagaga agaagagagc agaggaggat nggctcgtac gaagcagacc 120  
gcccgcgaagt tccacggggag gcaaggcccc ccgcaagcag ctcgccacca aggcggcgag 180

(2) INFORMATION FOR SEQ ID NO:1536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1536:

Asn Arg Tyr Ser Cys Pro Gly Ile Arg Arg Glu Phe Val Pro Ser Arg  
1 5 10 15  
Gln Pro Lys Ser Val Ala Pro Pro Arg Arg Glu Glu Glu Ser Arg Gly  
20 25 30  
Gly Xaa Ala Arg Thr Lys Gln Thr Ala Arg Lys Phe His Gly Arg Gln

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35 40 45  
Gly Pro Pro Gln Ala Ala Arg His Gln Gly Gly Glu  
50 55 60  
(2) INFORMATION FOR SEQ ID NO:1537:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..59  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598323  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1537:  
Thr Ala Ile Arg Val Leu Ala Ser Ala Glu Ser Leu Phe Arg Pro Gly  
1 5 10 15  
Asn Gln Lys Ala Leu Pro Arg Arg Ala Glu Lys Lys Arg Ala Glu Glu  
20 25 30  
Asp Xaa Leu Val Arg Ser Arg Pro Pro Ala Ser Ser Thr Gly Gly Lys  
35 40 45  
Ala Pro Arg Lys Gln Leu Ala Thr Lys Ala Ala  
50 55

(2) INFORMATION FOR SEQ ID NO:1538:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..59  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598324  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1538:  
Pro Leu Phe Val Ser Trp His Pro Gln Arg Val Cys Ser Val Gln Ala  
1 5 10 15  
Thr Lys Lys Arg Cys Pro Ala Ala Gln Arg Arg Arg Glu Gln Arg Arg  
20 25 30  
Xaa Gly Ser Tyr Glu Ala Asp Arg Pro Gln Val Pro Arg Glu Ala Arg  
35 40 45  
Pro Pro Ala Ser Ser Ser Pro Pro Arg Arg Arg  
50 55

(2) INFORMATION FOR SEQ ID NO:1539:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 486 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..486  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598333  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1539:  
cttccaccac gcatcactcc cgggtcgccg ccgcccgcgc cgccgcccgc gcgaaaaacc 60  
ctagcagget tcgcgctatc actcctaggg gcgcgaccat ggtggccaca aagaagacga 120  
agaaatccac ggacaacatc aacaacaagc tgcagcttgt tatgaagagt ggcaagtaca 180  
ctctcggtta caagaccgtc ctccaggactc tcaggaactc taagtccaag ctagtgatca 240  
tcgctaataa ctgcccgcgc ctccgtaagt ctgaaattga gtactatgct atgctggcca 300  
aggctcactgt ccaccacttc catagaaaca atgtctacct tggaaactgcc tgtggtaaat 360

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(2) INFORMATION FOR SEQ ID NO:1542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1542:

Met Lys Ser Gly Lys Tyr Thr Leu Gly Tyr Lys Thr Val Leu Arg Thr  
1                   5                   10                   15  
Leu Arg Asn Ser Lys Ser Lys Leu Val Ile Ile Ala Asn Asn Cys Pro  
          20                   25                   30  
Pro Leu Arg Lys Ser Glu Ile Glu Tyr Tyr Ala Met Leu Ala Lys Val  
          35                   40                   45  
Thr Val His His Phe His Arg Asn Asn Val Tyr Leu Gly Thr Ala Cys  
          50                   55                   60  
Gly Lys Tyr Phe Arg Val Cys Cys Leu Ser Ile Ile Asp Pro Gly Asp  
65                   70                   75                   80  
Ser Asp Ile Ile Lys Thr Thr Pro Gly Glu Gln  
          85                   90

(2) INFORMATION FOR SEQ ID NO:1543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..460
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1543:

agatccacaa caaatagcga aaccctagcy cawactcgac bkcctctgct ataagtagct 60  
ccactctctc tcttccaagc ytaccccagc ngccgcccgc gccaccgcca ccgccaccgy 120  
yacytgcncc agcgcgcgcg cgccgcagcc accatgggtc gcgtccgcac caagaccgtg 180  
aagaagacct ccaggcaggt gatcgagaag tactactccc gcatgaccct cgacttccac 240  
accaacaaga aggtgctgga ggaggtctcg attctgccct cgaagcgct ccgcaacaag 300  
gtggttggtc tcagtaccca cctgatgcgc cgcattccagc gcggcccagt ccgcggcattc 360  
tcgctcaagc tgcaggagga ggagcgcgag ncggcatgga cttcgtgccg gagaagtccg 420  
cgctcgaggt cgaagagatc cgcgtcgaca aggagaccat

(2) INFORMATION FOR SEQ ID NO:1544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598415

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1544:

Met Gly Arg Val Arg Thr Lys Thr Val Lys Lys Thr Ser Arg Gln Val  
1                   5                   10                   15  
Ile Glu Lys Tyr Tyr Ser Arg Met Thr Leu Asp Phe His Thr Asn Lys

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(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1598420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1549:

Met Ala Glu Ala Arg Val Pro Leu Ala Tyr Arg Asp Gln Cys Ala His  
1 5 10 15  
Leu Leu Ile Pro Leu Asn Lys Cys Arg Val Ala Glu Phe Tyr Leu Pro  
20 25 30  
Trp Lys Cys Glu Pro Glu Arg His Ala Tyr Glu Lys Cys Gln Tyr Glu  
35 40 45  
Leu Val Met Glu Arg Met Leu Gln Met Gln Lys Ile Arg Glu Ala Gln  
50 55 60  
Glu Thr Lys Val Lys Gly Gly Ala Pro Leu Ala Ser Ser Arg Pro Pro  
65 70 75 80  
Pro Ser Ser Pro Asp Thr Gly Pro Ser Pro Ile  
85 90

(2) INFORMATION FOR SEQ ID NO:1550:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 499 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..499

(D) OTHER INFORMATION: / Ceres Seq. ID 1598425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1550:

|                        |                        |                          |     |
|------------------------|------------------------|--------------------------|-----|
| agcgtcagac attccagtg   | gtgcctggca agtggcaa    | ac tgcagctgtc tagtcctcgg | 60  |
| ttcgcggaatc ttccacagag | atgcagacgg caggactcgc  | ttcaagctcc tcatctcgcg    | 120 |
| caggggggggt cgctgagat  | cacagcgaca atgggtgaagg | cagttgctgt cctcgccggc    | 180 |
| actgatgtca agggcaccat  | cttcttttca caggaggggg  | atgggtccgac caccgtgact   | 240 |
| ggaagtatct ctggcctcaa  | gccaggggctc catgggttcc | atgtgcacgc gcttggcgac    | 300 |
| accaccaacg gctgcatgtc  | gactgggcca cacttcaatc  | ctgttggcaa ggagcatggc    | 360 |
| gcaccggaag atgaggaccg  | ccatgccggg gatcttggga  | atgtgacagc gggagaagat    | 420 |
| ggtgttggtta atgtcaatat | tactgacagc cagatacctc  | ttgctggacc ccactcgatc    | 480 |
| attggccgag ctgttttgt   |                        |                          |     |

(2) INFORMATION FOR SEQ ID NO:1551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1598426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1551:

Ser Val Arg His Ser Ser Ala Cys Leu Ala Ser Gly Lys Leu Glu Leu  
1 5 10 15  
Ser Ser Pro Arg Phe Ala Asn Leu Pro Gln Arg Cys Arg Arg Gln Asp  
20 25 30  
Ser Leu Gln Ala Pro His Leu Ala Gln Gly Gly Ser Pro Glu Ile Thr  
35 40 45  
Ala Thr Met Val Lys Ala Val Ala Val Leu Ala Gly Thr Asp Val Lys  
50 55 60  
Gly Thr Ile Phe Phe Ser Gln Glu Gly Asp Gly Pro Thr Thr Val Thr  
65 70 75 80  
Gly Ser Ile Ser Gly Leu Lys Pro Gly Leu His Gly Phe His Val His  
85 90 95  
Ala Leu Gly Asp Thr Thr Asn Gly Cys Met Ser Thr Gly Pro His Phe

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100 105 110  
Asn Pro Val Gly Lys Glu His Gly Ala Pro Glu Asp Glu Asp Arg His  
115 120 125  
Ala Gly Asp Leu Gly Asn Val Thr Ala Gly Glu Asp Gly Val Val Asn  
130 135 140  
Val Asn Ile Thr Asp Ser Gln Ile Pro Leu Ala Gly Pro His Ser Ile  
145 150 155 160  
Ile Gly Arg Ala Val Leu  
165

(2) INFORMATION FOR SEQ ID NO:1552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1552:

Met Val Lys Ala Val Ala Val Leu Ala Gly Thr Asp Val Lys Gly Thr  
1 5 10 15  
Ile Phe Phe Ser Gln Glu Gly Asp Gly Pro Thr Thr Val Thr Gly Ser  
20 25 30  
Ile Ser Gly Leu Lys Pro Gly Leu His Gly Phe His Val His Ala Leu  
35 40 45  
Gly Asp Thr Thr Asn Gly Cys Met Ser Thr Gly Pro His Phe Asn Pro  
50 55 60  
Val Gly Lys Glu His Gly Ala Pro Glu Asp Glu Asp Arg His Ala Gly  
65 70 75 80  
Asp Leu Gly Asn Val Thr Ala Gly Glu Asp Gly Val Val Asn Val Asn  
85 90 95  
Ile Thr Asp Ser Gln Ile Pro Leu Ala Gly Pro His Ser Ile Ile Gly  
100 105 110  
Arg Ala Val Leu  
115

(2) INFORMATION FOR SEQ ID NO:1553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..472
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1553:

agcgctttcc tgtccgactc ccagccgtcg tctgctgcgt actccgcctc caatttggtc 60  
tgtttcttgc aagttgctct tgcggtagtt cccccwactg tcaccatgca gaacgaggag 120  
ggtaagactg tggacctcta tgttcccagg aagtgtctcg ccacanacag gatcatcact 180  
gccaaggacc atgcctctgt ccagatcaac attggccact tggatgcaa tggcctgtat 240  
gatggtcact tcacaacatt tgcctctctt gggtttgtcc gtgctcaggg cgatgcagac 300  
agtccttgg acaggctgtg gcagaagaag aaggctgata tcaagcagta gattttacat 360  
ctagtttacc aagaattgga cactgcctta gctatgtttt gaattcatgt cactatatgc 420  
aatgttgtga tttcagctgg taccttaaatt ctgaagattt agtatctttg tt

(2) INFORMATION FOR SEQ ID NO:1554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid

DO NOT REPRODUCE





(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1598458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1559:

Met Gly Ile Asp Leu Val Ala Gly Gly Arg Asn Lys Lys Thr Lys Arg  
1 5 10 15  
Thr Ala Xaa Lys Ser Asp Asp Val Tyr Leu Lys Leu Leu Val Lys Leu  
20 25 30  
Tyr Arg Phe Leu Val Arg Arg Thr Lys Ser Asn Phe Asn Ala Val Ile  
35 40 45  
Leu Lys Arg Leu Phe Met Ser Lys Thr Asn Arg Pro Pro Leu Ser Met  
50 55 60  
Arg Arg Leu Val Arg Phe Met Glu Gly Lys Gly Asp Gln Ile Ala Val  
65 70 75 80  
Ile Val Gly Thr Val Thr Asp Asp Lys Arg Ile Ser Glu Val Pro Ala  
85 90 95  
Met Lys Val Cys Ala Leu Arg Phe Thr Glu Thr Ala Arg Ala Arg Ile  
100 105 110  
Ile Asn Ala Gly Gly Asp Ala Ser Cys  
115 120

(2) INFORMATION FOR SEQ ID NO:1560:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1598459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1560:

Met Ser Lys Thr Asn Arg Pro Pro Leu Ser Met Arg Arg Leu Val Arg  
1 5 10 15  
Phe Met Glu Gly Lys Gly Asp Gln Ile Ala Val Ile Val Gly Thr Val  
20 25 30  
Thr Asp Asp Lys Arg Ile Ser Glu Val Pro Ala Met Lys Val Cys Ala  
35 40 45  
Leu Arg Phe Thr Glu Thr Ala Arg Ala Arg Ile Ile Asn Ala Gly Gly  
50 55 60  
Asp Ala Ser Cys  
65

(2) INFORMATION FOR SEQ ID NO:1561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..235

(D) OTHER INFORMATION: / Ceres Seq. ID 1598463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1561:

tawccctcac ccacccaacc ttcggcagty cccatcctct ctctgtggg cgctccctct 60  
ccccgcgcc ccaatcatcg cgctccctc gccacgcctc ayagggccgg ttgcgtasg 120  
agaaakgaga aasgaaggag gggakgcgg cktcgggcga katgagcgac tccttctgcc 180  
ccgactgcaa gaagcatag gaggtggcgt tcgaccactc ggcggkkgac atggt

(2) INFORMATION FOR SEQ ID NO:1562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

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(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..54  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598464  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1562:  
Xaa Pro Ser Pro Thr Gln Pro Ser Ala Xaa Pro Ile Leu Ser Pro Val  
1 5 10 15  
Gly Ala Pro Ser Pro Pro Pro Asn His Arg Ala Ser Leu Ala Thr  
20 25 30  
Pro Xaa Arg Ala Gly Ser Arg Xaa Arg Xaa Glu Lys Xaa Arg Arg Gly  
35 40 45  
Xaa Gly Xaa Arg Ala Xaa  
50

(2) INFORMATION FOR SEQ ID NO:1563:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 78 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1598465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1563:

Xaa Pro His Pro Pro Asn Leu Arg Gln Xaa Pro Ser Ser Leu Leu Trp  
1 5 10 15  
Ala Leu Pro Leu Pro Arg Pro Gln Ile Ile Ala Pro Pro Ser Pro Arg  
20 25 30  
Leu Xaa Gly Pro Val Arg Val Xaa Glu Xaa Arg Xaa Glu Gly Gly Xaa  
35 40 45  
Ala Val Xaa Gly Arg Xaa Glu Arg Leu Leu Leu Pro Arg Leu Gln Glu  
50 55 60  
Ala Tyr Gly Gly Gly Val Arg Pro Leu Gly Xaa Gly His Gly  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1564:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1598466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1564:

Xaa Leu Thr His Pro Thr Phe Gly Ser Xaa His Pro Leu Ser Cys Gly  
1 5 10 15  
Arg Ser Leu Ser Pro Ala Pro Lys Ser Ser Arg Leu Pro Arg His Ala  
20 25 30  
Ser Xaa Gly Arg Phe Ala Xaa Glu Lys Xaa Glu Xaa Lys Glu Gly Xaa  
35 40 45  
Arg Xaa Ser Gly Xaa Met Ser Asp Ser Phe Cys Pro Asp Cys Lys Lys  
50 55 60  
His Thr Glu Val Ala Phe Asp His Ser Ala Xaa Asp Met  
65 70 75

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(2) INFORMATION FOR SEQ ID NO:1565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..477
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1565:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aaactggctt | acctcttcgg | aaagggaaaa | cgccaccaca | cgcggtatga | attaggctct | 60  |
| ccgagtctcc | ggttccctcc | tctcggcggc | ggctcaggtc | cctctccatc | tccggcgtgg | 120 |
| cgcttggcgt | ctgacctcaa | caagcaagaa | agcaaattgg | aggcggcagg | gttgcgcatg | 180 |
| ccaccctcaa | gggcccagat | gtggtgaagg | agatcttcat | tggactgacc | ctgggtctga | 240 |
| tgcggggagg | catgtggaag | atgcaccact | ggaacgagca | gaggaagact | aggctcttct | 300 |
| atgacatgct | tgacaagggc | cagatcagcg | ttgtcgtcga | ggagtaaaga | gttcttccca | 360 |
| gttattttca | aagaactctc | tcgagagcat | gacaaagtga | ttgcttgctg | tggagatttg | 420 |
| tcctggaaat | aagcacaacc | atttggaac  | accagatttt | gtcgaatttt | cctttcc    |     |

(2) INFORMATION FOR SEQ ID NO:1566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1566:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Leu | Ala | Tyr | Leu | Phe | Gly | Lys | Gly | Lys | Arg | His | His | Thr | Arg | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Leu | Gly | Ser | Pro | Ser | Leu | Arg | Phe | Pro | Pro | Leu | Gly | Gly | Ser |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Pro | Ser | Pro | Ser | Pro | Ala | Trp | Arg | Leu | Ala | Ser | Asp | Leu | Asn | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Glu | Ser | Lys | Trp | Gln | Ala | Ala | Gly | Leu | Arg | Met | Pro | Pro | Ser | Arg |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ala | Arg | Val | Trp |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1567:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Gly | Arg | Val | Ala | His | Ala | Thr | Leu | Lys | Gly | Pro | Ser | Val |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Val | Lys | Glu | Ile | Phe | Ile | Gly | Leu | Thr | Leu | Gly | Leu | Ile | Ala | Gly | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Trp | Lys | Met | His | His | Trp | Asn | Glu | Gln | Arg | Lys | Thr | Arg | Ser | Phe |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Asp | Met | Leu | Asp | Lys | Gly | Gln | Ile | Ser | Val | Val | Glu | Glu |     |     |

00000000 00000000

50 55 60  
(2) INFORMATION FOR SEQ ID NO:1568:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..43  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598472  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1568:  
Met Thr Cys Leu Thr Arg Ala Arg Ser Ala Leu Ser Ser Arg Ser Lys  
1 5 10 15  
Glu Phe Phe Pro Val Ile Phe Lys Glu Leu Ser Arg Glu His Asp Lys  
20 25 30  
Val Ile Ala Cys Cys Gly Asp Leu Ser Trp Lys  
35 40

(2) INFORMATION FOR SEQ ID NO:1569:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 333 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..333  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598480  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1569:  
aaaccaggaa agcaaagygs ttctgcaagc acaggcagtg atcggaacc aaatccggac 60  
agtcttgagc tctctcagtc tcagcatttc agttcccaga ttccatagc cccagcccca 120  
caagtagcga aatggcagct gctccgttcg cgattgcygg ccggctctcc cccgttgccg 180  
gcctcccggg ccgcgcctgg aggcggcgcg acgggtttgc gtcgtccggg agagcccgct 240  
cgctcgccgt ggcgtccgcg gcgcaggaga acagggacaa cagtgtcgac gtacaggtta 300  
gccagaacgg cggcaacagg cagcagggca acg

(2) INFORMATION FOR SEQ ID NO:1570:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 111 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..111  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598481  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1570:  
Lys Pro Gly Lys Gln Xaa Xaa Phe Ala Ser Thr Gly Ser Asp Arg Gln  
1 5 10 15  
Pro Asn Pro Asp Ser Leu Glu Leu Ser Gln Ser Gln His Phe Ser Ser  
20 25 30  
Gln Ile His Ile Ala Pro Ala Pro Gln Val Ala Lys Trp Gln Leu Leu  
35 40 45  
Arg Ser Arg Leu Xaa Ala Gly Ser Pro Pro Leu Arg Ala Ser Arg Ser  
50 55 60  
Ala Pro Gly Gly Arg Arg Thr Gly Leu Arg Arg Pro Gly Glu Pro Ala  
65 70 75 80  
Arg Ser Pro Trp Arg Pro Arg Arg Arg Arg Thr Gly Thr Thr Val Ser  
85 90 95

00000000 101300





Ser Pro 85 90 95

(2) INFORMATION FOR SEQ ID NO:1576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..486
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1576:

|                                                                      |     |
|----------------------------------------------------------------------|-----|
| aaaagagcca gtccctgcgt ttccttactt cctggtaaag aaagaagcga mrcagggtact   | 60  |
| tgttggtgag cgcgagagaga ggagaggcgc agagcatcga cgatggcgag cggcacatga   | 120 |
| agagggagat cagcgagacc cagcacaccc tccgcttcgg cctcaatgcc ggcgtcaagg    | 180 |
| ccgacctcgc kccgccgcac ccgctccagt ccagcatcca atcggaggcc aagttctggg    | 240 |
| cggacaagaa gaagtttgga acagaggcca tctacggatc cgccttgaac atccgcaaga    | 300 |
| tctcgaatgcc caaatcctct caagggttcca aaggcccccct ggtgctttgc catcatctct | 360 |
| gcttgatgat gaggcactga caggttcctt agatgatttt ggttttgaag attatcttaa    | 420 |
| catgcctcaa gattctgaag gtttccgtca acctgacatg caccacggaa tggagggttcg   | 480 |
| ccttgg                                                               |     |

(2) INFORMATION FOR SEQ ID NO:1577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1577:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Lys Glu Pro Val Pro Ala Phe Pro Tyr Phe Leu Val Lys Lys Glu Ala |  |
| 1 5 10 15                                                       |  |
| Xaa Gln Val Leu Val Val Glu Arg Gly Glu Arg Arg Gly Ala Glu His |  |
| 20 25 30                                                        |  |
| Arg Arg Trp Arg Ala Ala His Glu Gly Asp Gln Arg Asp Pro Arg     |  |
| 35 40 45                                                        |  |
| His Pro Pro Leu Arg Pro Gln Cys Arg Arg Gln Gly Arg Pro Arg Xaa |  |
| 50 55 60                                                        |  |
| Ala Ala Pro Ala Pro Val Gln His Pro Ile Gly Gly Gln Val Leu Gly |  |
| 65 70 75 80                                                     |  |
| Gly Gln Glu Glu Val Trp Asp Arg Gly His Leu Arg Ile Arg Leu Glu |  |
| 85 90 95                                                        |  |
| His Pro Gln Asp Leu Asp Ala Gln Ile Leu Ser Arg Phe Gln Arg Pro |  |
| 100 105 110                                                     |  |
| Pro Gly Ala Leu Pro Ser Ser Leu Leu Gly Tyr Glu Ala Leu Thr Gly |  |
| 115 120 125                                                     |  |
| Ser Leu Asp Asp Phe Gly Phe Glu Asp Tyr Leu Asn Met Pro Gln Asp |  |
| 130 135 140                                                     |  |
| Ser Glu Gly Phe Arg Gln Pro Asp Met His His Gly Met Glu Val Arg |  |
| 145 150 155 160                                                 |  |
| Leu                                                             |  |

(2) INFORMATION FOR SEQ ID NO:1578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids

09589990 08663960

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..87  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598511  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1578:  
Met Lys Arg Glu Ile Ser Glu Thr His Asp Thr Leu Arg Phe Gly Leu  
1 5 10 15  
Asn Ala Gly Val Lys Ala Asp Leu Xaa Pro Pro His Pro Leu Gln Ser  
20 25 30  
Ser Ile Gln Ser Glu Ala Lys Phe Trp Ala Asp Lys Lys Lys Phe Gly  
35 40 45  
Thr Glu Ala Ile Tyr Gly Ser Ala Leu Asn Ile Arg Lys Ile Ser Met  
50 55 60  
Pro Lys Ser Ser Gln Gly Ser Lys Gly Pro Leu Val Leu Cys His His  
65 70 75 80  
Leu Cys Leu Asp Met Arg His  
85

(2) INFORMATION FOR SEQ ID NO:1579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..242  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1579:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| atctttttttt cgacttttga gcgcagaaac gagagggccg gagcagccgc agtcccggcg  | 60  |
| atcccgccgc cggtcgccct catacttccct cgtcactgcc ttcgttttctc tttccaacaa | 120 |
| tcaabatgag ccgtggcgnt acgcgggtgg tgggtcaaagt tctctgggtt acctctttgg  | 180 |
| aagcsgtgag ccccccaaac cagcagtggc accagctgta agtgctccac ctgctgctgc   | 240 |

ag

(2) INFORMATION FOR SEQ ID NO:1580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..42  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1580:

Ile Phe Phe Ser Thr Phe Glu Arg Arg Asn Glu Arg Ala Gly Ala Ala  
1 5 10 15  
Ala Val Pro Ala Ile Pro Pro Pro Val Ala Leu Ile Leu Pro Arg His  
20 25 30  
Cys Leu Arg Phe Ser Phe Gln Gln Ser Xaa  
35 40

(2) INFORMATION FOR SEQ ID NO:1581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:

DOCKET "101300"

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..80  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1598514  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1581:  
Ser Phe Phe Arg Leu Ser Ser Ala Glu Thr Arg Gly Pro Glu Gln Pro  
1                    5                    10                    15  
Gln Ser Arg Arg Ser Arg Arg Arg Ser Pro Ser Tyr Phe Leu Val Thr  
                    20                    25                    30  
Ala Phe Val Ser Leu Ser Asn Asn Gln Xaa Glu Pro Trp Xaa Tyr Ala  
                    35                    40                    45  
Gly Gly Gly Gln Ser Ser Leu Gly Tyr Leu Phe Gly Ser Xaa Glu Pro  
                    50                    55                    60  
Pro Lys Pro Ala Val Ala Pro Ala Val Ser Ala Pro Pro Ala Ala Ala  
65                    70                    75                    80

(2) INFORMATION FOR SEQ ID NO:1582:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 72 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..72  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1598515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1582:

Leu Phe Phe Asp Phe Arg Ala Gln Lys Arg Glu Gly Arg Ser Ser Arg  
1                    5                    10                    15  
Ser Pro Gly Asp Pro Ala Ala Gly Arg Pro His Thr Ser Ser Ser Leu  
                    20                    25                    30  
Pro Ser Phe Leu Phe Pro Thr Ile Xaa Met Ser Arg Gly Xaa Thr Arg  
                    35                    40                    45  
Val Val Val Lys Val Leu Trp Val Thr Ser Leu Glu Xaa Val Ser Pro  
                    50                    55                    60  
Pro Asn Gln Gln Trp His Gln Leu  
65                    70

(2) INFORMATION FOR SEQ ID NO:1583:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 424 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
    (B) LOCATION: 1..424  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1598516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1583:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ctagacgcac cccttcctcg tttcgccgcc tccgccgaca ccgactgcct acctcagctg | 60  |
| ccgtcgccat gggcagaagg ctgctagatg ctatcgccag atcaagaaca agccataccc | 120 |
| taagtccagg tactgccgtg gtgtccctga ccccaagatc aggatctacg atgttgggat | 180 |
| gaagaggaag ggtgttgatg agttccccta ttgtgtgcac cttgtctctt gggagaagga | 240 |
| gaatgtctcc agtgaggcgc ttgaggctgc cgcattgcc tgcaacaagt acatgaccaa  | 300 |
| gtctgcagga aaggatgctt tccaccttag ggtccgggtt caccgttcca tgtcctccgt | 360 |
| atcaacaaga tgctttcgtg tgctggggct gataggctcc agactggaat taggggtgcc | 420 |
| tttt                                                              |     |

0056980 "101300



(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

- (B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1598517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1584:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Arg | Thr | Pro | Ser | Ser | Phe | Arg | Arg | Leu | Arg | Arg | His | Arg | Leu | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Ser | Ala | Ala | Val | Ala | Met | Gly | Arg | Arg | Leu | Leu | Asp | Ala | Ile | Ala |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Arg | Ser | Arg | Thr | Ser | His | Thr | Leu | Ser | Pro | Gly | Thr | Ala | Val | Val | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Thr | Pro | Arg | Ser | Gly | Ser | Thr | Met | Leu | Gly |     |     |     |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..82
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1598518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1585:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..44
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1598519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1586:

| (x1) SEQUENCE DESCRIPTION: SEQ |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|--------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met                            | Thr | Lys | Ser | Ala | Gly | Lys | Asp | Ala | Phe | His | Leu | Arg | Val | Arg | Val |
| 1                              |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| His                            | Arg | Ser | Met | Ser | Ser | Val | Ser | Thr | Arg | Cys | Phe | Arg | Val | Leu | Gly |
|                                |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu                            | Ile | Gly | Ser | Arg | Leu | Glu | Leu | Gly | Val | Pro | Phe |     |     |     |     |

35 40  
(2) INFORMATION FOR SEQ ID NO:1587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..509
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1587:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| tccaccagcg | gcatttatag | caaccggtcc | agcactttca | cgctcagctc | cagcaatggc  | 60  |
| tgcctccacc | atggcgatct | cctccacggc | gatggccggc | acccccatca | aggtgggctc  | 120 |
| cttcggcgag | ggccgcatca | ccatgcgcaa | gaccgtgggc | aagcccaagg | tggcggcgctc | 180 |
| cggcagcccc | tggtacggcc | ccgaccgcgt | caagtacctc | ggccccttct | ccggcgagcc  | 240 |
| cccgagctac | ctcaccggcg | agttccccgg | cgactacggc | tgggacaccg | ccgggctgtc  | 300 |
| cgccgacccc | gagaccttcg | ccaagaaccg | cgagctggag | gtgatccact | cccgtggggc  | 360 |
| catgctcggc | gcgctcggct | gcgtcttccc | cgagctgctc | tcccgcaacg | gcgtcaagtt  | 420 |
| cggcgaggcc | gtctggttca | aggccggctc | ccagatcttc | agcgaggggc | ggctggacta  | 480 |
| cctcggcaac | cccagcctga | tccacgcgc  |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:1588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..169
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1588:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Thr | Ser | Gly | Ile | Tyr | Ser | Asn | Arg | Ser | Thr | Phe | Thr | Leu | Ser |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Ser | Asn | Gly | Cys | Leu | His | His | Gly | Asp | Leu | Leu | His | Gly | Asp |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     | Gly |
| Arg | His | Pro | His | Gln | Gly | Gly | Leu | Leu | Arg | Arg | Gly | Pro | His | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     | His |
| Ala | Gln | Asp | Arg | Gly | Gln | Ala | Gln | Gly | Gly | Gly | Val | Arg | Gln | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     | Leu |
| Val | Arg | Pro | Arg | Pro | Arg | Gln | Val | Pro | Arg | Pro | Leu | Leu | Arg | Arg |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Glu | Leu | Pro | His | Arg | Arg | Val | Pro | Arg | Arg | Leu | Arg | Leu | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  | His |
| Arg | Arg | Ala | Val | Arg | Arg | Pro | Arg | Asp | Leu | Arg | Gln | Glu | Pro | Arg |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 | Ala |
| Gly | Gly | Asp | Pro | Leu | Pro | Leu | Gly | His | Ala | Arg | Arg | Ala | Arg | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     | Arg |
| Leu | Pro | Arg | Ala | Ala | Leu | Pro | Gln | Arg | Arg | Gln | Val | Arg | Arg | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     | Arg |
| Leu | Val | Gln | Gly | Arg | Leu | Pro | Asp | Leu | Gln | Arg | Gly | Arg | Ala | Gly |
|     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Arg | Gln | Pro | Gln | Pro | Asp | Pro | Arg |     |     |     |     |     |     |
|     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

DOCKET# 00668950



(2) INFORMATION FOR SEQ ID NO:1591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..481
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1591:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| accccttaaa cctcgtcaa aaccgctgct cactgaatat ttccattttt acccttttct  | 60  |
| cgcccctacc cccgccaccg ccgccgccgt cgccgcagcc atggcgctgc gccgctgtct | 120 |
| cctccgcttc ctctcgatcc gcctcgttcc tcagagatct caacctcttg ccccgatctc | 180 |
| gactgcgacc cggaccctaa cctctttgtc cgaggccctc ggctccccag ctccccgggc | 240 |
| cctcgccctcc ccccggtgt actaccctc gcgctgccac ttccgcgacc gctcctccgg  | 300 |
| cgacgaggac gacggagaag acgaagaaga gcactacgac gatgagggga gcgatgggga | 360 |
| atggggggac gatgaggagg tgggtggcgc gaagaaaccg agcgggaaga ccgaagagga | 420 |
| gaaggtagcg gaggcggcgg agatcggcta caaggtgttg ggaccgctcg aggctgacga | 480 |

t

(2) INFORMATION FOR SEQ ID NO:1592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598536

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1592:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Leu | Lys | Pro | Ser | Ser | Lys | Pro | Leu | Leu | Thr | Glu | Tyr | Phe | His | Phe |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Tyr | Pro | Phe | Leu | Ala | Pro | Thr | Pro | Ala | Thr | Ala | Ala | Ala | Val | Ala | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Met | Ala | Ser | Arg | Arg | Cys | Leu | Leu | Arg | Phe | Leu | Ser | Ile | Arg | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Pro | Gln | Arg | Ser | Gln | Pro | Leu | Ala | Pro | Ile | Ser | Thr | Ala | Thr | Arg |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Thr | Leu | Thr | Ser | Leu | Ser | Glu | Ala | Leu | Gly | Ser | Pro | Ala | Pro | Arg | Ala |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Ala | Ser | Pro | Arg | Leu | Tyr | Tyr | Pro | Ser | Arg | Cys | His | Phe | Ala | Thr |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Arg | Ser | Ser | Gly | Asp | Glu | Asp | Asp | Gly | Glu | Asp | Glu | Glu | Glu | His | Tyr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Asp | Glu | Gly | Ser | Asp | Gly | Glu | Trp | Gly | Asp | Asp | Glu | Glu | Val | Val |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Ala | Lys | Lys | Pro | Ser | Gly | Lys | Thr | Glu | Glu | Glu | Lys | Val | Ala | Glu |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Ala | Ala | Glu | Ile | Gly | Tyr | Lys | Val | Leu | Gly | Pro | Leu | Glu | Ala | Asp | Asp |
|     |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |

(2) INFORMATION FOR SEQ ID NO:1593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

DOCKET# 08659960



50 55 60  
Ala Gly Gly Ala Tyr Thr Met Asn Thr Ala Ser Ala Val Thr Val Arg  
65 70 75 80  
Ala Arg Ser Ala Ala  
85

(2) INFORMATION FOR SEQ ID NO:1596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..57
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1596:

Met Glu Val Ser Gln His Ser Lys Tyr Phe Cys Gly Lys  
1 5 10 15  
Phe Ala Val Lys Arg Lys Ala Val Gly Ile Trp Gly Cys Lys Asp Cys  
20 25 30  
Gly Lys Val Lys Ala Gly Gly Ala Tyr Thr Met Asn Thr Ala Ser Ala  
35 40 45  
Val Thr Val Arg Ala Arg Ser Ala Ala  
50 55

(2) INFORMATION FOR SEQ ID NO:1597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..507
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1597:

acgcctcaaa tcgctccctg cctctgccct ctggtcacct cgtttccgct cccggctccc 60  
ctccggccac ccagacatcg tccgttcgct cgccaagaga caggaccgga gaccatggcg 120  
gaccagctca ccgacgacca gatcgccgag ttcaaggagg ccttcagcct cttcgacaag 180  
gacggcgacg gttgcatcac aaccaaggag ctcggaactg tcatgcgatc actgggtcag 240  
aaccacaccg aggctgagct ccaggacatg atcaacgagg tcgatgcgga cggcaacggc 300  
accatcgact tcccggagtt cctcaacctc atggcccgtg agatgaagga caccgactcc 360  
gaggaggagc tcaaggaggc gttcaggggtg ttcgacaagg accagaacgg cttcatctct 420  
gcggcggast ccgcacgtga tgaccaacct cggcgagaag ctgaccgacg aggaggtcga 480  
tgagatgac cgcgagccga cgtcgat

(2) INFORMATION FOR SEQ ID NO:1598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1598:

Thr Pro Gln Ile Ala Pro Cys Leu Cys Pro Leu Val Thr Ser Leu Pro  
1 5 10 15  
Leu Pro Ala Pro Leu Arg Pro Pro Arg His Arg Pro Phe Ala Arg Gln

DOCKET# 08688950

| Descriptive statistics                 |                | Univariate analysis |           | Multivariate analysis |           | Sensitivity analysis |           |
|----------------------------------------|----------------|---------------------|-----------|-----------------------|-----------|----------------------|-----------|
| Variable                               | Value          | OR                  | 95% CI    | OR                    | 95% CI    | OR                   | 95% CI    |
| Age (years)                            | 55.2 (SD 12.1) | 1.02                | 1.01-1.03 | 1.01                  | 1.00-1.02 | 1.01                 | 1.00-1.02 |
| Gender (male)                          | 65.3%          | 1.15                | 1.05-1.26 | 1.10                  | 1.00-1.21 | 1.10                 | 1.00-1.21 |
| Education (years)                      | 12.5 (SD 2.1)  | 1.05                | 1.04-1.06 | 1.04                  | 1.03-1.05 | 1.04                 | 1.03-1.05 |
| Income (USD/month)                     | 1,200 (SD 300) | 1.01                | 1.00-1.02 | 1.00                  | 0.99-1.01 | 1.00                 | 0.99-1.01 |
| Marital status (married)               | 78.9%          | 1.08                | 1.00-1.17 | 1.05                  | 0.97-1.14 | 1.05                 | 0.97-1.14 |
| Health insurance (private)             | 45.2%          | 1.25                | 1.15-1.36 | 1.20                  | 1.10-1.31 | 1.20                 | 1.10-1.31 |
| Comorbidities (hypertension)           | 32.1%          | 1.18                | 1.08-1.29 | 1.15                  | 1.05-1.26 | 1.15                 | 1.05-1.26 |
| Comorbidities (diabetes)               | 18.7%          | 1.12                | 1.03-1.22 | 1.10                  | 1.00-1.21 | 1.10                 | 1.00-1.21 |
| Comorbidities (heart disease)          | 25.4%          | 1.22                | 1.12-1.33 | 1.18                  | 1.08-1.29 | 1.18                 | 1.08-1.29 |
| Comorbidities (stroke)                 | 12.3%          | 1.15                | 1.05-1.26 | 1.12                  | 1.02-1.23 | 1.12                 | 1.02-1.23 |
| Comorbidities (chronic kidney disease) | 8.9%           | 1.10                | 1.00-1.21 | 1.08                  | 0.98-1.19 | 1.08                 | 0.98-1.19 |
| Comorbidities (asthma)                 | 15.6%          | 1.08                | 1.00-1.17 | 1.05                  | 0.97-1.14 | 1.05                 | 0.97-1.14 |
| Comorbidities (depression)             | 22.1%          | 1.15                | 1.05-1.26 | 1.12                  | 1.02-1.23 | 1.12                 | 1.02-1.23 |
| Comorbidities (anxiety)                | 19.8%          | 1.10                | 1.00-1.21 | 1.08                  | 0.98-1.19 | 1.08                 | 0.98-1.19 |
| Comorbidities (arthritis)              | 28.5%          | 1.18                | 1.08-1.29 | 1.15                  | 1.05-1.26 | 1.15                 | 1.05-1.26 |
| Comorbidities (chronic pain)           | 35.2%          | 1.25                | 1.15-1.36 | 1.20                  | 1.10-1.31 | 1.20                 | 1.10-1.31 |
| Comorbidities (obesity)                | 20.3%          | 1.12                | 1.03-1.22 | 1.10                  | 1.00-1.21 | 1.10                 | 1.00-1.21 |
| Comorbidities (hypertension)           | 32.1%          | 1.18                | 1.08-1.29 | 1.15                  | 1.05-1.26 | 1.15                 | 1.05-1.26 |
| Comorbidities (diabetes)               | 18.7%          | 1.12                | 1.03-1.22 | 1.10                  | 1.00-1.21 | 1.10                 | 1.00-1.21 |
| Comorbidities (heart disease)          | 25.4%          | 1.22                | 1.12-1.33 | 1.18                  | 1.08-1.29 | 1.18                 | 1.08-1.29 |
| Comorbidities (stroke)                 | 12.3%          | 1.15                | 1.05-1.26 | 1.12                  | 1.02-1.23 | 1.12                 | 1.02-1.23 |
| Comorbidities (chronic kidney disease) | 8.9%           | 1.10                | 1.00-1.21 | 1.08                  | 0.98-1.19 | 1.08                 | 0.98-1.19 |
| Comorbidities (asthma)                 | 15.6%          | 1.08                | 1.00-1.17 | 1.05                  | 0.97-1.14 | 1.05                 | 0.97-1.14 |
| Comorbidities (depression)             | 22.1%          | 1.15                | 1.05-1.26 | 1.12                  | 1.02-1.23 | 1.12                 | 1.02-1.23 |
| Comorbidities (anxiety)                | 19.8%          | 1.10                | 1.00-1.21 | 1.08                  | 0.98-1.19 | 1.08                 | 0.98-1.19 |
| Comorbidities (arthritis)              | 28.5%          | 1.18                | 1.08-1.29 | 1.15                  | 1.05-1.26 | 1.15                 | 1.05-1.26 |
| Comorbidities (chronic pain)           | 35.2%          | 1.25                | 1.15-1.36 | 1.20                  | 1.10-1.31 | 1.20                 | 1.10-1.31 |
| Comorbidities (obesity)                | 20.3%          | 1.12                | 1.03-1.22 | 1.10                  | 1.00-1.21 | 1.10                 | 1.00-1.21 |
| Comorbidities (hypertension)           | 32.1%          | 1.18                | 1.08-1.29 | 1.15                  | 1.05-1.26 | 1.15                 | 1.05-1.26 |
| Comorbidities (diabetes)               | 18.7%          | 1.12                | 1.03-1.22 | 1.10                  | 1.00-1.21 | 1.10                 | 1.00-1.21 |
| Comorbidities (heart disease)          | 25.4%          | 1.22                | 1.12-1.33 | 1.18                  | 1.08-1.29 | 1.18                 | 1.08-1.29 |
| Comorbidities (stroke)                 | 12.3%          | 1.15                | 1.05-1.26 | 1.12                  | 1.02-1.23 | 1.12                 | 1.02-1.23 |
| Comorbidities (chronic kidney disease) | 8.9%           | 1.10                | 1.00-1.21 | 1.08                  | 0.98-1.19 | 1.08                 | 0.98-1.19 |
| Comorbidities (asthma)                 | 15.6%          | 1.08                | 1.00-1.17 | 1.05                  | 0.97-1.14 | 1.05                 | 0.97-1.14 |
| Comorbidities (depression)             | 22.1%          | 1.15                | 1.05-1.26 | 1.12                  | 1.02-1.23 | 1.12                 | 1.02-1.23 |
| Comorbidities (anxiety)                | 19.8%          | 1.10                | 1.00-1.21 | 1.08                  | 0.98-1.19 | 1.08                 | 0.98-1.19 |
| Comorbidities (arthritis)              | 28.5%          | 1.18                | 1.08-1.29 | 1.15                  | 1.05-1.26 | 1.15                 | 1.05-1.26 |
| Comorbidities (chronic pain)           | 35.2%          | 1.25                | 1.15-1.36 | 1.20                  |           |                      |           |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1598562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1599:

(2) INFORMATION FOR SEQ ID NO:1600:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1598563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1600:

| (X1) SEQUENCE DESCRIPTION: 321 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|--------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met                            | Ala | Asp | Gln | Leu | Thr | Asp | Asp | Gln | Ile | Ala | Glu | Phe | Lys | Glu | Ala |
| 1                              |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Phe                            | Ser | Leu | Phe | Asp | Lys | Asp | Gly | Asp | Gly | Cys | Ile | Thr | Thr | Lys | Glu |
|                                |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Leu                            | Gly | Thr | Val | Met | Arg | Ser | Leu | Gly | Gln | Asn | Pro | Thr | Glu | Ala | Glu |
|                                |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |







20 25 30  
Gly Gln Arg Ala Ser Ser Ser Phe Leu Gly Gly Lys Thr Leu Leu Arg  
35 40 45  
Gln Ala Glu Ala Ala Gly  
50

(2) INFORMATION FOR SEQ ID NO:1606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..46

(D) OTHER INFORMATION: / Ceres Seq. ID 1598580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1606:

Thr Pro Arg Ser Pro Xaa Pro Gln Leu Ala Pro Ala Met Ala Leu Val  
1 5 10 15  
Ser Ala Ser Ser Ser Ser Thr Thr Ala Val Thr Xaa Ser Pro Gly Met  
20 25 30  
Gly Ser Gly Arg Arg Pro Pro Ser Ser Ala Ala Arg Arg Cys  
35 40 45

(2) INFORMATION FOR SEQ ID NO:1607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1598581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1607:

Arg His Ala Leu Gln Xaa His Ser Leu Arg Pro Gln Trp His Ser Ser  
1 5 10 15  
Pro Pro Pro Arg Pro Pro Pro Pro Pro Ser Xaa Leu Pro Gln Glu Trp  
20 25 30  
Ala Ala Gly Val Val Leu Leu Pro Arg Arg Gln Asp Ala Ala Glu Thr  
35 40 45  
Gly Arg Gly Gly Arg  
50

(2) INFORMATION FOR SEQ ID NO:1608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1598598

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1608:

cacaccgaga atcacaatac gaaacgaatt aatccccaat caacacagca agtcagcanc 60  
aagcaaagca gcgacccgag agatggacgc gaggatgttc gggctggaga cccccgggt 120  
ggcggcgctg catcacctgc tggacgtgcc cgacggcgac aaggcgggag gcggcgcacg 180

(2) INFORMATION FOR SEQ ID NO:1609:

(i) SEQUENCE CHARACTERISTICS:

DOCKET "0866355"

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 498 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..498  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1598610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1612:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| caagaaggca  | gtggagaact | ctcctttcct | ggagaagctg | aagaagaggg | gctacgaggt | 60  |
| cctgtacatg  | gttgatgcca | ttgatgagta | tgctgttggt | cagctcaagg | agtttgaggg | 120 |
| caagaagctt  | gtctcggcca | ccaaggaggg | tctgaagctt | gatgagaccg | aggatgagaa | 180 |
| gaagaggaag  | gaggagctga | aggagaagtt | tgagggtctg | tgcaagatca | tcaaggaggt | 240 |
| tctgggcgac  | aaggttgaga | aggttggtgt | gtctgaccgt | gtcgtggact | caccgtgctg | 300 |
| ccttggtcact | ggtgagtatg | gctggacagc | aacatggaga | ggatcatgaa | ggcgcaggcc | 360 |
| ctgagggact  | ctagcatgtc | ggggtacatg | tcgagcaaaa | agactatgga | aatcaacccg | 420 |
| gagaacccaa  | tcatggatga | gctccgtaag | cgcgccgagg | ctgacaggaa | tgacaagtca | 480 |
| gtcaaggatc  | ttgtgatg   |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1613:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 115 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..115  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1598611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1613:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Lys | Ala | Val | Glu | Asn | Ser | Pro | Phe | Leu | Glu | Lys | Leu | Lys | Lys | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Tyr | Glu | Val | Leu | Tyr | Met | Val | Asp | Ala | Ile | Asp | Glu | Tyr | Ala | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Gln | Leu | Lys | Glu | Phe | Glu | Gly | Lys | Lys | Leu | Val | Ser | Ala | Thr | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Gly | Leu | Lys | Leu | Asp | Glu | Thr | Glu | Asp | Glu | Lys | Lys | Arg | Lys | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Leu | Lys | Glu | Lys | Phe | Glu | Gly | Leu | Cys | Lys | Ile | Ile | Lys | Glu | Val |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Gly | Asp | Lys | Val | Glu | Lys | Val | Val | Val | Ser | Asp | Arg | Val | Val | Asp |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Pro | Cys | Cys | Leu | Val | Thr | Gly | Glu | Tyr | Gly | Trp | Thr | Ala | Thr | Trp |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Gly | Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 115 |

(2) INFORMATION FOR SEQ ID NO:1614:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 93 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..93  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1598612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1614:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Asp | Ala | Ile | Asp | Glu | Tyr | Ala | Val | Gly | Gln | Leu | Lys | Glu | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Gly | Lys | Lys | Leu | Val | Ser | Ala | Thr | Lys | Glu | Gly | Leu | Lys | Leu | Asp |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Thr | Glu | Asp | Glu | Lys | Lys | Arg | Lys | Glu | Glu | Leu | Lys | Glu | Lys | Phe |

35 40 45  
Glu Gly Leu Cys Lys Ile Ile Lys Glu Val Leu Gly Asp Lys Val Glu  
50 55 60  
Lys Val Val Val Ser Asp Arg Val Val Asp Ser Pro Cys Cys Leu Val  
65 70 75 80  
Thr Gly Glu Tyr Gly Trp Thr Ala Thr Trp Arg Gly Ser  
85 90

(2) INFORMATION FOR SEQ ID NO:1615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..375
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598623

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1615:

agggtgtactg tactgttagta ggttggttct ccattcatca ttcagctcac aggtccctcc 60  
gcctccgccg tatcggaggg agaggaagcg gaaggcttgg aaggagaaga gaatggcggg 120  
gcggcgccg gaggaggagt acgactacct gttcaagggtg gtgctgatcg gggactcggg 180  
cgtcggcaag tccaacctcc tctcccgtt caccgcgaac gagttctgcc tcgagtccaa 240  
gtccaccatc ggcgtcgagt tcgccacacg gacactccat gttgagggca agatcatcaa 300  
ggcgcagatc tgggacacgg caggccagga gcggtaccgg gcgatcacca gcgcctacta 360  
tcgcggggcg ctggg

(2) INFORMATION FOR SEQ ID NO:1616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1616:

Gly Val Leu Tyr Cys Ser Arg Leu Val Leu His Ser Ser Phe Ser Ser  
1 5 10 15  
Gln Val Pro Pro Pro Pro Pro Tyr Arg Arg Glu Arg Lys Arg Lys Ala  
20 25 30  
Trp Lys Glu Lys Arg Met Ala Gly Arg Arg Ala Glu Glu Tyr Asp  
35 40 45  
Tyr Leu Phe Lys Val Val Leu Ile Gly Asp Ser Gly Val Gly Lys Ser  
50 55 60  
Asn Leu Leu Ser Arg Phe Thr Arg Asn Glu Phe Cys Leu Glu Ser Lys  
65 70 75 80  
Ser Thr Ile Gly Val Glu Phe Ala Thr Arg Thr Leu His Val Glu Gly  
85 90 95  
Lys Ile Ile Lys Ala Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Tyr  
100 105 110  
Arg Ala Ile Thr Ser Ala Tyr Tyr Arg Gly Ala Leu  
115 120

(2) INFORMATION FOR SEQ ID NO:1617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

00000000 00000000



Pro Glu Ile Pro Glu Pro Ala Leu Gly Ile Asn Phe Ala Arg Asp Gly  
100 105 110  
Met Asn Glu Lys Asp Trp Leu Ala Leu Val Ala Val His Ser Asp Ser  
115 120 125  
Trp Leu Leu Ala Val Ala Phe Tyr Phe Ala Ala Arg Phe Gly Phe Asp  
130 135 140  
Lys Glu Ser Arg Arg Arg Leu Phe Asn Met Ile Asn  
145 150 155

(2) INFORMATION FOR SEQ ID NO:1620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1620:

Met Ile Lys Ala Leu Thr Asn Asp Val Glu Lys Phe Tyr Gln Leu Cys  
1 5 10 15  
Asp Pro Glu Lys Glu Asn Leu Cys Leu Tyr Gly Tyr Pro Asn Glu Thr  
20 25 30  
Trp Glu Val Thr Leu Pro Ala Glu Val Pro Pro Glu Ile Pro Glu  
35 40 45  
Pro Ala Leu Gly Ile Asn Phe Ala Arg Asp Gly Met Asn Glu Lys Asp  
50 55 60  
Trp Leu Ala Leu Val Ala Val His Ser Asp Ser Trp Leu Leu Ala Val  
65 70 75 80  
Ala Phe Tyr Phe Ala Ala Arg Phe Gly Phe Asp Lys Glu Ser Arg Arg  
85 90 95  
Arg Leu Phe Asn Met Ile Asn  
100

(2) INFORMATION FOR SEQ ID NO:1621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..476
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1621:

gctgacacat tccacccacc catcacccct tccttccttt ccattctctg tgcgcttgcg 60  
ccctccaagg ttctctgatt ccagacgcaa ccttgcggtc gcggggtcaa ggagccaggg 120  
ggtgcacagc gatcgttctg ccggagatcg aaaccctcag ctagggtctg aggcgccggg 180  
ctgcggccgc cgagatgtcg acgccggcga ggaagcggct gatgcgggac ttcaggcgcc 240  
tgcagcagga cccgcccgcc ggatcaccgg cgcgccgcac gacaacaaca tcatgctctg 300  
gaacgccgtc atattcgggc cggatgatac gccttgggac ggaggcacgt tcaagcttac 360  
cttgacgttt acagaagatt acccaacaa gccaccaact gttcgggtcg tctctaggat 420  
gtttcatcca aacatatatg ctgatggaag catctgcttg gatatcctac agaacc

(2) INFORMATION FOR SEQ ID NO:1622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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Met Arg Asp Phe Arg Arg Leu Gln Gln Asp Pro Pro Ala Gly Ser Pro  
1 5 10 15  
Ala Arg Arg Thr Thr Thr Thr Ser Cys Ser Gly Thr Pro Ser Tyr Ser  
20 25 30  
Gly Arg Met Ile Arg Leu Gly Thr Glu Ala Arg Ser Ser Leu Pro Cys  
35 40 45  
Ser Leu Gln Lys Ile Thr Gln Thr Ser His Gln Leu Phe Gly Ser Ser  
50 55 60  
Leu Gly Cys Phe Ile Gln Thr Tyr Met Leu Met Glu Ala Ser Ala Trp  
65 70 75 80  
Ile Ser Tyr Arg Thr  
85

(2) INFORMATION FOR SEQ ID NO:1625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..480
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1625:

aacataaaaa actcaccggg aagaaggaag gagaagctaa ccggcacgtc gtgaagctaa 60  
ccgggaagca gagacgtccg cccgtccccc gtcgtccgtc gtcattggccg ccgtggaggt 120  
gtgctgtaag gccgccacgg ggaagcccga cacgtcggc gactgccgt tctcgacag 180  
ggtgctgtc acgtggagg agaagaagg cccctacgag gtgaagctcg tcgacctcga 240  
caacaagccc gaatggttc tgaagatcag ccagagggt aagggtgctg tgttcaacgg 300  
tggtgatggc aaatgcatcg ctgattctga tgtaatcacc caaaccattg aggagaagtt 360  
cccaactcca tctctggtca ctctgtaga atatgcatca gtgggatcaa agattttccc 420  
agccttcac acattctga agagcaagga tgctagtgt ggttccgaga aggcgcttct 480

(2) INFORMATION FOR SEQ ID NO:1626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1626:

Met Ala Ala Val Glu Val Cys Val Lys Ala Ala Thr Gly Lys Pro Asp  
1 5 10 15  
Thr Leu Gly Asp Cys Pro Phe Ser Gln Arg Val Leu Leu Thr Leu Glu  
20 25 30  
Glu Lys Lys Val Pro Tyr Glu Val Lys Leu Val Asp Leu Asp Asn Lys  
35 40 45  
Pro Glu Trp Phe Leu Lys Ile Ser Pro Glu Gly Lys Val Pro Val Phe  
50 55 60  
Asn Gly Gly Asp Gly Lys Cys Ile Ala Asp Ser Asp Val Ile Thr Gln  
65 70 75 80  
Thr Ile Glu Glu Lys Phe Pro Thr Pro Ser Leu Val Thr Pro Val Glu  
85 90 95  
Tyr Ala Ser Val Gly Ser Lys Ile Phe Pro Ala Phe Ile Thr Phe Leu  
100 105 110  
Lys Ser Lys Asp Ala Ser Asp Gly Ser Glu Lys Ala Leu  
115 120 125

00689980 101300



[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..435
 (D) OTHER INFORMATION: / Ceres Seq. ID 1598644
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| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:1 |            |             |            |             |            |  |     |
|----------------------------------------|------------|-------------|------------|-------------|------------|--|-----|
| acaagcgctc                             | acagcttcca | ctagagaccg  | aagtaccgaa | cagatagaga  | ttggagaacc |  | 60  |
| atgatgagat                             | coggccttct | ctcgctatgt  | ttccacctag | ccctggccat  | cacactggct |  | 120 |
| gcaagtkttc                             | ctggccttgc | tcgtagtagg  | gtaatcgaca | tcgaaccgca  | actcaaaccg |  | 180 |
| acgctgcaac                             | tagaaccaaa | gcatgggtga  | tctcaaccag | acagaaaacca | atgaacccaa |  | 240 |
| accgacacca                             | caaoctgagc | caaaaaccgga | gcctaaaccg | gaacccaaaac | ctgcaccaca |  | 300 |
| atcagacacc                             | aaatcagagc | ctaaaaccgc  | accacagtca | gacccaaaac  | ctgcaccaca |  | 360 |
| accggaccta                             | aaaccagaa  | ccaaacctac  | accacagcca | gacccaaaac  | cttcaccaca |  | 420 |
| accagaccga                             | gaqcc      |             |            |             |            |  |     |

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
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(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..57
 (D) OTHER INFORMATION: / Ceres Seq. ID 1598645
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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Arg | Ser | Gly | Leu | Leu | Ser | Leu | Cys | Phe | His | Leu | Ala | Leu | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Thr | Leu | Ala | Ala | Ser | Xaa | Pro | Gly | Leu | Ala | Arg | Ser | Arg | Val | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Ile | Glu | Pro | Gln | Leu | Lys | Pro | Thr | Leu | Gln | Leu | Glu | Pro | Lys | His |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Val | Ser | Gln | Pro | Asp | Arg | Asn | Gln |     |     |     |     |     |     |     |
|     |     |     | 50  |     |     | 55  |     |     |     |     |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1636:

Pro Pro Pro Thr Ser Asp Ser Thr Thr Arg Leu Leu Ser Ser Ser  
1 5 10 15  
Ile Cys Leu Leu Pro Gln Thr Cys Arg Ala Ala Ala Arg Glu Ala Arg  
20 25 30  
Ala Trp Val Arg Ala Ala Arg Asn Ala Pro Gln Val Phe Arg Asp Asn  
35 40 45  
Ile Gln Gly Ile Thr Lys Pro Ala Ile  
50 55

(2) INFORMATION FOR SEQ ID NO:1637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1637:

Arg Arg Arg Leu Leu Ile Leu Pro Pro Pro Ala Ser Ser Arg Val Arg  
1 5 10 15  
Ser Val Cys Ser Pro Arg His Val Gly Pro Arg Gln Gly Arg Gln Gly  
20 25 30  
Pro Gly

(2) INFORMATION FOR SEQ ID NO:1638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1638:

Met Ser Gly Arg Gly Lys Gly Gly Lys Gly Leu Gly Lys Gly Gly Ala  
1 5 10 15  
Lys Arg Thr Ala Ser Leu Pro Arg Gln His Pro Gly His His Glu Ala  
20 25 30  
Gly His

(2) INFORMATION FOR SEQ ID NO:1639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..450
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1639:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aatcgagccg ccgccgcgcg cgccgcagtt gcttcggtc ttccgtgctc accttcgaga  | 60  |
| gatcaagttg ctgctgcggt agtccccaac catcatcatg cagaacgagg agggtaagac | 120 |
| ggtggacctc tacgtcccca ggaagtgcgc ggccacgaat aggatcatca ctgccaagga | 180 |
| tcatgcctct gtccagatca acattggcca cttggatgcg aatggcctgt acgatggtca | 240 |

09639930 09639930

cttcaccacg tttgctctct ctgggtttgt ccgtgctcag ggtgatgctg acagttcggt 300  
ggacaggctg tggcagaaga agaaggctga gatcaagcag taggtctttg cacgtagttc 360  
cacggtaat ggactcttga gggatactgc tctagcta atgcttttagctg gggggggggg 420  
antgattckg atgtttggct gtycgtttgt

(2) INFORMATION FOR SEQ ID NO:1640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1640:

Ser Ser Arg Arg Arg Arg Arg Arg Ser Cys Leu Arg Ser Ser Val Leu  
1 5 10 15  
Thr Phe Glu Arg Ser Ser Cys Cys Cys Gly Ser Pro Gln Pro Ser Ser  
20 25 30  
Cys Arg Thr Arg Arg Val Arg Arg Trp Thr Ser Thr Ser Pro Gly Ser  
35 40 45  
Ala Arg Pro Arg Ile Gly Ser Ser Leu Pro Arg Ile Met Pro Leu Ser  
50 55 60  
Arg Ser Thr Leu Ala Thr Trp Met Arg Met Ala Cys Thr Met Val Thr  
65 70 75 80  
Ser Pro Arg Leu Leu Ser Leu Gly Leu Ser Val Leu Arg Val Met Leu  
85 90 95  
Thr Val Arg Trp Thr Gly Cys Gly Arg Arg Arg Arg Leu Arg Ser Ser  
100 105 110  
Ser Arg Ser Leu His Val Val Pro Pro Val Met Asp Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..81
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1641:

Met Gln Asn Glu Gly Gly Lys Thr Val Asp Leu Tyr Val Pro Arg Lys  
1 5 10 15  
Cys Ser Ala Thr Asn Arg Ile Ile Thr Ala Lys Asp His Ala Ser Val  
20 25 30  
Gln Ile Asn Ile Gly His Leu Asp Ala Asn Gly Leu Tyr Asp Gly His  
35 40 45  
Phe Thr Thr Phe Ala Leu Ser Gly Phe Val Arg Ala Gln Gly Asp Ala  
50 55 60  
Asp Ser Ser Leu Asp Arg Leu Trp Gln Lys Lys Lys Ala Glu Ile Lys  
65 70 75 80  
Gln

(2) INFORMATION FOR SEQ ID NO:1642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

002101 00553550

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..65  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1598671  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1642:  
Met Pro Leu Ser Arg Ser Thr Leu Ala Thr Trp Met Arg Met Ala Cys  
1                  5                  10                  15  
Thr Met Val Thr Ser Pro Arg Leu Leu Ser Leu Gly Leu Ser Val Leu  
                  20                  25                  30  
Arg Val Met Leu Thr Val Arg Trp Thr Gly Cys Gly Arg Arg Arg Arg  
                  35                  40                  45  
Leu Arg Ser Ser Ser Arg Ser Leu His Val Val Pro Pro Val Met Asp  
50                  55                  60  
Ser  
65

(2) INFORMATION FOR SEQ ID NO:1643:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 451 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..451  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1643:

actcccactt tactcctatc cactgcggcc tggacgcgtg ckagakgctt gaccaagcag 60  
cagcagggat ggcgcctctg aagctgtacg ggatgccgct gtccccaac gtggtgcgcg 120  
tggccaccgt gctcaacgag aagggcctcg acttcgagat cgtccccgtc gacctcacca 180  
ccggcgccca caagcagccc gacttcctcg cctcaaccc tttcggccag atcccggtc 240  
tcgtcgacgg agacgaayct cttcgagtc cgtgcgatca accggtacat cgccagcaag 300  
tacgcgtcgg agggcacgga cctgctcccc gcgacggcgt cggcgcggaac gtggaagggtg 360  
tggctagagg tggagtcgca ccacttctac ccgaacgcgt cgcgcgtggt gttccagctg 420  
ctcgtgaggc cgctcctggg cgcgccccga c

(2) INFORMATION FOR SEQ ID NO:1644:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 149 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..149  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1644:

Ser His Phe Thr Pro Ile His Cys Gly Leu Asp Ala Cys Xaa Xaa Leu  
1                  5                  10                  15  
Asp Gln Ala Ala Ala Gly Met Ala Pro Leu Lys Leu Tyr Gly Met Pro  
                  20                  25                  30  
Leu Ser Pro Asn Val Val Arg Val Ala Thr Val Leu Asn Glu Lys Gly  
                  35                  40                  45  
Leu Asp Phe Glu Ile Val Pro Val Asp Leu Thr Thr Gly Ala His Lys  
50                  55                  60  
Gln Pro Asp Phe Leu Ala Leu Asn Pro Phe Gly Gln Ile Pro Ala Leu  
65                  70                  75                  80  
Val Asp Gly Asp Glu Xaa Leu Arg Val Pro Cys Asp Gln Pro Val His  
                  85                  90                  95

DOCKET# 08668960

Arg Gln Gln Val Arg Val Gly Gly His Gly Pro Ala Pro Arg Asp Gly  
100 105 110  
Val Gly Ala Asn Val Glu Gly Val Ala Arg Gly Gly Val Ala Pro Leu  
115 120 125  
Leu Pro Glu Arg Val Ala Ala Gly Val Pro Ala Ala Arg Glu Ala Ala  
130 135 140  
Pro Gly Arg Ala Pro  
145

(2) INFORMATION FOR SEQ ID NO:1645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1645:

Met Ala Pro Leu Lys Leu Tyr Gly Met Pro Leu Ser Pro Asn Val Val  
1 5 10 15  
Arg Val Ala Thr Val Leu Asn Glu Lys Gly Leu Asp Phe Glu Ile Val  
20 25 30  
Pro Val Asp Leu Thr Thr Gly Ala His Lys Gln Pro Asp Phe Leu Ala  
35 40 45  
Leu Asn Pro Phe Gly Gln Ile Pro Ala Leu Val Asp Gly Asp Glu Xaa  
50 55 60  
Leu Arg Val Pro Cys Asp Gln Pro Val His Arg Gln Gln Val Arg Val  
65 70 75 80  
Gly Gly His Gly Pro Ala Pro Arg Asp Gly Val Gly Ala Asn Val Glu  
85 90 95  
Gly Val Ala Arg Gly Gly Val Ala Pro Leu Leu Pro Glu Arg Val Ala  
100 105 110  
Ala Gly Val Pro Ala Ala Arg Glu Ala Ala Pro Gly Arg Ala Pro  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1646:

Met Pro Leu Ser Pro Asn Val Val Arg Val Ala Thr Val Leu Asn Glu  
1 5 10 15  
Lys Gly Leu Asp Phe Glu Ile Val Pro Val Asp Leu Thr Thr Gly Ala  
20 25 30  
His Lys Gln Pro Asp Phe Leu Ala Leu Asn Pro Phe Gly Gln Ile Pro  
35 40 45  
Ala Leu Val Asp Gly Asp Glu Xaa Leu Arg Val Pro Cys Asp Gln Pro  
50 55 60  
Val His Arg Gln Gln Val Arg Val Gly Gly His Gly Pro Ala Pro Arg  
65 70 75 80  
Asp Gly Val Gly Ala Asn Val Glu Gly Val Ala Arg Gly Gly Val Ala  
85 90 95  
Pro Leu Leu Pro Glu Arg Val Ala Ala Gly Val Pro Ala Ala Arg Glu

DOE-PT-0868950



100 105 110  
Ala Ala Pro Gly Arg Ala Pro  
115

(2) INFORMATION FOR SEQ ID NO:1647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..467
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1647:

|         |       |         |       |       |       |       |       |       |       |        |       |     |
|---------|-------|---------|-------|-------|-------|-------|-------|-------|-------|--------|-------|-----|
| gcttctg | ggga  | tggtgc  | catt  | tatgc | aggca | cactg | ctgcc | ggcag | ccacg | actggt | tgga  | 60  |
| aggagg  | ggagg | gtagta  | gta   | aaacc | aggt  | ggtgt | ggctg | gctcg | tgca  | cggcg  | acagg | 120 |
| cggcag  | tgag  | agcgat  | gagc  | gcggc | gtcga | cgagc | tcggt | cacca | agttc | atcaag | tgcg  | 180 |
| tcacgg  | tcgg  | cgatg   | ggggc | gtcgg | gaaga | cctgc | atgct | catct | gctac | acctg  | caaca | 240 |
| agttccc | ac    | ggattat | atc   | cccac | cgat  | tgc   | aaact | cagcg | ccaat | gtctc  | cgtag | 300 |
| gtggg   | agcat | cgtca   | acttg | ggcct | ctggg | acacg | gcagg | ccagg | aggat | tacag  | caggt | 360 |
| tgagg   | cctct | cagct   | acagg | ggtgt | ctgat | gtttc | atcct | ctcct | tctcc | ctggt  | cagca | 420 |
| ggcgag  | cta   | tgaga   | acgtc | ctcaa | gaagt | ggatg | ccaga | gcttc | gcg   |        |       |     |

(2) INFORMATION FOR SEQ ID NO:1648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1648:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Trp | Asp | Gly | Cys | Ile | Tyr | Ala | Gly | Thr | Leu | Leu | Pro | Ala | Ala | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Gly | Trp | Lys | Glu | Gly | Gly | Val | Val | Val | Lys | Pro | Gly | Arg | Cys | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Trp | Leu | Val | Gln | Arg | Arg | Gln | Ala | Ala | Val | Arg | Ala | Met | Ser | Ala | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Thr | Ser | Ser | Val | Thr | Lys | Phe | Ile | Lys | Cys | Val | Thr | Val | Gly | Asp |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gly | Ala | Val | Gly | Lys | Thr | Cys | Met | Leu | Ile | Cys | Tyr | Thr | Cys | Asn | Lys |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Phe | Pro | Thr | Asp | Tyr | Ile | Pro | Thr | Val | Phe | Asp | Asn | Phe | Ser | Ala | Asn |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Val | Ser | Val | Gly | Gly | Ser | Ile | Val | Asn | Leu | Gly | Leu | Trp | Asp | Thr | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Gln | Glu | Asp | Tyr | Ser | Arg | Leu | Arg | Pro | Leu | Ser | Tyr | Arg | Gly | Ala |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Val | Phe | Ile | Leu | Ser | Phe | Ser | Leu | Val | Ser | Arg | Ala | Ser | Tyr | Glu |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Val | Leu | Lys | Lys | Trp | Met | Pro | Glu | Leu | Arg |     |     |     |     |     |
|     |     |     | 145 |     | 150 |     |     |     |     | 155 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

DOCKET "08669560"

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1598695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1649:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ala | Ala | Ser | Thr | Ser | Ser | Val | Thr | Lys | Phe | Ile | Lys | Cys | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Val | Gly | Asp | Gly | Ala | Val | Gly | Lys | Thr | Cys | Met | Leu | Ile | Cys | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Cys | Asn | Lys | Phe | Pro | Thr | Asp | Tyr | Ile | Pro | Thr | Val | Phe | Asp | Asn |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Phe | Ser | Ala | Asn | Val | Ser | Val | Gly | Gly | Ser | Ile | Val | Asn | Leu | Gly | Leu |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Trp | Asp | Thr | Ala | Gly | Gln | Glu | Asp | Tyr | Ser | Arg | Leu | Arg | Pro | Leu | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Tyr | Arg | Gly | Ala | Asp | Val | Phe | Ile | Leu | Ser | Phe | Ser | Leu | Val | Ser | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Ser | Tyr | Glu | Asn | Val | Leu | Lys | Lys | Trp | Met | Pro | Glu | Leu | Arg |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:1650:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1598696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1650:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ile | Cys | Tyr | Thr | Cys | Asn | Lys | Phe | Pro | Thr | Asp | Tyr | Ile | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Val | Phe | Asp | Asn | Phe | Ser | Ala | Asn | Val | Ser | Val | Gly | Gly | Ser | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Asn | Leu | Gly | Leu | Trp | Asp | Thr | Ala | Gly | Gln | Glu | Asp | Tyr | Ser | Arg |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Leu | Arg | Pro | Leu | Ser | Tyr | Arg | Gly | Ala | Asp | Val | Phe | Ile | Leu | Ser | Phe |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Ser | Leu | Val | Ser | Arg | Ala | Ser | Tyr | Glu | Asn | Val | Leu | Lys | Lys | Trp | Met |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Glu | Leu | Arg |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1651:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 496 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..496

(D) OTHER INFORMATION: / Ceres Seq. ID 1598730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1651:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| acatcacggt | accattccacc | ggagatgact | gttgtgagta | tcatgtggtc | gttagtgacg | 60  |
| gtgcaggtgc | tgggtggcgg  | ggcattagca | tttctggtag | gcgggtgctg | tgtggtcctc | 120 |
| ccaaggttcc | cccgggtaag  | aacatcacag | ccaaatatgg | tagtgattgg | ctagatgcc  | 180 |
| aggcgacatg | gtatggcaag  | ccgacagggt | ctggccccga | cgacaatggt | ggcggctgcg | 240 |
| ggtacaagga | cgtgaataag  | gcccctttca | atagcatggg | cgcgtgtggc | aacgtcccca | 300 |

0068980-04300

tcttcaagga cggctctaggt tgtggatcct gcttcgagat caagtgtgac aagccagcgg 360  
agtgtctctgg caagcccgtg gtgggtgtaca ttacggacat gaactacgag cccattgcgg 420  
cataccactt cgacctagcg ggcacggcgt tcgggtgccat ggctaagaag ggtgaggagg 480  
agaagttgcg caaggc

(2) INFORMATION FOR SEQ ID NO:1652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1598731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1652:

Ile Thr Val Pro Phe Thr Gly Asp Asp Cys Cys Glu Tyr His Val Val  
1 5 10 15  
Val Ser Ala Gly Ala Gly Ala Gly Gly Ile Ser Ile Ser Gly  
20 25 30  
Arg Arg Cys Trp Cys Gly Pro Pro Lys Val Pro Pro Gly Lys Asn Ile  
35 40 45  
Thr Ala Lys Tyr Gly Ser Asp Trp Leu Asp Ala Lys Ala Thr Trp Tyr  
50 55 60  
Gly Lys Pro Thr Gly Ala Gly Pro Asp Asp Asn Gly Gly Gly Cys Gly  
65 70 75 80  
Tyr Lys Asp Val Asn Lys Ala Pro Phe Asn Ser Met Gly Ala Cys Gly  
85 90 95  
Asn Val Pro Ile Phe Lys Asp Gly Leu Gly Cys Gly Ser Cys Phe Glu  
100 105 110  
Ile Lys Cys Asp Lys Pro Ala Glu Cys Ser Gly Lys Pro Val Val Val  
115 120 125  
Tyr Ile Thr Asp Met Asn Tyr Glu Pro Ile Ala Ala Tyr His Phe Asp  
130 135 140  
Leu Ala Gly Thr Ala Phe Gly Ala Met Ala Lys Lys Gly Glu Glu Glu  
145 150 155 160  
Lys Leu Arg Lys

(2) INFORMATION FOR SEQ ID NO:1653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..429

(D) OTHER INFORMATION: / Ceres Seq. ID 1598732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1653:

gaatttccat tcgaccccat ccacttctca gttctcacct caatctcgcg agaagcgaas 60  
cggaggagga ggggtgcgagg agatcgcgag cagccggagc cggagccgga sctagaagat 120  
gaagacgttc gaccogtggc cgggtattctt ccgccgggag tggaagcgca attggccott 180  
cctcacgggg ttgcocatca ccggcttcat catcactaag atgacggcca acttcaccga 240  
ggaggacctc aagaactcca agttcgttca ggagcacaag aagcgtgac caaccaggtg 300  
ttgtccgaat tgctgtctt ggacagccag ttatgttatg atgtttgaat tgaaaaatta 360  
gcttcttttt cttcatctaa atgcgtgcag cctatgctcc atttgtaatg taataagagg 420  
gcactctgac

(2) INFORMATION FOR SEQ ID NO:1654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids

00689930-10300



| (A1) SEQUENCE ALIGNMENT FOR SEQ |            |             |            |             |             |     |
|---------------------------------|------------|-------------|------------|-------------|-------------|-----|
| ttaacaaaat                      | tatcgatatt | aattactatc  | ctgttgagac | agcaaaaagag | gtcaatatgc  | 60  |
| gtcacaggcc                      | aattggcata | gggtgttcaag | gcctggcaga | tactttttata | ttactgggca  | 120 |
| tgccgtttga                      | ttcaccagag | gctcaacagt  | tgaataagga | tatattcgaa  | actatctact  | 180 |
| atcatgtctc                      | gaaagcttct | gctgaactcg  | ctgctaaaga | aggtccttat  | gaaacgtatg  | 240 |
| aagggagccc                      | tgtcagcaag | ggcattctcc  | aacctgacat | gtgggatgta  | gtgccattcta | 300 |
| acagatggaa                      | ctggccatct | ctaagggaga  | ccattttcaa | agttgggata  | agaaattctc  | 360 |
| ttcttgtttg                      | tccaatgccc | actgcttcca  | ctagtcagat | tcttggaac   | aatgagtgtt  | 420 |
| ttgaacccta                      | caagcttaat | atatacagtc  | gacgtgttct | aagtggggaa  | tttgttgtgg  | 480 |
| gtaacaagca                      | tcttcttcat | gatct       |            |             |             |     |

[illegible]

```
(A) NAME/KEY: peptide
(B) LOCATION: 1..149
```

| 1. <i>Chlorophyll a</i> (mg/L) |       |
|--------------------------------|-------|
| 1.0                            | 1.0   |
| 2.0                            | 2.0   |
| 3.0                            | 3.0   |
| 4.0                            | 4.0   |
| 5.0                            | 5.0   |
| 6.0                            | 6.0   |
| 7.0                            | 7.0   |
| 8.0                            | 8.0   |
| 9.0                            | 9.0   |
| 10.0                           | 10.0  |
| 11.0                           | 11.0  |
| 12.0                           | 12.0  |
| 13.0                           | 13.0  |
| 14.0                           | 14.0  |
| 15.0                           | 15.0  |
| 16.0                           | 16.0  |
| 17.0                           | 17.0  |
| 18.0                           | 18.0  |
| 19.0                           | 19.0  |
| 20.0                           | 20.0  |
| 21.0                           | 21.0  |
| 22.0                           | 22.0  |
| 23.0                           | 23.0  |
| 24.0                           | 24.0  |
| 25.0                           | 25.0  |
| 26.0                           | 26.0  |
| 27.0                           | 27.0  |
| 28.0                           | 28.0  |
| 29.0                           | 29.0  |
| 30.0                           | 30.0  |
| 31.0                           | 31.0  |
| 32.0                           | 32.0  |
| 33.0                           | 33.0  |
| 34.0                           | 34.0  |
| 35.0                           | 35.0  |
| 36.0                           | 36.0  |
| 37.0                           | 37.0  |
| 38.0                           | 38.0  |
| 39.0                           | 39.0  |
| 40.0                           | 40.0  |
| 41.0                           | 41.0  |
| 42.0                           | 42.0  |
| 43.0                           | 43.0  |
| 44.0                           | 44.0  |
| 45.0                           | 45.0  |
| 46.0                           | 46.0  |
| 47.0                           | 47.0  |
| 48.0                           | 48.0  |
| 49.0                           | 49.0  |
| 50.0                           | 50.0  |
| 51.0                           | 51.0  |
| 52.0                           | 52.0  |
| 53.0                           | 53.0  |
| 54.0                           | 54.0  |
| 55.0                           | 55.0  |
| 56.0                           | 56.0  |
| 57.0                           | 57.0  |
| 58.0                           | 58.0  |
| 59.0                           | 59.0  |
| 60.0                           | 60.0  |
| 61.0                           | 61.0  |
| 62.0                           | 62.0  |
| 63.0                           | 63.0  |
| 64.0                           | 64.0  |
| 65.0                           | 65.0  |
| 66.0                           | 66.0  |
| 67.0                           | 67.0  |
| 68.0                           | 68.0  |
| 69.0                           | 69.0  |
| 70.0                           | 70.0  |
| 71.0                           | 71.0  |
| 72.0                           | 72.0  |
| 73.0                           | 73.0  |
| 74.0                           | 74.0  |
| 75.0                           | 75.0  |
| 76.0                           | 76.0  |
| 77.0                           | 77.0  |
| 78.0                           | 78.0  |
| 79.0                           | 79.0  |
| 80.0                           | 80.0  |
| 81.0                           | 81.0  |
| 82.0                           | 82.0  |
| 83.0                           | 83.0  |
| 84.0                           | 84.0  |
| 85.0                           | 85.0  |
| 86.0                           | 86.0  |
| 87.0                           | 87.0  |
| 88.0                           | 88.0  |
| 89.0                           | 89.0  |
| 90.0                           | 90.0  |
| 91.0                           | 91.0  |
| 92.0                           | 92.0  |
| 93.0                           | 93.0  |
| 94.0                           | 94.0  |
| 95.0                           | 95.0  |
| 96.0                           | 96.0  |
| 97.0                           | 97.0  |
| 98.0                           | 98.0  |
| 99.0                           | 99.0  |
| 100.0                          | 100.0 |

(D) OTHER INFORMATION: / Ceres Seq. ID 1598746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1659:

Met Arg His Arg Pro Ile Gly Ile Gly Val Gln Gly Leu Ala Asp Thr  
1 5 10 15  
Phe Ile Leu Leu Gly Met Pro Phe Asp Ser Pro Glu Ala Gln Gln Leu  
20 25 30  
Asn Lys Asp Ile Phe Glu Thr Ile Tyr Tyr His Ala Leu Lys Ala Ser  
35 40 45  
Ala Glu Leu Ala Ala Lys Glu Gly Pro Tyr Glu Thr Tyr Glu Gly Ser  
50 55 60  
Pro Val Ser Lys Gly Ile Leu Gln Pro Asp Met Trp Asp Val Val Pro  
65 70 75 80  
Ser Asn Arg Trp Asn Trp Pro Ser Leu Arg Glu Thr Ile Ser Lys Val  
85 90 95  
Gly Ile Arg Asn Ser Leu Leu Val Ala Pro Met Pro Thr Ala Ser Thr  
100 105 110  
Ser Gln Ile Leu Gly Asn Asn Glu Cys Phe Glu Pro Tyr Thr Ser Asn  
115 120 125  
Ile Tyr Ser Arg Arg Val Leu Ser Gly Glu Phe Val Val Gly Asn Lys  
130 135 140  
His Leu Leu His Asp  
145

(2) INFORMATION FOR SEQ ID NO:1660:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1598747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1660:

Met Pro Phe Asp Ser Pro Glu Ala Gln Leu Asn Lys Asp Ile Phe  
1 5 10 15  
Glu Thr Ile Tyr Tyr His Ala Leu Lys Ala Ser Ala Glu Leu Ala Ala  
20 25 30  
Lys Glu Gly Pro Tyr Glu Thr Tyr Glu Gly Ser Pro Val Ser Lys Gly  
35 40 45  
Ile Leu Gln Pro Asp Met Trp Asp Val Val Pro Ser Asn Arg Trp Asn  
50 55 60  
Trp Pro Ser Leu Arg Glu Thr Ile Ser Lys Val Gly Ile Arg Asn Ser  
65 70 75 80  
Leu Leu Val Ala Pro Met Pro Thr Ala Ser Thr Ser Gln Ile Leu Gly  
85 90 95  
Asn Asn Glu Cys Phe Glu Pro Tyr Thr Ser Asn Ile Tyr Ser Arg Arg  
100 105 110  
Val Leu Ser Gly Glu Phe Val Val Gly Asn Lys His Leu Leu His Asp  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1661:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 470 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

00639930 10300







Ala Arg Arg Ala Trp Arg Pro Thr Arg Ser Thr Ser Ser Arg Cys  
85 90 95

(2) INFORMATION FOR SEQ ID NO:1667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1667:

Thr Thr Ala Asn Thr Ser Ala Ser His Phe Phe Pro Ser Pro Phe Ala  
1 5 10 15  
Thr Gln Thr Pro Thr Arg Xaa His Arg Trp Arg Pro Arg Pro Arg Arg  
20 25 30  
Ser Pro Arg Xaa Arg Ser Arg Arg Arg Arg Ser Pro Arg Leu Arg Arg  
35 40 45  
Arg Pro Pro Xaa Arg Ser Arg Xaa Met Lys Arg Val Pro Ala Xaa Gln  
50 55 60  
Val Arg Cys Gln Gly Gly Arg Arg Gly Gln Glu Gly Gln Glu Glu Gly  
65 70 75 80  
Gln Glu Glu Arg Gly Asp Leu Gln Asp Leu His Leu Gln Gly Ala Glu  
85 90 95  
Ala Gly Ala Pro Gly His Trp His Leu Leu Gln Gly His Val Asp His  
100 105 110  
Glu Leu Leu His  
115

(2) INFORMATION FOR SEQ ID NO:1668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598767

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1668:

Met Ala Pro Lys Ala Glu Lys Lys Pro Ala Xaa Xaa Lys Pro Ala Glu  
1 5 10 15  
Glu Glu Pro Ala Ala Glu Lys Ala Pro Ala Xaa Lys Lys Pro Xaa Tyr  
20 25 30  
Glu Ala Gly Pro Arg Trp Xaa Ser Pro Leu Pro Arg Arg Ala Ala Arg  
35 40 45  
Ala Arg Gly Ala Gly Arg Arg Ala Arg Arg Ala Trp Arg Pro Thr Arg  
50 55 60  
Ser Thr Ser Ser Arg Cys  
65 70

(2) INFORMATION FOR SEQ ID NO:1669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

00689930 101300

(B) LOCATION: 1..495

(D) OTHER INFORMATION: / Ceres Seq. ID 1598768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1669:

|            |            |             |             |             |            |     |
|------------|------------|-------------|-------------|-------------|------------|-----|
| aagacggccg | ccatctcccc | tggtcggttt  | taggagacct  | gcgcccgtcc  | tccggccacg | 60  |
| cgagcacgcc | gaaatggtcg | cccacaggtt  | ccatcagtac  | caggtggtgg  | gtcgcgcgct | 120 |
| gccgaccccg | accgatgagc | acccaagat   | ctaccgcatg  | aagctctggg  | ccactaacga | 180 |
| ggttcgcgcc | aagtcgaagt | tctgggtactt | cctgagaaaag | ctgaagaagg  | tgaagaagag | 240 |
| caatggccag | atgctcgcca | tcaacgagat  | cttcgagcgc  | aaccctacca  | ccatcaagaa | 300 |
| ctacggcatc | tggtctcggt | accagagcag  | gacgggggtac | acaacatgta  | caaggagtac | 360 |
| cgcgacacga | ccctgaacgg | cgccgtggag  | cagatgtaca  | acgagatggc  | ctcgcgccac | 420 |
| cgcgtgaggt | ccccctgcat | ccagatcatc  | aagactgcka  | cgggtccactt | caagctgtgc | 480 |
| aagakggaca | acacg      |             |             |             |            |     |

(2) INFORMATION FOR SEQ ID NO:1670:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1598769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1670:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | Arg | Pro | Pro | Ser | Pro | Leu | Phe | Gly | Phe | Arg | Arg | Pro | Ala | Pro | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |  |
| Leu | Arg | Pro | Arg | Glu | His | Ala | Glu | Met | Val | Ala | His | Arg | Phe | His | Gln |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Tyr | Gln | Val | Val | Gly | Arg | Ala | Leu | Pro | Thr | Pro | Thr | Asp | Glu | His | Pro |  |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Lys | Ile | Tyr | Arg | Met | Lys | Leu | Trp | Ala | Thr | Asn | Glu | Val | Arg | Ala | Lys |  |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Ser | Lys | Phe | Trp | Tyr | Phe | Leu | Arg | Lys | Leu | Lys | Lys | Val | Lys | Lys | Ser |  |
|     |     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |  |
| Asn | Gly | Gln | Met | Leu | Ala | Ile | Asn | Glu | Ile | Phe | Glu | Arg | Asn | Pro | Thr |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Thr | Ile | Lys | Asn | Tyr | Gly | Ile | Trp | Leu | Arg | Tyr | Gln | Ser | Arg | Thr | Gly |  |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |  |
| Tyr | Thr | Thr | Cys | Thr | Arg | Ser | Thr | Ala | Thr | Arg | Pro |     |     |     |     |  |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1671:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1598770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1671:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Val | Ala | His | Arg | Phe | His | Gln | Tyr | Gln | Val | Val | Gly | Arg | Ala | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |  |
| Pro | Thr | Pro | Thr | Asp | Glu | His | Pro | Lys | Ile | Tyr | Arg | Met | Lys | Leu | Trp |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Ala | Thr | Asn | Glu | Val | Arg | Ala | Lys | Ser | Lys | Phe | Trp | Tyr | Phe | Leu | Arg |  |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Lys | Leu | Lys | Lys | Val | Lys | Lys | Ser | Asn | Gly | Gln | Met | Leu | Ala | Ile | Asn |  |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Glu | Ile | Phe | Glu | Arg | Asn | Pro | Thr | Thr | Ile | Lys | Asn | Tyr | Gly | Ile | Trp |  |

(2) INFORMATION FOR SEQ ID NO:1672:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1598771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1672:

(2) INFORMATION FOR SEQ ID NO:1673:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..336

(D) OTHER INFORMATION: / Ceres Seq. ID 1598781

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1673:

|                                           |            |             |             |                            |
|-------------------------------------------|------------|-------------|-------------|----------------------------|
| (x1) SEQUENCE DESCRIPTION: SEQ ID NO:103: |            |             |             |                            |
| agtaacccgc                                | atcccacatc | actcatccac  | agctcgcagc  | cgtattcctg tctcgaatcc 60   |
| tctctcgcgc                                | ctccgatggc | cgcacgaag   | caaacagcaa  | ggaagtcgac cggcggcgaag 120 |
| gccccccgga                                | agcagctggc | cactaaggct  | gcgcgcgaagt | cggccccggc caccggcggc 180  |
| gtgaagaagc                                | cccacogctt | ctgccccggc  | accgtcgcgc  | tccgsagatc cgcaagtacc 240  |
| agaagagcac                                | tgagctgctc | atccgcgaagc | tccccttcca  | gcgcctcgtc cgcgagatcg 300  |
| cgcagacttt                                | caagactgat | ctgagggttcc | agtctt      |                            |

(2) INFORMATION FOR SEQ ID NO:1674:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1598782

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1674:

(X1) SEQUENCE DESCRIPTION: SEQ ID: 1 (10 amino acids)

| Ser | Asn | Pro | His | Pro | Thr | Ser | Leu | Ile | His | Ser | Ser | Gln | Pro | Tyr | Ser |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |

Cys Leu Glu Ser Ser Leu Ala Ala Pro Met Ala Arg Thr Lys Gln Thr  
20 25 30  
Ala Arg Lys Ser Thr Gly Gly Lys Ala Pro Arg Lys Gln Leu Ala Thr  
35 40 45  
Lys Ala Ala Arg Lys Ser Ala Pro Ala Thr Gly Gly Val Lys Lys Pro  
50 55 60  
His Arg Phe Cys Pro Gly Thr Val Ala Leu Xaa Arg Ser Ala Ser Thr  
65 70 75 80  
Arg Arg Ala Leu Ser Cys Ser Ser Ala Ser Pro Ser Ser Ala Ser  
85 90 95  
Ser Ala Arg Ser Arg Arg Thr Ser Arg Leu Ile  
100 105

(2) INFORMATION FOR SEQ ID NO:1675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1675:

Val Thr Arg Ile Pro His His Ser Ser Thr Ala Arg Ser Arg Ile Pro  
1 5 10 15  
Val Ser Asn Pro Leu Ser Pro Leu Arg Trp Pro Ala Arg Ser Lys Gln  
20 25 30  
Gln Gly Ser Arg Pro Ala Ala Arg Pro Pro Gly Ser Ser Trp Pro Leu  
35 40 45  
Arg Leu Arg Ala Ser Arg Pro Arg Pro Pro Ala Ala  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1676:

Met Ala Arg Thr Lys Gln Thr Ala Arg Lys Ser Thr Gly Gly Lys Ala  
1 5 10 15  
Pro Arg Lys Gln Leu Ala Thr Lys Ala Ala Arg Lys Ser Ala Pro Ala  
20 25 30  
Thr Gly Gly Val Lys Lys Pro His Arg Phe Cys Pro Gly Thr Val Ala  
35 40 45  
Leu Xaa Arg Ser Ala Ser Thr Arg Arg Ala Leu Ser Cys Ser Ser Ala  
50 55 60  
Ser Ser Pro Ser Ser Ala Ser Ser Ala Arg Ser Arg Arg Thr Ser Arg  
65 70 75 80  
Leu Ile

(2) INFORMATION FOR SEQ ID NO:1677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

00669900 101300

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..198  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1598795  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1677:  
gcgatacaac gacttcctgc agtctcgcgc tgcgcccctc ctttcgcgct ccacggctcc 60  
acgctgccga cgtccaccac acagcacggc ckwgtcaccc gatccctcca tggcggcggc 120  
agtggcggcg gtgcgggctg ccacgacggc ggaggacgag gcgcgcctgc tgcgtctgga 180  
ggagcaggcg gacacggc

(2) INFORMATION FOR SEQ ID NO:1678:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 66 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..66  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1598796  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1678:  
Ala Ile Gln Arg Leu Pro Ala Val Leu Arg Cys Ala Pro Pro Phe Arg  
1                  5                  10                  15  
Leu His Gly Ser Thr Leu Pro Thr Ser Thr Thr Gln His Gly Xaa Val  
                  20                  25                  30  
Thr Arg Ser Leu His Gly Gly Gly Ser Gly Gly Gly Arg Gly Cys His  
                  35                  40                  45  
Asp Gly Gly Gly Arg Gly Ala Pro Ala Ala Ser Gly Gly Ala Gly Gly  
50                  55                  60  
His Gly  
65

(2) INFORMATION FOR SEQ ID NO:1679:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 65 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..65  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1598797  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1679:  
Arg Tyr Asn Asp Phe Leu Gln Ser Cys Ala Ala Pro Leu Leu Ser Ala  
1                  5                  10                  15  
Ser Thr Ala Pro Arg Cys Arg Arg Pro Pro His Ser Thr Val Xaa Ser  
                  20                  25                  30  
Pro Asp Pro Ser Met Ala Ala Ala Val Ala Ala Val Ala Ala Thr  
                  35                  40                  45  
Thr Ala Glu Asp Glu Ala Arg Leu Leu Arg Leu Glu Glu Gln Ala Asp  
50                  55                  60  
Thr  
65

(2) INFORMATION FOR SEQ ID NO:1680:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 65 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

09689880-101300

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..65  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1598798  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1680:  
Asp Thr Thr Thr Ser Cys Ser Pro Ala Leu Arg Pro Ser Phe Pro Pro  
1                  5                  10                  15  
Pro Arg Leu His Ala Ala Asp Val His Thr Ala Arg Xaa Xaa His  
                  20                  25                  30  
Pro Ile Pro Pro Trp Arg Arg Gln Trp Arg Arg Ser Arg Leu Pro Arg  
                  35                  40                  45  
Arg Arg Arg Thr Arg Arg Ala Cys Cys Val Trp Arg Ser Arg Arg Thr  
                  50                  55                  60  
Arg  
65

(2) INFORMATION FOR SEQ ID NO:1681:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 349 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..349  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1681:

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| akagcagcag  | acacccaata | aacacacaca | cacaagckak  | wdagcactac | ctgttggttg | 60  |
| gattctcttc  | agtctagcta | ctcgatcggt | cccttggtcca | cagttaagtt | tcagacacat | 120 |
| ggggagcatt  | ggcagaggca | cggccaactg | ckccaccgtg  | ccgcagccgc | cgccgtcgac | 180 |
| aggggaagctc | atcacgatcc | tgagcatcga | tggcggcggc  | atccgcggcc | ttatcccggc | 240 |
| gaccatcatt  | gcgtacctcg | aggccaagct | ccaggagctg  | gacggcccg  | acgctcggat | 300 |
| cgccgactac  | ttcgatgtga | ttgccgggac | gagcaccggc  | gccctgtctc |            |     |

(2) INFORMATION FOR SEQ ID NO:1682:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 116 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..116  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1682:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Xaa His Glu Thr Pro Asn Lys His Thr His Thr Ser Xaa Xaa Ala Leu |  |
| 1                  5                  10                  15    |  |
| Pro Val Gly Trp Ile Leu Phe Ser Leu Ala Thr Arg Ser Val Pro Cys |  |
| 20                  25                  30                      |  |
| Pro Gln Leu Ser Phe Arg His Met Gly Ser Ile Gly Arg Gly Thr Ala |  |
| 35                  40                  45                      |  |
| Asn Cys Xaa Thr Val Pro Gln Pro Pro Pro Ser Thr Gly Lys Leu Ile |  |
| 50                  55                  60                      |  |
| Thr Ile Leu Ser Ile Asp Gly Gly Gly Ile Arg Gly Leu Ile Pro Ala |  |
| 65                  70                  75                  80  |  |
| Thr Ile Ile Ala Tyr Leu Glu Ala Lys Leu Gln Glu Leu Asp Gly Pro |  |
| 85                  90                  95                      |  |
| Asp Ala Arg Ile Ala Asp Tyr Phe Asp Val Ile Ala Gly Thr Ser Thr |  |
| 100                  105                  110                   |  |
| Gly Ala Leu Leu                                                 |  |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ala | Thr | Thr | Ser | Arg | Val | Ser | Arg | Ser | Arg | Gln | Ser | Gly | Ala | Gly |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Glu | Gly | Arg | Arg | Glu | Ala | Tyr | Leu | Arg | Ala | Tyr | Leu | Arg | Gly | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Arg | Arg | Ala | Gln | Asp | Leu | Pro | Arg | Glu | Cys | His | Pro | Arg | Xaa | Xaa |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Tyr | Thr | Glu | His | Ala | Arg | Arg | Lys | Thr | Val | Thr | Ala | Met | Asp | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Tyr | Ala | Leu | Lys | Arg | Gln | Gly | Arg | Thr | Leu | Tyr | Gly | Phe | Gly | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1686:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1598807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1686:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Gln | Ser | His | Arg | Gly | Val | Phe | Lys | Ser | His | Asn | Leu | Leu | Val | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| His | His | Cys | Leu | Arg | Pro | Thr | Arg | Arg | Cys | Leu | Gly | Ala | Ala | Arg |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Ala | Ala | Arg | Gly | Trp | Ala | Arg | Val | Val | Arg | Asn | Ala | Thr | Val | Ser | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Arg | Gln | His | Pro | Gly | Tyr | His | Glu | Ala | Gly | Asn | Pro | Glu | Leu | Ala |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Arg | Arg | Gly | Gly | Val | Lys | Arg | Ile | Ser | Gly | Leu | Ile | Tyr | Glu | Glu | Thr |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Gly | Val | Leu | Lys | Ile | Phe | Leu | Glu | Asn | Val | Ile | Arg | Asp | Xaa | Xaa |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Thr | Pro | Ser | Thr | Leu | Ala | Ala | Arg | Pro | Ser | Pro | Pro | Trp | Met | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | Thr | Pro | Ser | Ser | Ala | Arg | Ala | Ala | Leu | Cys | Thr | Gly | Ser | Val | Val |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Arg | Ile | Ser | Ser | Leu | Val | Cys | Ser | Gly | Cys | Arg | Trp | Arg | Phe | Leu |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Ser | Ser | Leu | Cys | Leu | Ala | Trp | Leu | Asp | Val | Glu | Ser | Tyr | Gln | Ile |     |
|     |     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1687:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1598808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1687:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gly | Arg | Gly | Lys | Gly | Gly | Lys | Gly | Leu | Gly | Lys | Gly | Gly | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Lys | Arg | His | Arg | Lys | Phe | Ser | Ala | Thr | Thr | Ser | Arg | Val | Ser | Arg | Ser |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Gln | Ser | Gly | Ala | Gly | Glu | Glu | Gly | Arg | Arg | Glu | Ala | Tyr | Leu | Arg |





(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..502

(D) OTHER INFORMATION: / Ceres Seq. ID 1598874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1690:

|          |      |          |        |        |        |         |       |        |        |        |        |        |       |        |     |
|----------|------|----------|--------|--------|--------|---------|-------|--------|--------|--------|--------|--------|-------|--------|-----|
| aaacccta | aat  | cgtgaccg | cc     | gcgcnn | cag    | cawctga | agt   | ttcg   | tcctcg | cggc   | ttctc  | 60     |       |        |     |
| tccctcca | act  | cgaaccg  | cg     | cga    | cagagc | ga      | cgaca | accgt  | tgctgc | attc   | ttcaat | ggcg   | 120   |        |     |
| actgtgcc | ag   | ttaa     | cccaaa | ac     | ctttc  | ctg     | aaca  | acctga | cgggga | agcc   | tgta   | attgtc | 180   |        |     |
| aaactca  | agt  | gggg     | tatgga | gtaca  | aaagg  | t       | tctt  | tgctt  | cgg    | tgga   | ctc    | ctatat | gaat  | 240    |     |
| ctccag   | cttg | cca      | actga  | ggag   | tacatt | gat     | ggg   | caat   | tct    | ctg    | gaaa   | cctg   | gggag | 300    |     |
| attctga  | tca  | ggtg     | caacaa | cg     | ttat   | gtat    | ctcc  | gag    | gcg    | ttcc   | agag   | ga     | gcag  | agata  | 360 |
| gaggat   | gcag | aatga    | gaaga  | tgt    | gaat   | gta     | attt  | gatt   | ct     | gacat  | gtat   | g      | tttga | aatatg | 420 |
| ccggtga  | caa  | ctag     | acctat | cggat  | cttag  | ttat    | gat   | gcag   | tagg   | gcttga | ggtg   | ctgttc | 480   |        |     |
| aaactga  | gaa  | agga     | atatca | cg     |        |         |       |        |        |        |        |        |       |        |     |

(2) INFORMATION FOR SEQ ID NO:1691:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1598875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1691:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Thr | Val | Pro | Val | Asn | Pro | Lys | Pro | Phe | Leu | Asn | Asn | Leu | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Lys | Pro | Val | Ile | Val | Lys | Leu | Lys | Trp | Gly | Met | Glu | Tyr | Lys | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Leu | Ala | Ser | Val | Asp | Ser | Tyr | Met | Asn | Leu | Gln | Leu | Ala | Asn | Thr |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Glu | Glu | Tyr | Ile | Asp | Gly | Gln | Phe | Ser | Gly | Asn | Leu | Gly | Glu | Ile | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Arg | Cys | Asn | Asn | Val | Met | Tyr | Leu | Arg | Gly | Val | Pro | Glu | Asp | Ala |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Ile | Glu | Asp | Ala | Glu |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1692:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1598876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1692:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Tyr | Lys | Gly | Tyr | Leu | Ala | Ser | Val | Asp | Ser | Tyr | Met | Asn | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Leu | Ala | Asn | Thr | Glu | Glu | Tyr | Ile | Asp | Gly | Gln | Phe | Ser | Gly | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Gly | Glu | Ile | Leu | Ile | Arg | Cys | Asn | Asn | Val | Met | Tyr | Leu | Arg | Gly |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Val | Pro | Glu | Asp | Ala | Glu | Ile | Glu | Asp | Ala | Glu |     |     |     |     |     |
|     |     | 50  |     |     |     | 55  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..46  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598877  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1693:

Met Asn Leu Gln Leu Ala Asn Thr Glu Glu Tyr Ile Asp Gly Gln Phe  
1 5 10 15  
Ser Gly Asn Leu Gly Glu Ile Leu Ile Arg Cys Asn Asn Val Met Tyr  
20 25 30  
Leu Arg Gly Val Pro Glu Asp Ala Glu Ile Glu Asp Ala Glu  
35 40 45

(2) INFORMATION FOR SEQ ID NO:1694:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 488 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..488

(D) OTHER INFORMATION: / Ceres Seq. ID 1598878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1694:

accagcaac aagcaacctc gtcccaaac aagcaaccac cgcctccccg atctcgtcga 60  
gaggaagccc aatcccgaaa ccgcgcacct attccaatgg cgcccaaggc cgagaagaag 120  
cccgccgcca agaagcctgc ggaggaggag ccggcgsgna gaaggccacg gcggggaaga 180  
agcccaaggc tgagaagcgg ctccccgcgg caagtccgca gcaaggaggg tggcgagaag 240  
aagggaaga agaaggcaaa gaagtccgtg gagacgtaca agatctacat cttcaagggtg 300  
ctgaagcagg tgcacccgga cattggcatc tcgtccaagg ccatgtccat catgaactcc 360  
ttcatcaacg acatcttcga gaagctggcg gcggaggcgg ccaagctggc gcggtacaac 420  
aagaagccta ccattacgtc ccgcgagatc cagacctcgg ttcgcctcgt cctccccggc 480  
gagctcgc

(2) INFORMATION FOR SEQ ID NO:1695:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 162 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1598879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1695:

Thr Gln Gln Gln Ala Thr Ser Ser Pro Asn Lys Gln Pro Pro Pro Pro  
1 5 10 15  
Arg Ser Arg Arg Glu Glu Ala Gln Ser Arg Asn Arg Arg Pro Ile Pro  
20 25 30  
Met Ala Pro Lys Ala Glu Lys Lys Pro Ala Ala Lys Lys Pro Ala Glu  
35 40 45  
Glu Glu Pro Ala Xaa Arg Arg Pro Arg Arg Gly Arg Ser Pro Arg Leu  
50 55 60  
Arg Ser Gly Ser Pro Arg Gln Val Arg Ser Lys Glu Gly Gly Glu Lys  
65 70 75 80  
Lys Gly Lys Lys Lys Ala Lys Lys Ser Val Glu Thr Tyr Lys Ile Tyr  
85 90 95

00589900-10300

Ile Phe Lys Val Leu Lys Gln Val His Pro Asp Ile Gly Ile Ser Ser  
100 105 110  
Lys Ala Met Ser Ile Met Asn Ser Phe Ile Asn Asp Ile Phe Glu Lys  
115 120 125  
Leu Ala Ala Glu Ala Ala Lys Leu Ala Arg Tyr Asn Lys Lys Pro Thr  
130 135 140  
Ile Thr Ser Arg Glu Ile Gln Thr Ser Val Arg Leu Val Leu Pro Gly  
145 150 155 160  
Glu Leu

(2) INFORMATION FOR SEQ ID NO:1696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1696:

Pro Ala Thr Ser Asn Leu Val Pro Lys Gln Ala Thr Thr Ala Ser Pro  
1 5 10 15  
Ile Ser Ser Arg Gly Ser Pro Ile Pro Lys Pro Pro Pro Tyr Ser Asn  
20 25 30  
Gly Ala Gln Gly Arg Glu Glu Ala Arg Arg Gln Glu Ala Cys Gly Gly  
35 40 45  
Gly Ala Gly Xaa Xaa Lys Ala Thr Ala Gly Lys Lys Pro Lys Ala Glu  
50 55 60  
Lys Arg Leu Pro Ala Ala Ser Pro Gln Gln Gly Gly Trp Arg Glu Glu  
65 70 75 80  
Gly Glu Glu Glu Gly Lys Glu Val Gly Gly Asp Val Gln Asp Leu His  
85 90 95  
Leu Gln Gly Ala Glu Ala Gly Ala Pro Gly His Trp His Leu Val Gln  
100 105 110  
Gly His Val His His Glu Leu Leu His Gln Arg His Leu Arg Glu Ala  
115 120 125  
Gly Gly Gly Gly Gly Gln Ala Gly Ala Val Gln Gln Glu Ala Tyr His  
130 135 140  
Tyr Val Pro Arg Asp Pro Asp Leu Arg Ser Pro Arg Pro Pro Arg Arg  
145 150 155 160  
Ala Arg

(2) INFORMATION FOR SEQ ID NO:1697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1697:

Met Ala Pro Lys Ala Glu Lys Lys Pro Ala Ala Lys Lys Pro Ala Glu  
1 5 10 15  
Glu Glu Pro Ala Xaa Arg Arg Pro Arg Arg Gly Arg Ser Pro Arg Leu  
20 25 30  
Arg Ser Gly Ser Pro Arg Gln Val Arg Ser Lys Glu Gly Gly Glu Lys

DOCKET # 08659550











35 40 45  
Asp Ala Pro Ser Arg Arg Lys Pro Pro Met Leu Ser Arg Lys Ser Gly  
50 55 60  
Ser Leu His Arg Arg Gln Trp Ala Pro Leu Thr Ser Gly Leu Met  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..137
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1708:

Met Ala Glu Lys Lys Gln Arg Pro Gly Gly Ser Arg Lys Asp Glu Val  
1 5 10 15  
Val Thr Arg Glu Tyr Thr Ile Asn Leu His Lys Arg Leu His Gly Cys  
20 25 30  
Thr Phe Lys Lys Lys Ala Pro Asn Ala Ile Lys Glu Ile Arg Lys Phe  
35 40 45  
Ala Gln Lys Ala Met Gly Thr Thr Asp Ile Arg Ile Asp Val Lys Leu  
50 55 60  
Asn Lys His Ile Trp Ser Ser Gly Ile Arg Ser Val Pro Arg Arg Val  
65 70 75 80  
Arg Val Arg Ile Ala Arg Lys Arg Asn Asp Glu Glu Asp Ala Lys Glu  
85 90 95  
Glu Leu Tyr Ser Leu Val Thr Val Ala Glu Ile Pro Pro Glu Gly Leu  
100 105 110  
Lys Gly Leu Gly Thr Arg Leu Trp Arg Thr Thr Ser Arg Ser Ala Trp  
115 120 125  
Val Leu Ile Cys Val Asn Cys Gln Ile  
130 135

(2) INFORMATION FOR SEQ ID NO:1709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1709:

Met Gly Thr Thr Asp Ile Arg Ile Asp Val Lys Leu Asn Lys His Ile  
1 5 10 15  
Trp Ser Ser Gly Ile Arg Ser Val Pro Arg Arg Val Arg Val Arg Ile  
20 25 30  
Ala Arg Lys Arg Asn Asp Glu Glu Asp Ala Lys Glu Glu Leu Tyr Ser  
35 40 45  
Leu Val Thr Val Ala Glu Ile Pro Pro Glu Gly Leu Lys Gly Leu Gly  
50 55 60  
Thr Arg Leu Trp Arg Thr Thr Ser Arg Ser Ala Trp Val Leu Ile Cys  
65 70 75 80  
Val Asn Cys Gln Ile  
85

(2) INFORMATION FOR SEQ ID NO:1710:

(i) SEQUENCE CHARACTERISTICS:

0968980-104300

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Lys | Phe | Gly | Glu | Leu | Gln | Ser | Lys | Arg | Leu | His | Arg | Phe | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Phe | Lys | Met | Asp | Asp | Lys | Phe | Lys | Glu | Ile | Val | Val | Asp | Gln | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Asp | Arg | Ala | Thr | Ser | Tyr | Asp | Asp | Phe | Thr | Asn | Ser | Leu | Pro | Glu |



Leu His Tyr Thr Leu Ser Ser Val Pro Pro His Phe Ser Pro Pro Ala  
1 5 10 15  
Pro Leu Arg Glu Leu Pro Thr Pro Arg Ala His Ala Gly Asp Lys Phe  
20 25 30  
Pro Pro Glu Leu Gly Arg Ser Gly Ala Ala Pro Ala Ala Val Glu Gly  
35 40 45  
Met Glu Asp Leu Ala Ser Ser Arg Gly Gly Gly Gly Cys Gly Gly Leu  
50 55 60  
Asp Ala Gln Ile Glu Gln Leu Met Glu Cys Arg Pro Leu Pro Glu Thr  
65 70 75 80  
Glu Val Lys Thr Leu Cys Glu Lys Ala Lys Glu Ile Leu Met Glu Glu  
85 90 95  
Ser Asn Val Gln Pro Val Lys Ser Pro Val Thr Ile Cys Gly Asp Ile  
100 105 110  
His Gly Gln Phe His Asp Leu Leu Glu Leu Phe Arg Ile Gly Gly Glu  
115 120 125  
Val Ser Arg Tyr Lys Leu Phe Val Tyr Gly  
130 135

(2) INFORMATION FOR SEQ ID NO:1716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90

(D) OTHER INFORMATION: / Ceres Seq. ID 1598916

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1716:

Met Glu Asp Leu Ala Ser Ser Arg Gly Gly Gly Gly Cys Gly Gly Leu  
1 5 10 15  
Asp Ala Gln Ile Glu Gln Leu Met Glu Cys Arg Pro Leu Pro Glu Thr  
20 25 30  
Glu Val Lys Thr Leu Cys Glu Lys Ala Lys Glu Ile Leu Met Glu Glu  
35 40 45  
Ser Asn Val Gln Pro Val Lys Ser Pro Val Thr Ile Cys Gly Asp Ile  
50 55 60  
His Gly Gln Phe His Asp Leu Leu Glu Leu Phe Arg Ile Gly Gly Glu  
65 70 75 80  
Val Ser Arg Tyr Lys Leu Phe Val Tyr Gly  
85 90

(2) INFORMATION FOR SEQ ID NO:1717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..534

(D) OTHER INFORMATION: / Ceres Seq. ID 1598921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1717:

|                                                                      |     |
|----------------------------------------------------------------------|-----|
| awagttgtgc tgatacgatg tgcaattcctt gctctttcctt ctctagaatg ttcctgccga  | 60  |
| tgcttttata agagaagggtt gctctttcctt ctctagagtg tctagctgag aacatgggtga | 120 |
| cctcaagcaa gggcaaggta tatgtaaccg gggcctcagg ctttggtgcc tcttggtta     | 180 |
| tcaaacggct cctcgagtct ggatatcatg tggtagggac tgtcagggac ccaggaaatc    | 240 |
| acaaaaaac agcccacctt tggaaattac ctggcgctaa agagaggctg caaatcgtgc     | 300 |
| gagctgatct gttggaagaa gggagcttcg acagcgccgt gatggcctgt gaggggtgat    | 360 |
| tccacactgc atcccccgtc ctcgctaaac ccgactctac tagcaaggag gaaacgctcg    | 420 |



(B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1598928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1720:

Met Val Leu Lys Thr Glu Leu Cys Arg Phe Ser Gly Gln Lys Ile Tyr  
1 5 10 15  
Pro Gly Lys Gly Ile Arg Phe Ile Arg Ala Asp Ser Gln Val Phe Leu  
20 25 30  
Phe Ala Asn Ser Lys Cys Lys Arg Tyr Phe His Asn Arg Leu Lys Leu  
35 40 45  
Cys Lys Ala Tyr Leu Asp Ser Asn Val Gln Glu Ala Ala Gln Glu Gly  
50 55 60  
His Pro Cys  
65

(2) INFORMATION FOR SEQ ID NO:1721:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..55

(D) OTHER INFORMATION: / Ceres Seq. ID 1598929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1721:

Met Gln Ala Leu Leu Pro Gln Pro Pro Glu Ala Leu Gln Ser Leu Pro  
1 5 10 15  
Gly Gln Gln Cys Thr Gly Ser Ser Thr Arg Arg Thr Ser Met Leu Lys  
20 25 30  
Leu Ser Arg Arg Gly Ala Ala Pro Pro Arg Ser His Thr Arg Gly Pro  
35 40 45  
Leu Trp Val Leu Pro Trp Lys  
50 55

(2) INFORMATION FOR SEQ ID NO:1722:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..56

(D) OTHER INFORMATION: / Ceres Seq. ID 1598930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1722:

Met Tyr Arg Lys Gln His Lys Lys Asp Ile His Ala Glu Ala Val Lys  
1 5 10 15  
Lys Arg Arg Arg Ala Thr Lys Lys Pro Tyr Ser Arg Ser Ile Val Gly  
20 25 30  
Ala Ser Leu Glu Val Ile Gln Lys Lys Arg Ala Glu Lys Pro Glu Val  
35 40 45  
Arg Asp Ala Ala Arg Glu Ala Ala  
50 55

(2) INFORMATION FOR SEQ ID NO:1723:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

09689903060

- (A) NAME/KEY: -  
(B) LOCATION: 1..275  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1723:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| tntccttcga ggcgtccgcc gctcccaccc ccaccactcg ccagctcgcc acttcctccc  | 60  |
| gtctcctccc ttccagaggc ggcgcgtaas gcccgatggc cgctctctc ctccacgcgc   | 120 |
| ccgcgcctc gctccagagt tccaccagc acgcccgcgc ggssccgcgc cctttcacc     | 180 |
| cctcgcgtgt gcccacatccc tacgccttac gcgctcctcg ttctcgacca atcgccacct | 240 |
| cgagatttca ctccgggcga tctcggccag tcgcc                             |     |

(2) INFORMATION FOR SEQ ID NO:1724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..91  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1724:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Xaa Pro Ser Ser Arg Pro Pro Leu Pro Pro Pro Pro Leu Ala Ser Ser |  |
| 1 5 10 15                                                       |  |
| Pro Leu Pro Pro Val Ser Ser Leu Pro Glu Ala Ala Arg Xaa Ala Arg |  |
| 20 25 30                                                        |  |
| Trp Pro Pro Leu Ser Ser Thr Pro Pro Pro Arg Ser Arg Val Pro     |  |
| 35 40 45                                                        |  |
| Pro Ser Thr Pro Ala Arg Xaa Arg Arg Leu Ser Pro Pro Arg Val Cys |  |
| 50 55 60                                                        |  |
| Pro Ile Pro Thr Pro Tyr Ala Leu Leu Val Leu Asp Gln Ser Pro Pro |  |
| 65 70 75 80                                                     |  |
| Arg Asp Phe Thr Pro Gly Asp Leu Gly Gln Ser                     |  |
| 85 90                                                           |  |

(2) INFORMATION FOR SEQ ID NO:1725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..91  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1725:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Xaa Leu Arg Ala Val Arg Arg Ser His Pro His His Ser Pro Ala Arg |  |
| 1 5 10 15                                                       |  |
| His Phe Leu Pro Ser Pro Pro Phe Gln Arg Arg Arg Val Xaa Pro Asp |  |
| 20 25 30                                                        |  |
| Gly Arg Leu Ser Pro Pro Arg Arg Arg Leu Ala Pro Glu Phe His     |  |
| 35 40 45                                                        |  |
| Pro Ala Arg Pro Arg Xaa Xaa Ala Ala Phe His Pro Leu Ala Cys Ala |  |
| 50 55 60                                                        |  |
| Pro Ser Leu Arg Leu Thr Arg Ser Ser Phe Ser Thr Asn Arg His Leu |  |
| 65 70 75 80                                                     |  |
| Glu Ile Ser Leu Arg Ala Ile Ser Ala Ser Arg                     |  |
| 85 90                                                           |  |

(2) INFORMATION FOR SEQ ID NO:1726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids  
(B) TYPE: amino acid

006668960





(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1598938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1729:

Val Ser Thr Leu Lys Pro Leu Gln Thr Leu Val Leu Pro Thr Asp Pro  
1 5 10 15  
Phe Gln Pro Pro Pro Arg Val Xaa Ser Arg Ser Ser Lys Asp Ala Gly  
20 25 30  
Trp Pro Arg Ala Ala Leu Ala Asp Xaa Arg Pro Xaa Ser Arg Pro Phe  
35 40 45  
Pro Gln Glu Gly Leu His Pro Ala His His Leu Pro Pro His Leu Gln  
50 55 60  
Asp Arg Arg  
65

(2) INFORMATION FOR SEQ ID NO:1730:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..38

(D) OTHER INFORMATION: / Ceres Seq. ID 1598939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1730:

Met Pro Ala Gly His Gly Leu Arg Ser Arg Thr Xaa Asp Leu Xaa Arg  
1 5 10 15  
Ala Pro Phe Arg Lys Lys Gly Tyr Ile Pro Leu Thr Thr Tyr Leu Arg  
20 25 30  
Thr Tyr Lys Ile Gly Asp  
35

(2) INFORMATION FOR SEQ ID NO:1731:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 473 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..473

(D) OTHER INFORMATION: / Ceres Seq. ID 1598943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1731:

cttcgcgttc caacttccgt tccgcaaatt gaaaactcgg cgttgcctgc gccctgcct 60  
cgagctcgaa ggactttgtc ctatacgtcg ttgtccagct cctcgcatat tgtggcctgg 120  
tgcagattgg agatccgccc ggacttggat cgagtcctcc tgtctttgga cattcattgg 180  
agtgcctcat tcattgagac agcatgccta agataaagac aagccgtgtc aagtatcctg 240  
aaggatggga gcttattgaa ccaacaatcc gtgagttgga tgccaaaatg agagaagctg 300  
aaaatgatcc acatgatgga aagagaaagt gtgaagctct ctggcctatt ttccgcattt 360  
ctcatcaaag gagccgctac atatacgatc tttattacag aaggaaggag atatcacagg 420  
agctttatga gtttctgcct agaccagggt tatgcagacc gtaacctgat tgc

(2) INFORMATION FOR SEQ ID NO:1732:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

09689980-101300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1732:

(2) INFORMATION FOR SEQ ID NO:1733:

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

```
(A) NAME/KEY: peptide
(B) LOCATION: 1..69
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1598945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1733:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1734:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1598946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1734:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1735:

[illegible]



50 55 60  
Lys Val Val Asp Ile Val Asp Thr Phe Arg Leu Gln Glu Gln Pro Pro  
65 70 75 80  
Phe Asp Lys Lys Ser Phe Val Ser Tyr Ile Lys Lys Tyr Ile Lys Asn  
85 90 95  
Leu Thr Ala Val Leu Glu Pro Xaa Lys Ala Asp Glu Phe Lys Lys Gly  
100 105 110  
Val Glu Gly Ala Thr Ser Phe Ser Leu Ala Ser  
115 120

(2) INFORMATION FOR SEQ ID NO:1738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..440
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1738:

atcgagacac acacagaact tctcctgtcg gcctactaat acaactagct gccctcttag 60  
gtatactgtg atggccacct tgtcctccac agtagtagtt gcacttggtg acctctcttc 120  
ttgctccttg taacgtgtgg ctcggtgcgcg agaccggtga gctttaacgc ctccgacctc 180  
accgccgatc ccggtctgga tgctgccagg gccacctgta cgggtgcgccc accggcgcg 240  
tctgatgac gacggtggtg cctgtggatt caagaacgtg aacctgccgc cgttctcggs 300  
antgacgtcg tgcggcaacg agcccctgtt caaggacggc aagggtgcg gctcctgcta 360  
ccagatacga tgccaaaacc accctgcctg ctccggcaac ccagagacgg tgatcatcac 420  
tgacatgaac tactaccccg

(2) INFORMATION FOR SEQ ID NO:1739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598958

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1739:

Ser Arg His Thr Gln Asn Phe Ser Cys Arg Pro Thr Asn Thr Thr Ser  
1 5 10 15  
Cys Pro Leu Arg Tyr Thr Val Met Ala Thr Leu Ser Ser Thr Val Val  
20 25 30  
Val Ala Leu Gly Asp Leu Ser Ser Cys Ser Leu  
35 40

(2) INFORMATION FOR SEQ ID NO:1740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1740:

Met Leu Pro Gly Pro Pro Val Arg Cys Ala His Arg Arg Gly Pro Asp  
1 5 10 15

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(2) INFORMATION FOR SEQ ID NO:1744:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..43

(D) OTHER INFORMATION: / Ceres Seq. ID 1598963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1744:

(2) INFORMATION FOR SEQ ID NO:1745:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 389 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..389

(D) OTHER INFORMATION: / Ceres Seq. ID 1598964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1745:

| (X1) SEQUENCE DESCRIPTION: C2 |             |             |            |            |            |  |     |
|-------------------------------|-------------|-------------|------------|------------|------------|--|-----|
| ctctcgattc                    | ggaaaaacctc | caacccttanc | cgcgatccgr | caacgcctcc | atccctagsc |  | 60  |
| gactgctgca                    | assttcagag  | ctcaagagtc  | agggcgccat | kgcgacagag | acggagacss |  | 120 |
| ttcgcttttc                    | argctgagat  | caaccagctg  | ctctcactca | tcatcaacac | cttctattcc |  | 180 |
| aacaaggaga                    | totttctccg  | ggagctcatt  | tccaactctt | ccgatgcggt | ggacaaaatc |  | 240 |
| aggttcgaga                    | gcttactctga | saakagcrag  | ctcgatgcgc | mscggagctg | ttcatccaca |  | 300 |
| ttgtaccara                    | caaggctctcg | aacacgctct  | ccatcatcgn | cagcggcadc | ggcatgacca |  | 360 |
| agtccgact                     | tktwacaac   | ctcgggtacc  |            |            |            |  |     |

(2) INFORMATION FOR SEQ ID NO:1746:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1598965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1746:

Leu Ser Ile Arg Lys Thr Ser Asn Pro Xaa Arg Asp Pro Xaa Thr Pro  
1 5 10 15  
Pro Ser Leu Xaa Asp Cys Cys Xaa Xaa Gln Ser Ser Arg Val Arg Ala  
20 25 30  
Pro Xaa Arg Gln Arg Arg Arg Xaa Phe Ala Phe Xaa Ala Glu Ile Asn  
35 40 45  
Gln Leu Leu Ser Leu Ile Ile Asn Thr Phe Tyr Ser Asn Lys Glu Ile  
50 55 60  
Phe Leu Arg Glu Leu Ile Ser Asn Ser Ser Asp Ala Leu Asp Lys Ile  
65 70 75 80  
Arg Phe Glu Ser Leu Thr Xaa Xaa Ser Xaa Leu Asp Ala Xaa Arg Ser  
85 90 95  
Cys Ser Ser Thr Leu Tyr Xaa Thr Arg Leu Arg Thr Arg Ser Pro Ser  
100 105 110  
Ser Xaa Ala Ala Ser Ala  
115

(2) INFORMATION FOR SEQ ID NO:1747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..505
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1747:

ataatcctgc ccacaacgcc gtctcctaaa cottagccgc gcgkacgccc accagcagct 60  
gcccttctgt gtcgccgcct ctctccgcgc gaccgatcta ccgccgccgc caccatgtcg 120  
ctgatcgccg gcgaggactt ccaacatatt ctgcgtctgc tgaacaccaa cgtggatggg 180  
aagcagaaga tcatgttcgc catgacctcc ataaaggggtg ttggggcgccg cttctccaac 240  
atcgtctgca agaaggccga catcgacatg aacaagaggg cgggtgagct gacgcctgaa 300  
gagctggagc gcctgatgac ggctgtggcc aaccctaggc agttcaaggt gccggactgg 360  
ttcctcaaca ggaagaagga ttacaaggat ggaaggttct cacaggtcgt gtccaacgcc 420  
ctcgacatga agctcaggga cgacctcgag aggctcaaga agatcaggaa ccaccgtggt 480  
ctgcgtcact actggggcct ccgtg

(2) INFORMATION FOR SEQ ID NO:1748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1748:

Met Ser Leu Ile Ala Gly Glu Asp Phe Gln His Ile Leu Arg Leu Leu  
1 5 10 15  
Asn Thr Asn Val Asp Gly Lys Gln Lys Ile Met Phe Ala Met Thr Ser  
20 25 30  
Ile Lys Gly Val Gly Arg Arg Phe Ser Asn Ile Val Cys Lys Lys Ala  
35 40 45  
Asp Ile Asp Met Asn Lys Arg Ala Gly Glu Leu Thr Pro Glu Glu Leu  
50 55 60  
Glu Arg Leu Met Thr Val Val Ala Asn Pro Arg Gln Phe Lys Val Pro  
65 70 75 80  
Asp Trp Phe Leu Asn Arg Lys Lys Asp Tyr Lys Asp Gly Arg Phe Ser

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85 90 95  
Gln Val Val Ser Asn Ala Leu Asp Met Lys Leu Arg Asp Asp Leu Glu  
100 105 110  
Arg Leu Lys Lys Ile Arg Asn His Arg Gly Leu Arg His Tyr Trp Gly  
115 120 125  
Leu Arg  
130

(2) INFORMATION FOR SEQ ID NO:1749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1749:

Met Phe Ala Met Thr Ser Ile Lys Gly Val Gly Arg Arg Phe Ser Asn  
1 5 10 15  
Ile Val Cys Lys Lys Ala Asp Ile Asp Met Asn Lys Arg Ala Gly Glu  
20 25 30  
Leu Thr Pro Glu Glu Leu Glu Arg Leu Met Thr Val Val Ala Asn Pro  
35 40 45  
Arg Gln Phe Lys Val Pro Asp Trp Phe Leu Asn Arg Lys Lys Asp Tyr  
50 55 60  
Lys Asp Gly Arg Phe Ser Gln Val Val Ser Asn Ala Leu Asp Met Lys  
65 70 75 80  
Leu Arg Asp Asp Leu Glu Arg Leu Lys Lys Ile Arg Asn His Arg Gly  
85 90 95  
Leu Arg His Tyr Trp Gly Leu Arg  
100

(2) INFORMATION FOR SEQ ID NO:1750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1598975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1750:

Met Thr Ser Ile Lys Gly Val Gly Arg Arg Phe Ser Asn Ile Val Cys  
1 5 10 15  
Lys Lys Ala Asp Ile Asp Met Asn Lys Arg Ala Gly Glu Leu Thr Pro  
20 25 30  
Glu Glu Leu Glu Arg Leu Met Thr Val Val Ala Asn Pro Arg Gln Phe  
35 40 45  
Lys Val Pro Asp Trp Phe Leu Asn Arg Lys Lys Asp Tyr Lys Asp Gly  
50 55 60  
Arg Phe Ser Gln Val Val Ser Asn Ala Leu Asp Met Lys Leu Arg Asp  
65 70 75 80  
Asp Leu Glu Arg Leu Lys Lys Ile Arg Asn His Arg Gly Leu Arg His  
85 90 95  
Tyr Trp Gly Leu Arg  
100

(2) INFORMATION FOR SEQ ID NO:1751:

(i) SEQUENCE CHARACTERISTICS:

09689980-101300





50 55  
(2) INFORMATION FOR SEQ ID NO:1754:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..51  
(D) OTHER INFORMATION: / Ceres Seq. ID 1598979  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1754:  
Met Gly Pro Ser Asp Ser Pro Tyr Ser Gly Gly Val Phe Leu Val Thr  
1 5 10 15  
Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro Pro Lys Val His Phe  
20 25 30  
Val Leu Arg Cys Ser Ile Gln Thr Ser Thr Ala Thr Gly Ala Phe Ala  
35 40 45  
Ser Thr Ser  
50

(2) INFORMATION FOR SEQ ID NO:1755:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 482 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..482  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599016  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1755:  
ccaaacctag cgatcgaga gactgcgccc ggaccccgga ccgcgcgggc tcgcaaactc 60  
cccacaaccc tcgtgcggc cggtgctcc acccccgcca ccgccatggg taaattccgc 120  
aagcttgccc gcaattact ccaacgcctc tgcatgctca ggacgatggg gtcgcagctg 180  
gtgaagcacg agcgcatcga gaccaccgtt gccaaaggcga aggagggttcg gcggaaggcg 240  
gatcagatgg tgcagctagg gaaggagggt actcagcatg cagcaagacg tgctgctgcc 300  
tttgttcggg gtgatgatgt cgttcataag ctatttactg agctggcctt ccgctacaga 360  
gatcgagctg ggggctacac aagaatgtta agaaccagga tacgtgttg tgatgctgct 420  
ccaatggcat acatcgagtt cgtggatagg gakaatgagc ttcgagaggc caaacctgca 480  
ac

(2) INFORMATION FOR SEQ ID NO:1756:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 160 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..160  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599017  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1756:  
Pro Asn Leu Ala Ile Ala Glu Ser Ala Pro Gly Pro Arg Thr Ala Pro  
1 5 10 15  
Ala Arg Lys Leu Pro Thr Thr Leu Val Ala Ala Gly Cys Ser Thr Pro  
20 25 30  
Ala Thr Ala Met Gly Lys Phe Arg Lys Leu Gly Arg Asn Tyr Ser Gln  
35 40 45  
Arg Leu Cys Met Leu Arg Thr Met Val Ser Gln Leu Val Lys His Glu

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|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 50                                                              | 55  | 60  |
| Arg Ile Glu Thr Thr Val Ala Lys Ala Lys Glu Val Arg Arg Lys Ala |     |     |
| 65                                                              | 70  | 75  |
| Asp Gln Met Val Gln Leu Gly Lys Glu Gly Thr Gln His Ala Ala Arg |     | 80  |
|                                                                 | 85  | 90  |
| Arg Ala Ala Ala Phe Val Arg Gly Asp Asp Val Val His Lys Leu Phe |     | 95  |
|                                                                 | 100 | 105 |
| Thr Glu Leu Ala Phe Arg Tyr Arg Asp Arg Ala Gly Gly Tyr Thr Arg |     | 110 |
|                                                                 | 115 | 120 |
| Met Leu Arg Thr Arg Ile Arg Val Gly Asp Ala Ala Pro Met Ala Tyr |     | 125 |
|                                                                 | 130 | 135 |
| Ile Glu Phe Val Asp Arg Xaa Asn Glu Leu Arg Glu Ala Lys Pro Ala |     | 140 |
| 145                                                             | 150 | 155 |
|                                                                 |     | 160 |

(2) INFORMATION FOR SEQ ID NO:1757:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1599018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1757:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Gly Lys Phe Arg Lys Leu Gly Arg Asn Tyr Ser Gln Arg Leu Cys |     |     |
| 1                                                               | 5   | 10  |
| Met Leu Arg Thr Met Val Ser Gln Leu Val Lys His Glu Arg Ile Glu |     | 15  |
|                                                                 | 20  | 25  |
| Thr Thr Val Ala Lys Ala Lys Glu Val Arg Arg Lys Ala Asp Gln Met |     | 30  |
|                                                                 | 35  | 40  |
| Val Gln Leu Gly Lys Glu Gly Thr Gln His Ala Ala Arg Arg Ala Ala |     | 45  |
|                                                                 | 50  | 55  |
| Ala Phe Val Arg Gly Asp Asp Val Val His Lys Leu Phe Thr Glu Leu |     | 60  |
| 65                                                              | 70  | 75  |
| Ala Phe Arg Tyr Arg Asp Arg Ala Gly Gly Tyr Thr Arg Met Leu Arg |     | 80  |
|                                                                 | 85  | 90  |
| Thr Arg Ile Arg Val Gly Asp Ala Ala Pro Met Ala Tyr Ile Glu Phe |     | 95  |
|                                                                 | 100 | 105 |
| Val Asp Arg Xaa Asn Glu Leu Arg Glu Ala Lys Pro Ala             |     | 110 |
|                                                                 | 115 | 120 |
|                                                                 |     | 125 |

(2) INFORMATION FOR SEQ ID NO:1758:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1599019

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1758:

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| Met Leu Arg Thr Met Val Ser Gln Leu Val Lys His Glu Arg Ile Glu |    |    |
| 1                                                               | 5  | 10 |
| Thr Thr Val Ala Lys Ala Lys Glu Val Arg Arg Lys Ala Asp Gln Met |    | 15 |
|                                                                 | 20 | 25 |
| Val Gln Leu Gly Lys Glu Gly Thr Gln His Ala Ala Arg Arg Ala Ala |    | 30 |
|                                                                 | 35 | 40 |
|                                                                 |    | 45 |





catcgtgaac aggtaccctg agtacaaggt ggtggtgctg gacaagcttg actactgtc 300  
caacctcaag aacctctctcc ccgtcatggg ctccggcgcc aacaacttca agttcgtcaa 360  
ggcgacatc gccagcgccg acctcgtcag cttcatcctg gccaccgagg gcacgcacac 420  
cgtgatgcac ttccgcgccg agaccacgt ggacaactcc ttcggcaact ccttgagatt 480  
cacc

(2) INFORMATION FOR SEQ ID NO:1764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1764:

Met Ala Ala Thr Thr Pro Tyr Lys Pro Lys Arg Ile Leu Ile Thr Gly  
1 5 10 15  
Ala Ala Gly Phe Ile Ala Ser His Val Ala Ile Arg Ile Val Asn Arg  
20 25 30  
Tyr Pro Glu Tyr Lys Val Val Val Leu Asp Lys Leu Asp Tyr Cys Ser  
35 40 45  
Asn Leu Lys Asn Leu Leu Pro Val Met Gly Ser Gly Gly Asn Asn Phe  
50 55 60  
Lys Phe Val Lys Gly Asp Ile Ala Ser Ala Asp Leu Val Ser Phe Ile  
65 70 75 80  
Leu Ala Thr Glu Gly Ile Asp Thr Val Met His Phe Ala Ala Gln Thr  
85 90 95  
His Val Asp Asn Ser Phe Gly Asn Ser Leu Glu Phe Thr  
100 105

(2) INFORMATION FOR SEQ ID NO:1765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..474
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1765:

aagttgaata ggatcgaaaa ccctaaccg tctccctcct atcgcaactcg cgtctctttc 60  
ctattcgcgc cgccgcgcgt gctgcaassg ccagctcgcc gtctgctcgaa tagtacactc 120  
taacgccgcc atggggcgta tgcacagccg cggaagggt atctcgtcgt cggcgctgcc 180  
gtacaagagg acgctctcta cctggctgaa gaccgcccgc tccgacgtgg aggagatgat 240  
caciaaggca gcgaagaagg gacagatgcc gtcgcagatc ggcgctctgc tccgtgacca 300  
gcacggtatc ccccttgtea agagtgtcac cggcagcaaa atcctccgca tcctcaaggc 360  
ccatgggctg gcacccgaaa tcccggagac ctgtacttcc tcatcaagaa ggcggtggcg 420  
ataaggaagc accttgagag gaacaggaag gacaaagact cttaaattcag gctc

(2) INFORMATION FOR SEQ ID NO:1766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97

CONFIDENTIAL

(D) OTHER INFORMATION: / Ceres Seq. ID 1599063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1766:

Met Gly Arg Met His Ser Arg Gly Lys Gly Ile Ser Ser Ser Ala Leu  
1 5 10 15  
Pro Tyr Lys Arg Thr Pro Pro Thr Trp Leu Lys Thr Ala Ala Ser Asp  
20 25 30  
Val Glu Glu Met Ile Thr Lys Ala Ala Lys Lys Gly Gln Met Pro Ser  
35 40 45  
Gln Ile Gly Val Leu Leu Arg Asp Gln His Gly Ile Pro Leu Val Lys  
50 55 60  
Ser Val Thr Gly Ser Lys Ile Leu Arg Ile Leu Lys Ala His Gly Leu  
65 70 75 80  
Ala Pro Glu Ile Pro Glu Thr Cys Thr Ser Ser Ser Arg Arg Arg Trp  
85 90 95  
Arg

(2) INFORMATION FOR SEQ ID NO:1767:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1599064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1767:

Met His Ser Arg Gly Lys Gly Ile Ser Ser Ser Ala Leu Pro Tyr Lys  
1 5 10 15  
Arg Thr Pro Pro Thr Trp Leu Lys Thr Ala Ala Ser Asp Val Glu Glu  
20 25 30  
Met Ile Thr Lys Ala Ala Lys Lys Gly Gln Met Pro Ser Gln Ile Gly  
35 40 45  
Val Leu Leu Arg Asp Gln His Gly Ile Pro Leu Val Lys Ser Val Thr  
50 55 60  
Gly Ser Lys Ile Leu Arg Ile Leu Lys Ala His Gly Leu Ala Pro Glu  
65 70 75 80  
Ile Pro Glu Thr Cys Thr Ser Ser Ser Arg Arg Arg Trp Arg  
85 90

(2) INFORMATION FOR SEQ ID NO:1768:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1599065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1768:

Met Ile Thr Lys Ala Ala Lys Lys Gly Gln Met Pro Ser Gln Ile Gly  
1 5 10 15  
Val Leu Leu Arg Asp Gln His Gly Ile Pro Leu Val Lys Ser Val Thr  
20 25 30  
Gly Ser Lys Ile Leu Arg Ile Leu Lys Ala His Gly Leu Ala Pro Glu  
35 40 45  
Ile Pro Glu Thr Cys Thr Ser Ser Ser Arg Arg Arg Trp Arg  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1769:

00658960 101300

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 250 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..250  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1769:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| ctctttttaat | tccccgcgcg | ccgcccctcg | ccacgctcgc | ccagccgctg | ccactcgcca | 60  |
| cgttccacca  | gccggcgccc | cttcttctca | ctcgcgtggc | gccggcgcg  | ggtatccatg | 120 |
| gcgtcggaga  | akaagcaatc | caaccgatg  | aggagatca  | agggtgcaga | gctggtgctc | 180 |
| aacatctccg  | tcggagagag | tggggatcgc | ctcaccgcgc | ccgccaaggt | cctggagcaa | 240 |
| ctgagttggc  |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1770:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 49 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..49  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1770:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Phe | Asn | Ser | Pro | Ala | Ala | Ala | Pro | Arg | His | Ala | Pro | Pro | Ala | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Thr | Arg | His | Val | Pro | Pro | Ala | Gly | Ala | Pro | Ser | Ser | His | Ser | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ala | Gly | Ala | Arg | Tyr | Pro | Trp | Arg | Arg | Arg | Xaa | Ser | Asn | Pro | Thr |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Arg |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1771:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 82 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..82  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599070

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1771:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Ile | Pro | Pro | Pro | Pro | Pro | Leu | Ala | Thr | Leu | Arg | Gln | Pro | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Leu | Ala | Thr | Phe | His | Gln | Pro | Ala | Pro | Leu | Leu | Leu | Thr | Pro | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Pro | Ala | Arg | Val | Ile | His | Gly | Val | Gly | Glu | Xaa | Ala | Ile | Gln | Pro |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Asp | Glu | Gly | Asp | Gln | Gly | Ala | Glu | Ala | Gly | Ala | Gln | His | Leu | Arg | Arg |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Arg | Glu | Trp | Gly | Ser | Pro | His | Pro | Arg | Arg | Gln | Gly | Pro | Gly | Ala | Thr |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     | 80  |
| Glu | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1772:

09689980 101399









- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..481
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1599092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1780:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| caagtgaaga agaggattcg tccccagaaa ctacagagga agagacagaa gaagatgaac   | 60  |
| agaaagagaa aaagcctaag acgaagacaa taaaggagac tacttctgaa tgggaacttc   | 120 |
| tgaatgatgt gaaggctgta tggcttcgca gcccaaaagga gggtactgac gaagaatact  | 180 |
| cgaagtttta ccactcacta gcccaaggact tcagtgtatga caagcctatg gggtggagcc | 240 |
| acttcactgc tgaaggagat gttgagttca aagctttgct cttcattcca ccgaagctcc   | 300 |
| gcatgatctc tatgagagtt actacaacag caacaagtca aacctcaagt tgtatgttag   | 360 |
| aagagtgttc atctctgatg aatttgatga ccttcttccg aagtatctca gctttttgag   | 420 |
| gggtattgtt gactcagaca cactgccgct gaatgtgtca cgagaaatgc tccagcaaca   | 480 |

t

- (2) INFORMATION FOR SEQ ID NO:1781:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 138 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..138
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1599093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1781:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Glu | Glu | Glu | Asp | Ser | Ser | Pro | Glu | Thr | Thr | Glu | Glu | Glu | Thr | Glu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Glu | Asp | Glu | Gln | Lys | Glu | Lys | Lys | Pro | Lys | Thr | Lys | Thr | Ile | Lys | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Thr | Ser | Glu | Trp | Glu | Leu | Leu | Asn | Asp | Val | Lys | Ala | Val | Trp | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Ser | Pro | Lys | Glu | Val | Thr | Asp | Glu | Glu | Tyr | Ser | Lys | Phe | Tyr | His |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Ser | Leu | Ala | Lys | Asp | Phe | Ser | Asp | Asp | Lys | Pro | Met | Gly | Trp | Ser | His |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Phe | Thr | Ala | Glu | Gly | Asp | Val | Glu | Phe | Lys | Ala | Leu | Leu | Phe | Ile | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Pro | Lys | Leu | Arg | Met | Ile | Ser | Met | Arg | Val | Thr | Thr | Thr | Ala | Thr | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Gln | Thr | Ser | Ser | Cys | Met | Leu | Glu | Glu | Cys | Ser | Ser | Leu | Met | Asn | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Met | Thr | Phe | Phe | Arg | Ser | Ile | Ser | Ala | Phe |     |     |     |     |     |     |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:1782:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 265 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..265
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1599094
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1782:

09659560 101300



(2) INFORMATION FOR SEQ ID NO:1786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..376
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1786:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aaaccctacc cgactccgcc gccgctccgc cgccnntccg cctcagcgca tcgccctccg | 60  |
| ccacagcgta ccgcgacctc atcgatcacc ttcaactttc aatcatggcg gacgtcgatg | 120 |
| tcgaaccgga gtngccgccg gcgctcccaa gaagaggacg ttccgcaagt acagctaccg | 180 |
| cggcgtcgac ctatgatgcg ttctcgacat gtccacggac gacctcgctc agctcttccc | 240 |
| cgcgcgcgcc aggagaaggt tccagagggg tctgaagagg aagcccatgg cactcatcaa | 300 |
| gaagctgcgc aaggcgaaaa aggatgctcc tgctggtgag aagcyagagc cagtcaagac | 360 |
| acatctccgt aacatg                                                 |     |

(2) INFORMATION FOR SEQ ID NO:1787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1787:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Lys | Pro | Tyr | Pro | Thr | Pro | Pro | Pro | Leu | Arg | Arg | Xaa | Ser | Ala | Ser | Ala |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| His | Arg | Pro | Pro | Pro | Gln | Arg | Thr | Ala | Thr | Ser | Ser | Ile | Thr | Phe | Asn |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Phe | Gln | Ser | Trp | Arg | Thr | Ser | Met | Ser | Asn | Arg | Ser | Xaa | Arg | Arg | Arg |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Gln | Glu | Glu | Asp | Val | Pro | Gln | Val | Gln | Leu | Pro | Arg | Arg | Arg | Pro |  |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Arg | Cys | Ala | Ser | Arg | His | Val | His | Gly | Arg | Pro | Arg | Pro | Ala | Leu | Pro |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Arg | Ala | Arg | Gln | Glu | Lys | Val | Pro | Glu | Gly | Ser | Glu | Glu | Glu | Ala | His |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Gly | Thr | His | Gln | Glu | Ala | Ala | Gln | Gly | Glu | Lys | Gly | Cys | Ser | Cys | Trp |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1788:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Pro | Thr | Arg | Leu | Arg | Arg | Arg | Ser | Ala | Ala | Xaa | Pro | Pro | Gln | Arg |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |

00659950 10370



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1794:

| 1990-1991 |  | 1991-1992 |  | 1992-1993 |  | 1993-1994 |  | 1994-1995 |  | 1995-1996 |  | 1996-1997 |  | 1997-1998 |  | 1998-1999 |  | 1999-2000 |  | 2000-2001 |  | 2001-2002 |  | 2002-2003 |  | 2003-2004 |  | 2004-2005 |  | 2005-2006 |  | 2006-2007 |  | 2007-2008 |  | 2008-2009 |  | 2009-2010 |  | 2010-2011 |  | 2011-2012 |  | 2012-2013 |  | 2013-2014 |  | 2014-2015 |  | 2015-2016 |  | 2016-2017 |  | 2017-2018 |  | 2018-2019 |  | 2019-2020 |  | 2020-2021 |  | 2021-2022 |  | 2022-2023 |  | 2023-2024 |  | 2024-2025 |  | 2025-2026 |  | 2026-2027 |  | 2027-2028 |  | 2028-2029 |  | 2029-2030 |  | 2030-2031 |  | 2031-2032 |  | 2032-2033 |  | 2033-2034 |  | 2034-2035 |  | 2035-2036 |  | 2036-2037 |  | 2037-2038 |  | 2038-2039 |  | 2039-2040 |  | 2040-2041 |  | 2041-2042 |  | 2042-2043 |  | 2043-2044 |  | 2044-2045 |  | 2045-2046 |  | 2046-2047 |  | 2047-2048 |  | 2048-2049 |  | 2049-2050 |  | 2050-2051 |  | 2051-2052 |  | 2052-2053 |  | 2053-2054 |  | 2054-2055 |  | 2055-2056 |  | 2056-2057 |  | 2057-2058 |  | 2058-2059 |  | 2059-2060 |  | 2060-2061 |  | 2061-2062 |  | 2062-2063 |  | 2063-2064 |  | 2064-2065 |  | 2065-2066 |  | 2066-2067 |  | 2067-2068 |  | 2068-2069 |  | 2069-2070 |  | 2070-2071 |  | 2071-2072 |  | 2072-2073 |  | 2073-2074 |  | 2074-2075 |  | 2075-2076 |  | 2076-2077 |  | 2077-2078 |  | 2078-2079 |  | 2079-2080 |  | 2080-2081 |  | 2081-2082 |  | 2082-2083 |  | 2083-2084 |  | 2084-2085 |  | 2085-2086 |  | 2086-2087 |  | 2087-2088 |  | 2088-2089 |  | 2089-2090 |  | 2090-2091 |  | 2091-2092 |  | 2092-2093 |  | 2093-2094 |  | 2094-2095 |  | 2095-2096 |  | 2096-2097 |  | 2097-2098 |  | 2098-2099 |  | 2099-2100 |  | 2100-2101 |  | 2101-2102 |  | 2102-2103 |  | 2103-2104 |  | 2104-2105 |  | 2105-2106 |  | 2106-2107 |  | 2107-2108 |  | 2108-2109 |  | 2109-2110 |  | 2110-2111 |  | 2111-2112 |  | 2112-2113 |  | 2113-2114 |  | 2114-2115 |  | 2115-2116 |  | 2116-2117 |  | 2117-2118 |  | 2118-2119 |  | 2119-2120 |  | 2120-2121 |  | 2121-2122 |  | 2122-2123 |  | 2123-2124 |  | 2124-2125 |  | 2125-2126 |  | 2126-2127 |  | 2127-2128 |  | 2128-2129 |  | 2129-2130 |  | 2130-2131 |  | 2131-2132 |  | 2132-2133 |  | 2133-2134 |  | 2134-2135 |  | 2135-2136 |  | 2136-2137 |  | 2137-2138 |  | 2138-2139 |  | 2139-2140 |  | 2140-2141 |  | 2141-2142 |  | 2142-2143 |  | 2143-2144 |  | 2144-2145 |  | 2145-2146 |  | 2146-2147 |  | 2147-2148 |  | 2148-2149 |  | 2149-2150 |  | 2150-2151 |  | 2151-2152 |  | 2152-2153 |  | 2153-2154 |  | 2154-2155 |  | 2155-2156 |  | 2156-2157 |  | 2157-2158 |  | 2158-2159 |  | 2159-2160 |  | 2160-2161 |  | 2161-2162 |  | 2162-2163 |  | 2163-2164 |  | 2164-2165 |  | 2165-2166 |  | 2166-2167 |  | 2167-2168 |  | 2168-2169 |  | 2169-2170 |  | 2170-2171 |  | 2171-2172 |  | 2172-2173 |  | 2173-2174 |  | 2174-2175 |  | 2175-2176 |  | 2176-2177 |  | 2177-2178 |  | 2178-2179 |  | 2179-2180 |  | 2180-2181 |  | 2181-2182 |  | 2182-2183 |  | 2183-2184 |  | 2184-2185 |  | 2185-2186 |  | 2186-2187 |  | 2187-2188 |  | 2188-2189 |  | 2189-2190 |  | 2190-2191 |  | 2191-2192 |  | 2192-2193 |  | 2193-2194 |  | 2194-2195 |  | 2195-2196 |  | 2196-2197 |  | 2197-2198 |  | 2198-2199 |  | 2199-2200 |  | 2200-2201 |  | 2201-2202 |  | 2202-2203 |  | 2203-2204 |  | 2204-2205 |  | 2205-2206 |  | 2206-2207 |  | 2207-2208 |  | 2208-2209 |  | 2209-2210 |  | 2210-2211 |  | 2211-2212 |  | 2212-2213 |  | 2213-2214 |  | 2214-2215 |  | 2215-2216 |  | 2216-2217 |  |
|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|
|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|



ggccggccct gctcgtagct tggaggcggc ggcattctcc ggcaatgggg tgcaaggcgt 60  
gcgacaagcc caagcccaac taccgcaagg cctgtgggtcg ccggagagga ccagaagctc 120  
cgcgactaca ttctcctcca cggccacggc tgctggagcg cgctccccgc gaaagccggg 180  
ctccagcggg acggcaagag ctgcaggctg cggtggatca actaccttcg gccggggctg 240  
aagcacggca tgttctcccc ggagaggagg agacgggtgat gagcctccac gccacgctcg 300  
gcaacaagtg gtccaggatc gcacggcaact tgcttggcag gaccgacaac gaggtcaaga 360  
actactggaa ctctacctc aagaagaggg tcgaggccaa ggaccagggg cccagcacgc 420  
ccgcgcc

(2) INFORMATION FOR SEQ ID NO:1795:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1599135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1795:

Ala Gly Pro Ala Arg Ser Leu Glu Ala Ala Ala Phe Ser Gly Asn Gly  
1 5 10 15  
Val Gln Gly Val Arg Gln Ala Gln Ala Gln Leu Pro Gln Gly Leu Trp  
20 25 30  
Ser Pro Glu Arg Thr Arg Ser Ser Ala Thr Thr Phe Ser Ser Thr Ala  
35 40 45  
Thr Ala Ala Gly Ala Arg Ser Pro Arg Lys Pro Gly Ser Ser Gly Thr  
50 55 60  
Ala Arg Ala Ala Gly Cys Gly Gly Ser Thr Thr Phe Gly Arg Gly  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1796:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..141

(D) OTHER INFORMATION: / Ceres Seq. ID 1599136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1796:

Pro Ala Leu Leu Val Ala Trp Arg Arg His Ser Pro Ala Met Gly  
1 5 10 15  
Cys Lys Ala Cys Asp Lys Pro Lys Pro Asn Tyr Arg Lys Ala Cys Gly  
20 25 30  
Arg Arg Arg Gly Pro Glu Ala Pro Arg Leu His Ser Pro Pro Arg Pro  
35 40 45  
Arg Leu Leu Glu Arg Ala Pro Arg Glu Ser Arg Ala Pro Ala Glu Arg  
50 55 60  
Gln Glu Leu Gln Ala Ala Val Asp Gln Leu Pro Ser Ala Gly Ala Glu  
65 70 75 80  
Ala Arg His Val Leu Pro Gly Glu Glu Glu Thr Val Met Ser Leu His  
85 90 95  
Ala Thr Leu Gly Asn Lys Trp Ser Arg Ile Ala Arg His Leu Pro Gly  
100 105 110  
Arg Thr Asp Asn Glu Val Lys Asn Tyr Trp Asn Ser Tyr Leu Lys Lys  
115 120 125  
Arg Val Glu Ala Lys Asp Gln Gly Pro Ser Thr Pro Ala  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1797:

00669990 10300

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 127 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..127  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599137  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1797:  
Met Gly Cys Lys Ala Cys Asp Lys Pro Lys Pro Asn Tyr Arg Lys Ala  
1                  5                  10                  15  
Cys Gly Arg Arg Arg Gly Pro Glu Ala Pro Arg Leu His Ser Pro Pro  
                  20                  25                  30  
Arg Pro Arg Leu Leu Glu Arg Ala Pro Arg Glu Ser Arg Ala Pro Ala  
                  35                  40                  45  
Glu Arg Gln Glu Leu Gln Ala Val Asp Gln Leu Pro Ser Ala Gly  
50                  55                  60  
Ala Glu Ala Arg His Val Leu Pro Gly Glu Glu Thr Val Met Ser  
65                  70                  75                  80  
Leu His Ala Thr Leu Gly Asn Lys Trp Ser Arg Ile Ala Arg His Leu  
                  85                  90                  95  
Pro Gly Arg Thr Asp Asn Glu Val Lys Asn Tyr Trp Asn Ser Tyr Leu  
                  100                 105                 110  
Lys Lys Arg Val Glu Ala Lys Asp Gln Gly Pro Ser Thr Pro Ala  
115                 120                 125

(2) INFORMATION FOR SEQ ID NO:1798:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 493 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..493  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1798:

aagaaaaaaaa aaacacgcac ccgcgtccgc gtgctctctg cccctgccc ccctcccatc 60  
tgccgcgccc tctcatcca ccgccgtcc cgcgcgcgcc agcccaaggc caggcatccg 120  
ccagcctctc gcaccaacgcg tatcgsskcc cgcccgaccg gctcgtggcg atggcgtacc 180  
gggcggaaga cgactacgac tacctattca aggtggtgct catcggggac tccggcgctc 240  
gcaagtccaa cctgctctcg cgcttcacgc gcaacgagtt cagcctcgag tccaagtcca 300  
ccatcggcgt cgagttcgcc acccgagca tccacgtcga cgacaaggtc gtcaaggccc 360  
agatctggga caccgcccgt caggaaaggc accgtgctat caccgagcgc tactaccgcg 420  
gasakttagg ggcgctcgtc gtctacgagt gcacgcggca cgtcaccttc gagaacgtgg 480  
agaggktggw atg

(2) INFORMATION FOR SEQ ID NO:1799:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 142 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..142  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1799:

Lys Lys Lys Lys Thr Arg Thr Arg Val Arg Val Leu Ser Ala Pro Cys

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1 5 10 15  
Pro Pro Pro Ile Cys Ala Ala Leu Leu Ile His Arg Pro Ser Arg Arg  
20 25 30  
Arg Gln Pro Lys Ala Arg His Pro Pro Ala Ser Arg Thr Thr Arg Ile  
35 40 45  
Xaa Xaa Arg Pro Thr Gly Ser Trp Arg Trp Arg Thr Gly Arg Thr Thr  
50 55 60  
Thr Thr Thr Thr Tyr Ser Arg Trp Cys Ser Ser Gly Thr Pro Ala Ser  
65 70 75 80  
Ala Ser Pro Thr Cys Ser Arg Ala Ser Arg Ala Thr Ser Ser Ala Ser  
85 90 95  
Ser Pro Ser Pro Pro Ser Ala Ser Ser Ser Pro Pro Ala Ala Ser Thr  
100 105 110  
Ser Thr Thr Arg Ser Ser Arg Pro Arg Ser Gly Thr Pro Pro Val Arg  
115 120 125  
Lys Gly Thr Val Leu Ser Arg Ala Arg Thr Thr Ala Xaa Xaa  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1800:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1599140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1800:

Arg Lys Lys Lys His Ala Pro Ala Ser Ala Cys Ser Leu Pro Pro Ala  
1 5 10 15  
Pro Leu Pro Ser Ala Pro Pro Ser Ser Ser Thr Ala Arg Pro Ala Ala  
20 25 30  
Ala Ser Pro Arg Pro Gly Ile Arg Gln Pro Leu Ala Pro Arg Val Ser  
35 40 45  
Xaa Pro Ala Arg Pro Ala Arg Gly Asp Gly Val Pro Gly Gly Arg Arg  
50 55 60  
Leu Arg Leu Pro Ile Gln Gly Gly Ala His Arg Gly Leu Arg Arg Arg  
65 70 75 80  
Gln Val Gln Pro Ala Leu Ala Leu His Ala Gln Arg Val Gln Pro Arg  
85 90 95  
Val Gln Val His His Arg Arg Arg Val Arg His Pro Gln His Pro Arg  
100 105 110  
Arg Arg Gln Gly Arg Gln Gly Pro Asp Leu Gly His Arg Arg Ser Gly  
115 120 125  
Lys Val Pro Cys Tyr His Glu Arg Val Leu Pro Arg Xaa Xaa Arg Gly  
130 135 140  
Ala Arg Arg Leu Arg Val His Ala Ala Arg His Leu Arg Glu Arg Gly  
145 150 155 160  
Glu Xaa Xaa Met

(2) INFORMATION FOR SEQ ID NO:1801:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

09688880 101340

(D) OTHER INFORMATION: / Ceres Seq. ID 1599141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1801:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Lys | Lys | Asn | Thr | His | Pro | Arg | Pro | Arg | Ala | Leu | Cys | Pro | Leu | Pro |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ser | His | Leu | Arg | Arg | Pro | Pro | His | Pro | Pro | Pro | Val | Pro | Pro | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ala | Gln | Gly | Gln | Ala | Ser | Ala | Ser | Leu | Ser | His | His | Ala | Tyr | Xaa |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Xaa | Pro | Pro | Asp | Arg | Leu | Val | Ala | Met | Ala | Tyr | Arg | Ala | Asp | Asp | Asp |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Tyr | Asp | Tyr | Leu | Phe | Lys | Val | Val | Leu | Ile | Gly | Asp | Ser | Gly | Val | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Ser | Asn | Leu | Leu | Ser | Arg | Phe | Thr | Arg | Asn | Glu | Phe | Ser | Leu | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ser | Lys | Ser | Thr | Ile | Gly | Val | Glu | Phe | Ala | Thr | Arg | Ser | Ile | His | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Asp | Lys | Val | Val | Lys | Ala | Gln | Ile | Trp | Asp | Thr | Ala | Gly | Gln | Glu |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Arg | Tyr | Arg | Ala | Ile | Thr | Ser | Ala | Tyr | Tyr | Arg | Gly | Xaa | Leu | Gly | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Val | Val | Tyr | Glu | Cys | Thr | Arg | His | Val | Thr | Phe | Glu | Asn | Val | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg | Xaa |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1802:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 505 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..505

(D) OTHER INFORMATION: / Ceres Seq. ID 1599152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1802:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| cattcgcac  | gaagactgat | tggngtgta  | gagccatctc | tgccacaaac | ttgtatctac | 60  |
| gtgtaaatca | tatttatgtc | aattctgatg | atataaagga | aactggctac | acttacatta | 120 |
| tgccaaagaa | catattgaag | aaattcatat | gcatagcaga | tctgcgtaca | caaatcgctg | 180 |
| gattcttata | tgggctgagt | ccacaggaca | atcctcaagt | caaagagatt | aggtgtatag | 240 |
| ccatccctcc | gcagcatgga | acacaccaga | tggtgactct | gccatcaa   | attcctgaac | 300 |
| atgagttcct | taatgatctt | gaacccttgg | gatggatgca | tacacagcca | aatgaagctc | 360 |
| cacagctatc | accacaggac | ctgacatcac | atgccaagat | tctggagaac | aacaaacaat | 420 |
| gggatggtga | gaagtgcac  | attctgacat | gcagcttcac | cccaggatct | tgctcgctga | 480 |
| ctgcttacaa | gctgacacca | agtgg      |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1803:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1599153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1803:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ala | Ser | Lys | Thr | Asp | Trp | Xaa | Val | Arg | Ala | Ile | Ser | Ala | Thr | Asn |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Tyr | Leu | Arg | Val | Asn | His | Ile | Tyr | Val | Asn | Ser | Asp | Asp | Ile | Lys |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

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Glu Thr Gly Tyr Thr Tyr Ile Met Pro Lys Asn Ile Leu Lys Lys Phe  
35 40 45  
Ile Cys Ile Ala Asp Leu Arg Thr Gln Ile Ala Gly Phe Leu Tyr Gly  
50 55 60  
Leu Ser Pro Gln Asp Asn Pro Gln Val Lys Glu Ile Arg Cys Ile Ala  
65 70 75 80  
Ile Pro Pro Gln His Gly Thr His Gln Met Val Thr Leu Pro Ser Asn  
85 90 95  
Leu Pro Glu His Glu Phe Leu Asn Asp Leu Glu Pro Leu Gly Trp Met  
100 105 110  
His Thr Gln Pro Asn Glu Ala Pro Gln Leu Ser Pro Gln Asp Leu Thr  
115 120 125  
Ser His Ala Lys Ile Leu Glu Asn Asn Lys Gln Trp Asp Gly Glu Lys  
130 135 140  
Cys Ile Ile Leu Thr Cys Ser Phe Thr Pro Gly Ser Cys Ser Leu Thr  
145 150 155 160  
Ala Tyr Lys Leu Thr Pro Ser  
165

(2) INFORMATION FOR SEQ ID NO:1804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1599154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1804:

Met Pro Lys Asn Ile Leu Lys Lys Phe Ile Cys Ile Ala Asp Leu Arg  
1 5 10 15  
Thr Gln Ile Ala Gly Phe Leu Tyr Gly Leu Ser Pro Gln Asp Asn Pro  
20 25 30  
Gln Val Lys Glu Ile Arg Cys Ile Ala Ile Pro Pro Gln His Gly Thr  
35 40 45  
His Gln Met Val Thr Leu Pro Ser Asn Leu Pro Glu His Glu Phe Leu  
50 55 60  
Asn Asp Leu Glu Pro Leu Gly Trp Met His Thr Gln Pro Asn Glu Ala  
65 70 75 80  
Pro Gln Leu Ser Pro Gln Asp Leu Thr Ser His Ala Lys Ile Leu Glu  
85 90 95  
Asn Asn Lys Gln Trp Asp Gly Glu Lys Cys Ile Ile Leu Thr Cys Ser  
100 105 110  
Phe Thr Pro Gly Ser Cys Ser Leu Thr Ala Tyr Lys Leu Thr Pro Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..462

(D) OTHER INFORMATION: / Ceres Seq. ID 1599163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1805:

aagtaaaaaa aagttcacgc gcatgggtcgg tctgcgactg cctctgaccg ctgaccgcac

tgctcccttc tctgtttctc tctccccact tctgagacttc ctccattcgc ggtttgcctc 120  
tctgccttcc ctacctcaga tcttccctca gattgccatg gcggaccagc tcaccgacga 180  
ccagatcgcc gagttcaagg aagcattcag cctcttcgac aaggacggcg acggctgcat 240  
caccaccaag gaacttgaac tgtgatgccc tctgtggggc agaaccctac tgaggctgag 300  
cttcaggaca tgatcaacga ggttgatgct gatggcaatg gaaccatcga cttccctgag 360  
tttctcaacc tgatggcacg caagatgaag gacacagact ctgaggagga gctcaaggag 420  
gccttccgcg tgttcgacaa ggaccagaac ggcttcatct ct

(2) INFORMATION FOR SEQ ID NO:1806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1599164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1806:

Ser Lys Lys Lys Phe Thr Arg Met Val Gly Leu Arg Leu Pro Leu Thr  
1 5 10 15  
Ala Asp Arg Thr Ala Pro Phe Ser Cys Ser Leu Ser Pro Leu Arg Asp  
20 25 30  
Phe Leu His Ser Arg Phe Ala Ser Leu Pro Ser Leu Pro Gln Ile Leu  
35 40 45  
Pro Gln Ile Ala Met Ala Asp Gln Leu Thr Asp Asp Gln Ile Ala Glu  
50 55 60  
Phe Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile  
65 70 75 80  
Thr Thr Lys Glu Leu Glu Leu  
85

(2) INFORMATION FOR SEQ ID NO:1807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1599165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1807:

Met Val Gly Leu Arg Leu Pro Leu Thr Ala Asp Arg Thr Ala Pro Phe  
1 5 10 15  
Ser Cys Ser Leu Ser Pro Leu Arg Asp Phe Leu His Ser Arg Phe Ala  
20 25 30  
Ser Leu Pro Ser Leu Pro Gln Ile Leu Pro Gln Ile Ala Met Ala Asp  
35 40 45  
Gln Leu Thr Asp Asp Gln Ile Ala Glu Phe Lys Glu Ala Phe Ser Leu  
50 55 60  
Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys Glu Leu Glu Leu  
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:1808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

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- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..39
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1599198
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1816:

Met Tyr Arg Xaa Xaa His Lys Lys Asp Ile His Ala Glu Ala Val Lys  
1                   5                   10                   15  
Lys Arg Xaa Arg Ala Asn Lys Lys Pro Tyr Ser Xaa Ser Ile Val Xaa  
                  20                   25                   30  
Ala Ser Leu Glu Val Ile Gln  
                  35

- (2) INFORMATION FOR SEQ ID NO:1817:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 442 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..442
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1599222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1817:  
tccacttcac gccccgccgc cgccgccgcg tctcctctgc aggtaagaag gtaaggaaga           60  
gggcgaaatg gtgaagcaca acaacgttat cccaacggc acttcaagaa gcactggcag           120  
aactatgtca agacatggtt caaccagccc gcccgcaagc agaggcgccg catcgctcgt           180  
caaaagaagg ctgtgaagat attcccacgc ccaactgctg gccctcttcg ccccatcgtg           240  
caatgccaga ccctcaagta caacatgaag tcgagggctg ggagaggatt tacccttgag           300  
gagctgaakg ctgccggcat tccaaagaag cttgccccaa ccattggcat ttctgtggat           360  
caccgccgca agaacaaatc tctcgaggga ctgcaggcca atgtccagag gcttaagacg           420  
tacaaggcca agctggttat ct

- (2) INFORMATION FOR SEQ ID NO:1818:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 42 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..42
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1599223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1818:  
Met Val Lys His Asn Asn Val Ile Pro Asn Gly Thr Ser Arg Ser Thr  
1                   5                   10                   15  
Gly Arg Thr Met Ser Arg His Gly Ser Thr Ser Pro Pro Ala Ser Arg  
                  20                   25                   30  
Gly Ala Ala Ser Leu Val Lys Arg Arg Leu  
                  35                   40

- (2) INFORMATION FOR SEQ ID NO:1819:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 54 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:

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- (A) NAME/KEY: peptide
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1819:

Met Val Gln Pro Ala Arg Pro Gln Ala Glu Ala Pro His Arg Ser Ser  
1 5 10 15  
Lys Glu Gly Cys Glu Asp Ile Pro Thr Pro Asn Cys Trp Pro Ser Ser  
20 25 30  
Pro His Arg Ala Met Pro Asp Pro Gln Val Gln His Glu Val Glu Gly  
35 40 45  
Trp Glu Arg Ile Tyr Pro  
50

(2) INFORMATION FOR SEQ ID NO:1820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..59
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1820:

Met Lys Ser Arg Ala Gly Arg Gly Phe Thr Leu Glu Glu Leu Xaa Ala  
1 5 10 15  
Ala Gly Ile Pro Lys Lys Leu Ala Pro Thr Ile Gly Ile Ser Val Asp  
20 25 30  
His Arg Arg Lys Asn Lys Ser Leu Glu Gly Leu Gln Ala Asn Val Gln  
35 40 45  
Arg Leu Lys Thr Tyr Lys Ala Lys Leu Val Ile  
50 55

(2) INFORMATION FOR SEQ ID NO:1821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..487
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1821:

attctataaa acctctgccc gggggctagg gtttcctccc agccgctcgc gtttcgcgctc 60  
tgccctcagcc cgccgcaaga gaggttaagtt caggagacat cttcgagaag ctgaaatggc 120  
tcctaaagct gctcctgcca agaagggtga tgccaagacc caggccttga aggttgccaa 180  
ggctgtgaag tctggggcag ccaagaagaa gaccaagaag atccgcacgt ctgtgacatt 240  
tcaccgcccc acgaccctga agaaggctag ggaccccaag taccacgaa tcagcactac 300  
cggaaggaac aagcttgatc agtaccaaat tctcaagtac ccccttacca cagaatcagc 360  
gatgaagaag attgaagata acaacactct ggtcttcatt gttgacctca aggcagacaa 420  
gaagaagatc aaggctgccg tcaagaagat gtatgacatc caggcaaaga aggtcaacac 480  
cttgatc

(2) INFORMATION FOR SEQ ID NO:1822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:



Met Ala Val Pro Leu Leu Thr Gln Lys Ile Val Lys Lys Arg Val Lys  
1 5 10 15  
Gln Phe Lys Arg Pro His Leu Asp Arg Tyr Lys Cys Leu Asn Pro Ser  
20 25 30

Trp Arg Arg Pro Lys Gly Ile Asp Ser Arg Val Arg Arg Lys Phe Lys  
35 40 45  
Gly Cys Thr Leu Met Pro Asn Ile Gly Tyr Gly Ser Asp Lys Lys Thr  
50 55 60  
Arg His Tyr Leu Pro Asn Lys Phe Lys Lys Phe Val Val His Asn Val  
65 70 75 80  
Ser Glu Leu Glu Leu Leu Leu Met His Asn Arg Thr Tyr Cys Ala Glu  
85 90 95  
Ile Ala His Asn Val Ser Thr Arg Lys Arg Lys Glu Ile Val Glu Arg  
100 105 110  
Ala Ala Gln Met Asp Ile Val Val Thr Asn Lys Leu Ala Arg Leu Arg  
115 120 125  
Ser Gln Glu Asp Glu  
130

(2) INFORMATION FOR SEQ ID NO:1827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..81
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1827:

Met Pro Asn Ile Gly Tyr Gly Ser Asp Lys Lys Thr Arg His Tyr Leu  
1 5 10 15  
Pro Asn Lys Phe Lys Lys Phe Val Val His Asn Val Ser Glu Leu Glu  
20 25 30  
Leu Leu Leu Met His Asn Arg Thr Tyr Cys Ala Glu Ile Ala His Asn  
35 40 45  
Val Ser Thr Arg Lys Arg Lys Glu Ile Val Glu Arg Ala Ala Gln Met  
50 55 60  
Asp Ile Val Val Thr Asn Lys Leu Ala Arg Leu Arg Ser Gln Glu Asp  
65 70 75 80  
Glu

(2) INFORMATION FOR SEQ ID NO:1828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..497
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1828:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| agaaaaccta tagcttgcag cgccacctac accgagcagc caagcgagga agcgaagacc  | 60  |
| catttccccg agcgcaagag taccatggcg gcggcggcag tttatggcgg cctcaagggg  | 120 |
| aagcttggcg tcgaggatgc ccccgagctg cagctgaatc gcatccgcat caccctctca  | 180 |
| tccaagaacg tcaagaacct ggagaaagtt tgtgcggatt tggtaaaggg agccaaggat  | 240 |
| aagcatctga ggggttaaggg gcctgtcagg atccctacta aggttctcca catcaccacc | 300 |
| cgaaatccc cttgcggtga aggaacaaac acatgggacc ggtttgagtt ccgcatccat   | 360 |
| aagagggtga tcgacctgat cagctcccca gacgtggtga agcagatcac ctctatcacc  | 420 |
| attgagccgg gtgttgaggt cgaggtgacc gttgcagacg tgtaatgacg atctatatat  | 480 |
| tcgtgttgct tttgttt                                                 |     |

(2) INFORMATION FOR SEQ ID NO:1829:

(i) SEQUENCE CHARACTERISTICS:

00000000 00000000



(B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1599246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1831:

Met Ala Ala Ala Val Tyr Gly Gly Leu Lys Gly Lys Leu Gly Val  
1 5 10 15  
Glu Asp Ala Pro Glu Leu Gln Leu Asn Arg Ile Arg Ile Thr Leu Ser  
20 25 30  
Ser Lys Asn Val Lys Asn Leu Glu Lys Val Cys Ala Asp Leu Val Lys  
35 40 45  
Gly Ala Lys Asp Lys His Leu Arg Val Lys Gly Pro Val Arg Ile Pro  
50 55 60  
Thr Lys Val Leu His Ile Thr Thr Arg Lys Ser Pro Cys Gly Glu Gly  
65 70 75 80  
Thr Asn Thr Trp Asp Arg Phe Glu Phe Arg Ile His Lys Arg Val Ile  
85 90 95  
Asp Leu Ile Ser Ser Pro Asp Val Val Lys Gln Ile Thr Ser Ile Thr  
100 105 110  
Ile Glu Pro Gly Val Glu Val Glu Val Thr Val Ala Asp Val  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1832:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 504 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..504

(D) OTHER INFORMATION: / Ceres Seq. ID 1599263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1832:

ggagcaggac aggttgcat tgcctctgag ttctgatcg ttgtattcca gtttcttccg 60  
tgagttttgt gggatcgca ggaagaagga tgctgtgctg cggaggcaac tgcgggtgcg 120  
gcgccggctg caagtgcggc ascggtgctg gagggtgcaa gatgtaccgc gacatggctg 180  
agcaggtgac caccaccacc accaccaga ctctcatcat ggggtgttga ccatccaagg 240  
gcggggtcga ggcggccgcg gagctgagaa cggcgggtgc aagtgcggcg ccaactgcac 300  
ctgcgacccc tgcacctgca agtgagacta cgacgggtggc ggcgatgaag ctgcagggtc 360  
tgcaggccct gatggggtcg gaaggactct ttatctctct agctaattaa taagctctag 420  
ctagtatata atattctagc agtgtcgttt gctgtgtttt gttcagagtca gtttagacagt 480  
cagccgcgtg ccatgggcca tggg

(2) INFORMATION FOR SEQ ID NO:1833:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1599264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1833:

Met Ser Cys Cys Gly Gly Asn Cys Gly Cys Gly Ala Gly Cys Lys Cys  
1 5 10 15  
Gly Xaa Gly Cys Gly Gly Cys Lys Met Tyr Pro Asp Met Ala Glu Gln  
20 25 30  
Val Thr Thr Thr Thr Thr Thr Gln Thr Leu Ile Met Gly Val Ala Pro  
35 40 45  
Ser Lys Gly Gly Val Glu Ala Ala Glu Leu Arg Thr Ala Gly Ala  
50 55 60  
Ser Ala Ala Pro Thr Ala Pro Ala Thr Pro Ala Pro Ala Ser Glu Thr

DOCKET# 08558360



(2) INFORMATION FOR SEQ ID NO:1834:

(A) LENGTH: 82 amino acids

(C) STRANDEDNESS:

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1599265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1834:

(2) INFORMATION FOR SEQ ID NO:1835:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1599266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1835:

(2) INFORMATION FOR SEQ ID NO:1836:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 483 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..483

(D) OTHER INFORMATION: / Ceres Seq. ID 1599267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1836:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| acattctgtt | ctcgtttctc | ttcctctctc | tcaactcaac | tactcaaagc | ggtagattaa | 60  |
| ccggctctag | cgtmsggtgt | tgctacatct | ctcttgcca  | tgggggcatg | cgcgacgaag | 120 |
| ccgggtgacc | tcaaggtcaa | ggcgaggcg  | cctctggtcg | cggaggacgc | cgcggcgcca | 180 |
| ctggssgctg | cagacgagaa | ggcgaaggcc | gccgaggtcc | ccgtggccgc | cgcgcgcgag | 240 |
| gtcgaccagg | ccgatgtcag | ccgccggagt | ccctcagcga | cctgctcaaa | cgggacgccg | 300 |
| agggcagttg | acggggagga | kkaggccgac | caggaggcgg | agaaggctcg | gggctgggga | 360 |
| gccancgagt | gctgccgctg | ccgctgccgg | ggaaacgatg | gggtcaccgc | aagcaacagt | 420 |
| gcaggcctcg | gtcgcaaccg | agcaggacga | cacggccgaa | gaactcaagg | atggtcttcc | 480 |
| gag        |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1599268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1837:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Ala | Cys | Ala | Thr | Lys | Pro | Gly | Asp | Leu | Lys | Val | Lys | Gly | Glu |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Ala | Pro | Leu | Val | Ala | Glu | Asp | Ala | Ala | Pro | Leu | Xaa | Ala | Ala | Ala | Asp |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Glu | Lys | Ala | Lys | Ala | Ala | Glu | Val | Pro | Val | Ala | Ala | Ala | Ala | Glu | Val |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Asp | Gln | Ala | Asp | Val | Ser | Arg | Arg | Ser | Pro | Ser | Ala | Thr | Cys | Ser | Asn |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gly | Thr | Pro | Arg | Ala | Val | Asp | Gly | Glu | Xaa | Xaa | Ala | Asp | Gln | Glu | Ala |  |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Glu | Lys | Val | Val | Gly | Trp | Gly | Ala | Xaa | Glu | Cys | Cys | Arg | Cys | Arg | Cys |  |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |  |
| Arg | Gly | Asn | Asp | Gly | Val | Thr | Ala | Ser | Asn | Ser | Ala | Gly | Leu | Gly | Arg |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |
| Asn | Arg | Ala | Gly | Arg | His | Gly | Arg | Thr | Gln | Gly | Trp | Ser | Ser | Glu |     |  |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1599269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1838:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Ala | Ala | Gly | Val | Pro | Gln | Arg | Pro | Ala | Gln | Thr | Gly | Arg | Arg |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Gly | Gln | Leu | Thr | Gly | Arg | Xaa | Arg | Pro | Thr | Arg | Arg | Arg | Arg | Arg | Ser |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Trp | Ala | Gly | Glu | Pro | Xaa | Ser | Ala | Ala | Ala | Ala | Ala | Ala | Gly | Glu | Thr |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Met | Gly | Ser | Pro | Gln | Ala | Thr | Val | Gln | Ala | Ser | Val | Ala | Thr | Glu | Gln |  |
|     | 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |

Asp Asp Thr Ala Glu Glu Leu Lys Asp Gly Leu Pro  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..502
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1839:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| gaaaaaggaa | cagaagggag | aaagaaaagc | agtcgagcag | cggtasscgg  | tagssrgaga | 60  |
| gtcaggattc | aggacgcggc | gaggccacca | tgagcactct | caagtctctgc | cgggaatgca | 120 |
| acaacatgct | gtaccgcggg | gaggacaagg | agacgcgcac | cctcctgtac  | gcgtgccaaa | 180 |
| cgtgcgagca | tgaggagatt | gccactgata | cttgtgtgta | caaaagggtt  | atccgcaagc | 240 |
| ctggtggtga | gccaaggat  | gtcctgaagg | atgcagcaac | tgatcctagc  | ctgcctcgca | 300 |
| ccagaagcgt | catagtgtac | aactgcaacc | atccagaagc | tgcctttttt  | caggccccga | 360 |
| ctaagggaga | acaagccatg | acgctgtact | tcatctgctg | caacccaagc  | tgcgggcaca | 420 |
| ggtggaggga | ctgagaagga | tctggcttgg | tcttcgctgc | aaacctgccg  | tatttgtag  | 480 |
| cctatcrat  | aaatattgta | gg         |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:1840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1840:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Lys | Lys | Glu | Gln | Lys | Gly | Glu | Arg | Lys | Ala | Val | Glu | Gln | Arg | Xaa | Xaa |  |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |  |
| Val | Xaa | Xaa | Glu | Ser | Gly | Phe | Arg | Thr | Arg | Arg | Gly | His | His | Glu | His |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Gln | Val | Leu | Pro | Gly | Met | Gln | Gln | His | Ala | Val | Pro | Ala | Gly | Gly |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Gln | Gly | Asp | Ala | His | Pro | Pro | Val | Arg | Val | Pro | Asn | Val | Arg | Ala |     |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1841:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Thr | Leu | Lys | Phe | Cys | Arg | Glu | Cys | Asn | Asn | Met | Leu | Tyr | Pro |  |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |  |
| Arg | Glu | Asp | Lys | Glu | Thr | Arg | Thr | Leu | Leu | Tyr | Ala | Cys | Gln | Thr | Cys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu | His | Glu | Glu | Ile | Ala | Thr | Asp | Thr | Cys | Val | Tyr | Lys | Arg | Val | Ile |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |  |

Arg Lys Pro Gly Gly Glu Pro Lys Asp Val Leu Lys Asp Ala Ala Thr  
50 55 60  
Asp Pro Ser Leu Pro Arg Thr Arg Ser Val Arg Cys Tyr Asn Cys Asn  
65 70 75 80  
His Pro Glu Ala Ala Phe Phe Gln Ala Pro Thr Lys Gly Glu Gln Ala  
85 90 95  
Met Thr Leu Tyr Phe Ile Cys Cys Asn Pro Ser Cys Gly His Arg Trp  
100 105 110  
Arg Asp

(2) INFORMATION FOR SEQ ID NO:1842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1842:

Met Leu Tyr Pro Arg Glu Asp Lys Glu Thr Arg Thr Leu Leu Tyr Ala  
1 5 10 15  
Cys Gln Thr Cys Glu His Glu Glu Ile Ala Thr Asp Thr Cys Val Tyr  
20 25 30  
Lys Arg Val Ile Arg Lys Pro Gly Gly Glu Pro Lys Asp Val Leu Lys  
35 40 45  
Asp Ala Ala Thr Asp Pro Ser Leu Pro Arg Thr Arg Ser Val Arg Cys  
50 55 60  
Tyr Asn Cys Asn His Pro Glu Ala Ala Phe Phe Gln Ala Pro Thr Lys  
65 70 75 80  
Gly Glu Gln Ala Met Thr Leu Tyr Phe Ile Cys Cys Asn Pro Ser Cys  
85 90 95  
Gly His Arg Trp Arg Asp  
100

(2) INFORMATION FOR SEQ ID NO:1843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..487
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1843:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| tccaacgcgg  | cacagagcct | cattcatctc | cattcgaaac | accctcgac  | ccacactcnc | 60  |
| ccttggtccc  | cagcctaaat | ccccgcaang | atggctcgca | cgaagcakac | ggcgcgcaag | 120 |
| tccaacgkck  | gcaaggcccc | gaggaagcag | ctggcgacca | aggcggcgcg | caagtcggcc | 180 |
| cctgcgaccg  | gcggcgtaga | gaagccgcac | cgcttcgcc  | cgggcaccgt | ggcgtgcgc  | 240 |
| gagatccgca  | agtaccagaa | gagcacggag | ctgctcatcc | gcaagctgcc | cttcacgcgc | 300 |
| ctgggtccgcg | agatcgcgca | ggacttcaag | accgacctcc | gcttcagtc  | ctccgccgtc | 360 |
| gccgcgctgc  | aggaggccgc | cgaggcttac | ctcgtcggcc | tgttcgagga | caccaacctc | 420 |
| tgcgccatcc  | acgccaagcg | cgtcaccatc | atgcccaagg | acatccagct | cgccccgccg | 480 |
| atccgcg     |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid

0966980 10100

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..161  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599279  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1844:

Gln Arg Gly Thr Glu Pro His Ser Ser Pro Phe Glu Thr Pro Ser His  
1                   5                   10                   15  
Pro His Xaa Pro Phe Val Pro Ser Leu Asn Pro Arg Xaa Asp Gly Ser  
                  20                   25                   30  
His Glu Ala Xaa Gly Ala Gln Val His Xaa Xaa Gln Gly Pro Glu Glu  
                  35                   40                   45  
Ala Ala Gly Asp Gln Gly Gly Ala Gln Val Gly Pro Cys Asp Arg Arg  
                  50                   55                   60  
Arg Glu Glu Ala Ala Pro Leu Pro Pro Gly His Arg Gly Ala Ala Arg  
65                   70                   75                   80  
Asp Pro Gln Val Pro Glu Glu His Gly Ala Ala His Pro Gln Ala Ala  
                  85                   90                   95  
Leu Pro Ala Pro Gly Pro Arg Asp Arg Ala Gly Leu Gln Asp Arg Pro  
                  100                   105                   110  
Pro Leu Pro Val Leu Arg Arg Arg Arg Ala Ala Gly Gly Arg Arg Gly  
                  115                   120                   125  
Leu Pro Arg Arg Pro Val Arg Gly His Gln Pro Leu Arg His Pro Arg  
                  130                   135                   140  
Gln Ala Arg His His His Ala Gln Gly His Pro Ala Arg Pro Pro His  
145                   150                   155                   160  
Pro

- (2) INFORMATION FOR SEQ ID NO:1845:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 132 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..132  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1599280  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1845:

Met Ala Arg Thr Lys Xaa Thr Ala Arg Lys Ser Thr Xaa Xaa Lys Ala  
1                   5                   10                   15  
Pro Arg Lys Gln Leu Ala Thr Lys Ala Ala Arg Lys Ser Ala Pro Ala  
                  20                   25                   30  
Thr Gly Gly Val Lys Lys Pro His Arg Phe Arg Pro Gly Thr Val Ala  
                  35                   40                   45  
Leu Arg Glu Ile Arg Lys Tyr Gln Lys Ser Thr Glu Leu Leu Ile Arg  
                  50                   55                   60  
Lys Leu Pro Phe Gln Arg Leu Val Arg Glu Ile Ala Gln Asp Phe Lys  
65                   70                   75                   80  
Thr Asp Leu Arg Phe Gln Ser Ser Ala Val Ala Ala Leu Gln Glu Ala  
                  85                   90                   95  
Ala Glu Ala Tyr Leu Val Gly Leu Phe Glu Asp Thr Asn Leu Cys Ala  
                  100                   105                   110  
Ile His Ala Lys Arg Val Thr Ile Met Pro Lys Asp Ile Gln Leu Ala  
                  115                   120                   125  
Arg Arg Ile Arg  
                  130

- (2) INFORMATION FOR SEQ ID NO:1846:

00000000 00000000

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 373 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
    (B) LOCATION: 1..373  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599297

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1846:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| ccagcagcct cccgnatccc caaagcctcc gaccccccctc ctctctccct ccgcccgcgcg | 60  |
| tgcgcacgcr gggaacaagc gacatgggcg tctacacctt cgtgtgcgcg aacaacggcg   | 120 |
| kckaktggac cgccaagcag cactccggcg agatcgaggc ttccgcccgt accccatacg   | 180 |
| agctgcagcg ccgcctcgtc gccgtgcct ccgcggccga ctctgcctac gggtcagtc     | 240 |
| gtcctttctcc atggtcaccc ccagctccgc cgtgttccag gtgatcgtag gtgctgttg   | 300 |
| tggtgggtgca atgatggtga gcggagggtg ccgcgggtgct gctgcatctg gtggtgctgc | 360 |
| tgccgaggct ccc                                                      |     |

- (2) INFORMATION FOR SEQ ID NO:1847:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 124 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..124  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599298

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1847:

|                                                                      |  |
|----------------------------------------------------------------------|--|
| Pro Ala Ala Ser Xaa Ile Pro Lys Ala Ser Asp Pro Leu Pro Leu Ser      |  |
| 1                    5                    10                    15   |  |
| Leu Arg Arg Arg Cys Ala Arg Xaa Glu Gln Ala Thr Trp Ala Ser Thr      |  |
| 20                    25                    30                       |  |
| Pro Ser Cys Ala Ala Thr Thr Ala Xaa Xaa Gly Pro Pro Ser Ser Thr      |  |
| 35                    40                    45                       |  |
| Pro Ala Arg Ser Arg Leu Pro Pro Leu Pro His Thr Ser Cys Ser Ala      |  |
| 50                    55                    60                       |  |
| Ala Ser Ser Pro Leu Pro Pro Arg Pro Thr Leu Pro Thr Gly Pro Val      |  |
| 65                    70                    75                    80 |  |
| Val Leu Leu His Gly His Pro Gln Leu Arg Arg Val Pro Gly Asp Arg      |  |
| 85                    90                    95                       |  |
| Arg Cys Cys Trp Trp Trp Cys Asn Asp Gly Glu Arg Arg Trp Arg Arg      |  |
| 100                    105                    110                    |  |
| Cys Cys Cys Ile Trp Trp Cys Cys Arg Gly Ser                          |  |
| 115                    120                                           |  |

- (2) INFORMATION FOR SEQ ID NO:1848:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 124 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..124  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599299

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1848:

|                                                                    |  |
|--------------------------------------------------------------------|--|
| Gln Gln Pro Pro Xaa Ser Pro Lys Pro Pro Thr Pro Phe Leu Ser Pro    |  |
| 1                    5                    10                    15 |  |
| Ser Ala Ala Ala Ala His Xaa Gly Asn Lys Arg His Gly Arg Leu His    |  |

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20 25 30  
Leu Arg Val Pro Gln Gln Arg Xaa Xaa Asp Arg Gln Ala Ala Leu  
35 40 45  
Arg Arg Asp Arg Gly Phe Arg Arg Tyr Pro Ile Arg Ala Ala Ala Pro  
50 55 60  
Pro Arg Arg Arg Cys Leu Arg Gly Arg Leu Cys Leu Arg Val Gln Ser  
65 70 75 80  
Ser Phe Ser Met Val Thr Pro Ser Ser Ala Val Phe Gln Val Ile Val  
85 90 95  
Gly Ala Val Gly Gly Gly Ala Met Met Val Ser Gly Gly Gly Gly  
100 105 110  
Ala Ala Ala Ser Gly Gly Ala Ala Glu Ala Pro  
115 120

(2) INFORMATION FOR SEQ ID NO:1849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..93  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1849:

Ser Ser Leu Pro Xaa Pro Gln Ser Leu Arg Pro Pro Ser Ser Leu Pro  
1 5 10 15  
Pro Pro Pro Leu Arg Thr Xaa Gly Thr Ser Asp Met Gly Val Tyr Thr  
20 25 30  
Phe Val Cys Arg Asn Asn Gly Xaa Xaa Trp Thr Ala Lys Gln His Ser  
35 40 45  
Gly Glu Ile Glu Ala Ser Ala Ala Thr Pro Tyr Glu Leu Gln Arg Arg  
50 55 60  
Leu Val Ala Ala Ala Ser Ala Ala Asp Ser Ala Tyr Gly Ser Ser Arg  
65 70 75 80  
Pro Ser Pro Trp Ser Pro Pro Ala Pro Pro Cys Ser Arg  
85 90

(2) INFORMATION FOR SEQ ID NO:1850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..477  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1850:

aaacagccaa agaacagaaa aaaatataaa aaggtgggcg tgcaactttc ccttccttcg 60  
ccgaagccgc gcgacggaaa ccccaaacc aacctcatct cttttctcgg cctctaccgc 120  
cccctcgatc ggtcgcccg ttagctatga cgccgggaag ctccggccgc ggatccggst 180  
cgctcgttcct cggaacttca ggctcctaga agagcttgaa cgtggagaga agggcattgg 240  
agatgggaca gtgagctatg gaatggatga cgcagatgac atctacatgc gatcatggac 300  
tggcactatt attggccctc ataataccgt ccatgagggt cgcattctacc agctgaagtt 360  
gttctgcgac aaggactacc ctgagaagcc accatcagtt cgatttcatt caagaataaa 420  
tttaacatgc gttaatcatg aaactggagt gggtgaccgc aagaagttca gcgtttct

(2) INFORMATION FOR SEQ ID NO:1851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids  
(B) TYPE: amino acid

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- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..158  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599316  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1851:

Asn Ser Gln Arg Thr Glu Lys Asn Ile Lys Arg Trp Ala Cys Asn Phe  
1 5 10 15  
Pro Phe Leu Arg Arg Ser Arg Ala Thr Glu Thr Pro Asn Pro Thr Ser  
20 25 30  
Ser Leu Phe Ser Ala Ser Thr Ala Pro Ser Ile Gly Arg Pro Val Ser  
35 40 45  
Tyr Asp Ala Gly Lys Leu Gly Arg Arg Ile Arg Xaa Val Val Pro Arg  
50 55 60  
Asn Phe Arg Leu Leu Glu Glu Leu Glu Arg Gly Glu Lys Gly Ile Gly  
65 70 75 80  
Asp Gly Thr Val Ser Tyr Gly Met Asp Asp Ala Asp Asp Ile Tyr Met  
85 90 95  
Arg Ser Trp Thr Gly Thr Ile Ile Gly Pro His Asn Thr Val His Glu  
100 105 110  
Gly Arg Ile Tyr Gln Leu Lys Leu Phe Cys Asp Lys Asp Tyr Pro Glu  
115 120 125  
Lys Pro Pro Ser Val Arg Phe His Ser Arg Ile Asn Leu Thr Cys Val  
130 135 140  
Asn His Glu Thr Gly Val Val Asp Pro Lys Lys Phe Ser Val  
145 150 155

(2) INFORMATION FOR SEQ ID NO:1852:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 477 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..477  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1852:

actcaccact catcaccagc tagtagctct agcaaagcac ttgccatcta cgcacgcgcg 60  
cattccaaac agcccgacga gctagcagag cgncaggcac ctctccagg aacatggccc 120  
gcacgcagca gttggcagta gtggcgacan gtggtggcct tgggtgtgct ggcggcggcg 180  
acgtcggagg cgcccatcag ctgcggggcag gtggcgctcg ccacgcgcgc ctgcacatcc 240  
tacgcgcgcg gccagggctc agggccctcc gccggctgct gcagcggcgt caggagcctc 300  
aacaacgcgc cccgcaccac cgccgaccgc cgcgcgcgct gtaactgcct caagaacgcc 360  
gcckccgkyt gcagcggcct caacgccggt aacgcgcgca gcatccctc caagtgcggc 420  
gtcrsatccc octacacat cagcacctcc accgactgct ccagggtgaa ctgaacc

(2) INFORMATION FOR SEQ ID NO:1853:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..46  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1853:

Thr His His Ser Ser Pro Ala Ser Ser Ser Ser Lys Ala Leu Ala Ile

00559300 00559300



(2) INFORMATION FOR SEQ ID NO:1854:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1599319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1854:

(2) INFORMATION FOR SEQ ID NO:1855:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 504 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..504

(D) OTHER INFORMATION: / Ceres Seq. ID 1599320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1855:

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| ctaataccatc | gcagagcgcc | gccggngta   | gcgctactgc | tagaggagag | gaagcggaaa | 60  |
| gggcggcggc  | ggcgcttggt | gtcagtcaa   | gatccaacct | ccggactcgc | gatggggcgg | 120 |
| cggatcctca  | acgatgctst | gcgcacgatg  | gtcaacgcag | accggcgggg | gaacgcgctc | 180 |
| gcgcttctcc  | gacccatctc | cggcgctcatg | gtctccttcc | tcaacatcat | gaagtaccga | 240 |
| gggtatatca  | aaaaatttga | ggtcattgat  | gagaatagag | ttgggaaaat | tagagtggag | 300 |
| cttgatggac  | gtcttaaaga | ttgcaaagct  | ctcacctaca | ggcaagacct | caaagctaag | 360 |
| gagatagaac  | gatacacagt | taggatgtct  | ccaacacgcc | akggtgctat | gttgtgatta | 420 |
| ctactccga   | tggtgttttg | gatcatgagg  | aagcaatcag | gcagaacgtg | ggtgggcagg | 480 |
| tccttgqgtt  | attttccatt | gact        |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1856:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1599321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1856:

Leu Ile His Arg Arg Ala Pro Pro Xaa Val Ala Leu Leu Leu Glu Glu

| Table 1. Demographic characteristics of the study population |              |
|--------------------------------------------------------------|--------------|
| <b>Age (years)</b>                                           |              |
| 18-24                                                        | 100 (10.0)   |
| 25-34                                                        | 150 (15.0)   |
| 35-44                                                        | 200 (20.0)   |
| 45-54                                                        | 250 (25.0)   |
| 55-64                                                        | 300 (30.0)   |
| 65-74                                                        | 350 (35.0)   |
| 75-84                                                        | 400 (40.0)   |
| 85-94                                                        | 450 (45.0)   |
| 95-104                                                       | 500 (50.0)   |
| 105-114                                                      | 550 (55.0)   |
| 115-124                                                      | 600 (60.0)   |
| 125-134                                                      | 650 (65.0)   |
| 135-144                                                      | 700 (70.0)   |
| 145-154                                                      | 750 (75.0)   |
| 155-164                                                      | 800 (80.0)   |
| 165-174                                                      | 850 (85.0)   |
| 175-184                                                      | 900 (90.0)   |
| 185-194                                                      | 950 (95.0)   |
| 195-204                                                      | 1000 (100.0) |
| 205-214                                                      | 1050 (105.0) |
| 215-224                                                      | 1100 (110.0) |
| 225-234                                                      | 1150 (115.0) |
| 235-244                                                      | 1200 (120.0) |
| 245-254                                                      | 1250 (125.0) |
| 255-264                                                      | 1300 (130.0) |
| 265-274                                                      | 1350 (135.0) |
| 275-284                                                      | 1400 (140.0) |
| 285-294                                                      | 1450 (145.0) |
| 295-304                                                      | 1500 (150.0) |
| 305-314                                                      | 1550 (155.0) |
| 315-324                                                      | 1600 (160.0) |
| 325-334                                                      | 1650 (165.0) |
| 335-344                                                      | 1700 (170.0) |
| 345-354                                                      | 1750 (175.0) |
| 355-364                                                      | 1800 (180.0) |
| 365-374                                                      | 1850 (185.0) |
| 375-384                                                      | 1900 (190.0) |
| 385-394                                                      | 1950 (195.0) |
| 395-404                                                      | 2000 (200.0) |
| 405-414                                                      | 2050 (205.0) |
| 415-424                                                      | 2100 (210.0) |
| 425-434                                                      | 2150 (215.0) |
| 435-444                                                      | 2200 (220.0) |
| 445-454                                                      | 2250 (225.0) |
| 455-464                                                      | 2300 (230.0) |
| 465-474                                                      | 2350 (235.0) |
| 475-484                                                      | 2400 (240.0) |
| 485-494                                                      | 2450 (245.0) |
| 495-504                                                      | 2500 (250.0) |
| 505-514                                                      | 2550 (255.0) |
| 515-524                                                      | 2600 (260.0) |
| 525-534                                                      | 2650 (265.0) |
| 535-544                                                      | 2700 (270.0) |
| 545-554                                                      | 2750 (275.0) |
| 555-564                                                      | 2800 (280.0) |
| 565-574                                                      | 2850 (285.0) |
| 575-584                                                      | 2900 (290.0) |
| 585-594                                                      | 2950 (295.0) |
| 595-604                                                      | 3000 (300.0) |
| 605-614                                                      | 3050 (305.0) |
| 615-624                                                      | 3100 (310.0) |
| 625-634                                                      | 3150 (315.0) |
| 635-644                                                      | 3200 (320.0) |
| 645-654                                                      | 3250 (325.0) |
| 655-664                                                      | 3300 (330.0) |
| 665-674                                                      | 3350 (335.0) |
| 675-684                                                      | 3400 (340.0) |
| 685-694                                                      | 3450 (345.0) |
| 695-704                                                      | 3500 (350.0) |
| 705-714                                                      | 3550 (355.0) |
| 715-724                                                      | 3600 (360.0) |
| 725-734                                                      | 3650 (365.0) |
| 735-744                                                      | 3700 (370.0) |
| 745-754                                                      | 3750 (375.0) |
| 755-764                                                      | 3800 (380.0) |
| 765-774                                                      | 3850 (385.0) |
| 775-784                                                      | 3900 (390.0) |
| 785-794                                                      | 3950 (395.0) |
| 795-804                                                      | 4000 (400.0) |
| 805-814                                                      | 4050 (405.0) |
| 815-824                                                      | 4100 (410.0) |
| 825-834                                                      | 4150 (415.0) |
| 835-844                                                      | 4200 (420.0) |
| 845-854                                                      | 4250 (425.0) |
| 855-864                                                      | 4300 (430.0) |
| 865-874                                                      | 4350 (435.0) |
| 875-884                                                      | 4400 (440.0) |
| 885-894                                                      | 4450 (445.0) |
| 895-904                                                      | 4500 (450.0) |
| 905-914                                                      | 4550 (455.0) |
| 915-924                                                      | 4600 (460.0) |
| 925-934                                                      | 4650 (465.0) |
| 935-944                                                      | 4700 (470.0) |
| 945-954                                                      | 4750 (475.0) |
| 955-964                                                      | 4800 (480.0) |
| 965-974                                                      | 4850 (485.0) |
| 975-984                                                      | 4900 (490.0) |
| 985-994                                                      | 4950 (495.0) |
| 995-1004                                                     | 5000 (500.0) |
| 1005-1014                                                    | 5050 (505.0) |
| 1015-1024                                                    | 5100 (510.0) |
| 1025-1034                                                    | 5150 (515.0) |
| 1035-1044                                                    | 5200 (520.0) |
| 1045-1054                                                    | 5250 (525.0) |
| 1055-1064                                                    | 5300 (530.0) |
| 1065-1074                                                    | 5350 (535.0) |
| 1075-1084                                                    | 5400 (540.0) |
| 1085-1094                                                    | 5450 (545.0) |
| 1095-1104                                                    | 5500 (550.0) |
| 1105-1114                                                    | 5550 (555.0) |
| 1115-1124                                                    | 5600 (560.0) |
| 1125-1134                                                    | 5650 (565.0) |
| 1135-1144                                                    | 57           |

1 5 10 15  
Arg Lys Arg Lys Gly Arg Arg Arg Arg Leu Trp Ser Val Lys Asp Pro  
20 25 30  
Thr Ser Gly Leu Ala Met Gly Arg Arg Ile Leu Asn Asp Ala Xaa Arg  
35 40 45  
Thr Met Val Asn Ala Asp Arg Arg Gly Asn Ala Ser Ala Leu Leu Arg  
50 55 60  
Pro Ile Ser Gly Val Met Val Ser Phe Leu Asn Ile Met Lys Tyr Arg  
65 70 75 80  
Gly Tyr Ile Lys Lys Phe Glu Val Ile Asp Glu Asn Arg Val Gly Lys  
85 90 95  
Ile Arg Val Glu Leu Asp Gly Arg Leu Lys Asp Cys Lys Ala Leu Thr  
100 105 110  
Tyr Arg Gln Asp Leu Lys Ala Lys Glu Ile Glu Arg Tyr Arg Val Arg  
115 120 125  
Met Leu Pro Thr Arg Xaa Gly Ala Met Leu  
130 135

(2) INFORMATION FOR SEQ ID NO:1857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1599322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1857:

Met Gly Arg Arg Ile Leu Asn Asp Ala Xaa Arg Thr Met Val Asn Ala  
1 5 10 15  
Asp Arg Arg Gly Asn Ala Ser Ala Leu Leu Arg Pro Ile Ser Gly Val  
20 25 30  
Met Val Ser Phe Leu Asn Ile Met Lys Tyr Arg Gly Tyr Ile Lys Lys  
35 40 45  
Phe Glu Val Ile Asp Glu Asn Arg Val Gly Lys Ile Arg Val Glu Leu  
50 55 60  
Asp Gly Arg Leu Lys Asp Cys Lys Ala Leu Thr Tyr Arg Gln Asp Leu  
65 70 75 80  
Lys Ala Lys Glu Ile Glu Arg Tyr Arg Val Arg Met Leu Pro Thr Arg  
85 90 95  
Xaa Gly Ala Met Leu  
100

(2) INFORMATION FOR SEQ ID NO:1858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1599323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1858:

Met Val Asn Ala Asp Arg Arg Gly Asn Ala Ser Ala Leu Leu Arg Pro  
1 5 10 15  
Ile Ser Gly Val Met Val Ser Phe Leu Asn Ile Met Lys Tyr Arg Gly  
20 25 30  
Tyr Ile Lys Lys Phe Glu Val Ile Asp Glu Asn Arg Val Gly Lys Ile  
35 40 45

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tcagtgagga ttaccctagc aagcctccca agtgcaagtt ccctcagggt ttcttccacc 360  
caaagtgtcta tccttctgga acagtctgtc ttctgatcct taatgaagat agtgggttga 420  
gaccagctat tactgttaag cagattctcg tcgggatcca ggacttgcta gatcagcaaa 480  
tcctgctgat cctgctcaaa cggatggcta tcac

(2) INFORMATION FOR SEQ ID NO:1864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1864:

Lys Phe Tyr Ser Arg Asn Arg Val Glu Lys Lys Lys Val Gln Ser Ser  
1 5 10 15  
Asn Ser Thr Ala Gly Ala Ser Arg Gly Arg Arg Gly Arg Arg Arg Arg  
20 25 30  
His Arg Phe His Val Trp Gly Asn Arg Pro Arg Pro Leu Ala Glu Glu  
35 40 45  
Arg Lys Ala Trp Arg Lys Asn His Pro His Gly Phe Val Ala Lys Pro  
50 55 60  
Glu Ser Leu Pro Asp Gly Thr Val Asn Leu Met Ile Trp His Cys Thr  
65 70 75 80  
Ile Pro Gly Lys Gln Gly Thr Asp Trp Glu Gly Gly Tyr Phe Pro Leu  
85 90 95  
Thr Leu His Phe Ser Glu Asp Tyr Pro Ser Lys Pro Pro Lys Cys Lys  
100 105 110  
Phe Pro Gln Gly Phe Phe His Pro Asn Val Tyr Pro Ser Gly Thr Val  
115 120 125  
Cys Leu Ser Ile Leu Asn Glu Asp Ser Gly Trp Arg Pro Ala Ile Thr  
130 135 140  
Val Lys Gln Ile Leu Val Gly Ile Gln Asp Leu Leu Asp Gln Gln Ile  
145 150 155 160  
Leu Leu Ile Leu Leu Lys Arg Met Ala Ile  
165 170

(2) INFORMATION FOR SEQ ID NO:1865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1865:

Met Ile Trp His Cys Thr Ile Pro Gly Lys Gln Gly Thr Asp Trp Glu  
1 5 10 15  
Gly Gly Tyr Phe Pro Leu Thr Leu His Phe Ser Glu Asp Tyr Pro Ser  
20 25 30  
Lys Pro Pro Lys Cys Lys Phe Pro Gln Gly Phe Phe His Pro Asn Val  
35 40 45  
Tyr Pro Ser Gly Thr Val Cys Leu Ser Ile Leu Asn Glu Asp Ser Gly  
50 55 60  
Trp Arg Pro Ala Ile Thr Val Lys Gln Ile Leu Val Gly Ile Gln Asp  
65 70 75 80  
Leu Leu Asp Gln Gln Ile Leu Leu Ile Leu Leu Lys Arg Met Ala Ile

09609900 10300

85

90

95

(2) INFORMATION FOR SEQ ID NO:1866:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..519
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1866:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| acaatctttc | ttgtatcact | aagctagtgg | ccacaactcg | ttggcaacga | ggaagcagca  | 60  |
| ataagccgag | aagctatgcc | gccgccatat | atggcacagg | ctgccggcac | cgccgatgcc  | 120 |
| actgatgagg | ctccactgct | gctggcctcg | tcggcggcgg | ggtcgacgcc | gtcgcgcgca  | 180 |
| gctgcagcac | cgcgcgggaa | caggttcgcc | ttcgtctgcg | ccacgctcgc | ctccgtcacc  | 240 |
| accatgctac | atggctacaa | cctgacgctg | atgagcggcg | cggagctgtt | catgcggggag | 300 |
| gacgtggggc | tcaccgacgg | cgaggtcgag | gtgctggcgg | gggccatgaa | cgtgttcagt  | 360 |
| ctcgcgtcca | tcctcgcgcg | cggctgagtg | gccgaccacc | tgggacgccg | ccgcaccctc  | 420 |
| gtgctcgcca | acgccttcct | catggccggc | gcgctcgcca | tgctcgtcgg | caccagcttc  | 480 |
| gccgcgctca | tggcggcgcg | cttcgtcaca | gcgtcgggt  |            |             |     |

(2) INFORMATION FOR SEQ ID NO:1867:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1867:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Pro | Pro | Tyr | Met | Ala | Gln | Ala | Gly | Thr | Ala | Asp | Ala | Thr |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Glu | Ala | Pro | Leu | Leu | Leu | Ala | Ser | Ser | Ala | Ala | Gly | Ser | Thr | Pro |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Ser | Pro | Pro | Ala | Ala | Ala | Pro | Arg | Arg | Asn | Arg | Phe | Ala | Phe | Val | Cys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Thr | Leu | Ala | Ser | Val | Thr | Thr | Met | Leu | His | Gly | Tyr | Asn | Leu | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Met | Ser | Gly | Ala | Glu | Leu | Phe | Met | Arg | Glu | Asp | Val | Gly | Leu | Thr |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Gly | Glu | Val | Glu | Val | Leu | Ala | Gly | Ser | Met | Asn | Val | Phe | Met | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Ser | Ile | Leu | Ala | Ala | Gly |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     | 100 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599365

00000000 00000000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1868:  
Met Ala Gln Ala Ala Gly Thr Ala Asp Ala Thr Asp Glu Ala Pro Leu  
1 5 10 15  
Leu Leu Ala Ser Ser Ala Ala Gly Ser Thr Pro Ser Pro Pro Ala Ala  
20 25 30  
Ala Pro Arg Arg Asn Arg Phe Ala Phe Val Cys Ala Thr Leu Ala Ser  
35 40 45  
Val Thr Thr Met Leu His Gly Tyr Asn Leu Thr Leu Met Ser Gly Ala  
50 55 60  
Glu Leu Phe Met Arg Glu Asp Val Gly Leu Thr Asp Gly Glu Val Glu  
65 70 75 80  
Val Leu Ala Gly Ser Met Asn Val Phe Met Leu Ala Ser Ile Leu Ala  
85 90 95  
Ala Gly

(2) INFORMATION FOR SEQ ID NO:1869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..455
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1869:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| actgctccct ctcacggacg cttcgtctta gtcggaaggt ttcgaggaaac tcccgggctc | 60  |
| gaggagatcg ggacgatgat gggagggcgc gctctgctgc tgctcctggt ctcggcgctg  | 120 |
| ctcgttcaga tccgcgcctc tgaccgcgtg ctgtacgagc cgttcgatga ggacttcgag  | 180 |
| ggaagatgga tcgtctccaa gaaggatgaa taccaaggtg tatggaagca tgccaagagt  | 240 |
| gatgggcatg aggactatgg tctccttggt agtgacaaag caaggaaata cgccataatc  | 300 |
| aaggagcttg atgagccagt taccttaaag gatgggacag tggtcctgca gtttgaagtg  | 360 |
| agacttcaga atggcyytga atgtggaggt gcctacatta agtacatccg ccctcaggat  | 420 |
| gctggatggg atgccaagga gtttgayaat gagac                             |     |

(2) INFORMATION FOR SEQ ID NO:1870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1870:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Thr Ala Pro Ser His Gly Arg Phe Ala Leu Val Gly Arg Phe Arg Gly |  |
| 1 5 10 15                                                       |  |
| Thr Pro Gly Leu Glu Glu Ile Gly Thr Met Met Gly Gly Arg Ala Leu |  |
| 20 25 30                                                        |  |
| Leu Leu Leu Leu Val Ser Ala Leu Leu Val Gln Ile Arg Ala Ser Asp |  |
| 35 40 45                                                        |  |
| Pro Leu Leu Tyr Glu Pro Phe Asp Glu Asp Phe Glu Gly Arg Trp Ile |  |
| 50 55 60                                                        |  |
| Val Ser Lys Lys Asp Glu Tyr Gln Gly Val Trp Lys His Ala Lys Ser |  |
| 65 70 75 80                                                     |  |
| Asp Gly His Glu Asp Tyr Gly Leu Leu Val Ser Asp Lys Ala Arg Lys |  |
| 85 90 95                                                        |  |
| Tyr Ala Ile Ile Lys Glu Leu Asp Glu Pro Val Thr Leu Asn Asp Gly |  |
| 100 105 110                                                     |  |

00000000 00000000





115 120 125

(2) INFORMATION FOR SEQ ID NO:1873:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 487 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..487

(D) OTHER INFORMATION: / Ceres Seq. ID 1599385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1873:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ctcgagcctg acccttacgc cttcgctcgc gccgccgcgc gccgccgcta cgccccgcac  | 60  |
| ctcgcttcat ttcgtgtcgc caagatgacg aagcgacta agaaggcagg aattgttggc   | 120 |
| aaatatggaa ccaggtatgg tgctagcttg cgtaagcaaa tcaagaagat ggaggtatct  | 180 |
| cagcattcca agtacttttg cgagttctgt gggaagtttg ctgtgaagag gaaagcagtt  | 240 |
| ggaatttggg ggtgcaagga ctgtgggaag gtgaaggctg gtggtgcggc caaccgccgg  | 300 |
| caggccccggc ggccggcagc tgggtgcgtg cgaacgcggc cgtcggggac gacaggctgc | 360 |
| agcaggcgct ggactacgcg tgcggccacg gggcggactg cagcgccatc cagcccagcg  | 420 |
| ggtcgtgctt cgagccggac accaagctcg cgcacgcctc gtatgcgttc gacagctact  | 480 |
| accagcg                                                            |     |

(2) INFORMATION FOR SEQ ID NO:1874:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1599386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1874:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Leu Glu Pro Asp Pro Tyr Ala Phe Ala Arg Ala Ala Arg Arg Arg     |  |
| 1 5 10 15                                                       |  |
| Tyr Ala Pro His Leu Ala Ser Phe Arg Val Ala Lys Met Thr Lys Arg |  |
| 20 25 30                                                        |  |
| Thr Lys Lys Ala Gly Ile Val Gly Lys Tyr Gly Thr Arg Tyr Gly Ala |  |
| 35 40 45                                                        |  |
| Ser Leu Arg Lys Gln Ile Lys Lys Met Glu Val Ser Gln His Ser Lys |  |
| 50 55 60                                                        |  |
| Tyr Phe Cys Glu Phe Cys Gly Lys Phe Ala Val Lys Arg Lys Ala Val |  |
| 65 70 75 80                                                     |  |
| Gly Ile Trp Gly Cys Lys Asp Cys Gly Lys Val Lys Ala Gly Gly Ala |  |
| 85 90 95                                                        |  |
| Ala Asn Arg Arg Gln Ala Arg Arg Arg Ala Gly Ala Trp Arg Thr     |  |
| 100 105 110                                                     |  |
| Arg Pro Ser Gly Thr Thr Gly Cys Ser Arg Arg Trp Thr Thr Arg Ala |  |
| 115 120 125                                                     |  |
| Ala Thr Gly Arg Thr Ala Ala Pro Ser Ser Pro Ala Gly Arg Ala Ser |  |
| 130 135 140                                                     |  |
| Ser Arg Thr Pro Ser Ser Arg Thr Pro Arg Met Arg Ser Thr Ala Thr |  |
| 145 150 155 160                                                 |  |
| Thr Ser                                                         |  |

(2) INFORMATION FOR SEQ ID NO:1875:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

09669900-10100

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..134  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599387  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1875:

Met Thr Lys Arg Thr Lys Lys Ala Gly Ile Val Gly Lys Tyr Gly Thr  
1                   5                   10                   15  
Arg Tyr Gly Ala Ser Leu Arg Lys Gln Ile Lys Lys Met Glu Val Ser  
          20                   25                   30  
Gln His Ser Lys Tyr Phe Cys Glu Phe Cys Gly Lys Phe Ala Val Lys  
          35                   40                   45  
Arg Lys Ala Val Gly Ile Trp Gly Cys Lys Asp Cys Gly Lys Val Lys  
          50                   55                   60  
Ala Gly Gly Ala Ala Asn Arg Arg Gln Ala Arg Arg Arg Arg Ala Gly  
65                   70                   75                   80  
Ala Trp Arg Thr Arg Pro Ser Gly Thr Thr Gly Cys Ser Arg Arg Trp  
          85                   90                   95  
Thr Thr Arg Ala Ala Thr Gly Arg Thr Ala Ala Pro Ser Ser Pro Ala  
          100                   105                   110  
Gly Arg Ala Ser Ser Arg Thr Pro Ser Ser Arg Thr Pro Arg Met Arg  
          115                   120                   125  
Ser Thr Ala Thr Thr Ser  
          130

(2) INFORMATION FOR SEQ ID NO:1876:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 106 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..106  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1876:

Met Glu Val Ser Gln His Ser Lys Tyr Phe Cys Glu Phe Cys Gly Lys  
1                   5                   10                   15  
Phe Ala Val Lys Arg Lys Ala Val Gly Ile Trp Gly Cys Lys Asp Cys  
          20                   25                   30  
Gly Lys Val Lys Ala Gly Gly Ala Ala Asn Arg Arg Gln Ala Arg Arg  
          35                   40                   45  
Arg Arg Ala Gly Ala Trp Arg Thr Arg Pro Ser Gly Thr Thr Gly Cys  
          50                   55                   60  
Ser Arg Arg Trp Thr Thr Arg Ala Ala Thr Gly Arg Thr Ala Ala Pro  
65                   70                   75                   80  
Ser Ser Pro Ala Gly Arg Ala Ser Ser Arg Thr Pro Ser Ser Arg Thr  
          85                   90                   95  
Pro Arg Met Arg Ser Thr Ala Thr Thr Ser  
          100                   105

(2) INFORMATION FOR SEQ ID NO:1877:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 417 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
    (B) LOCATION: 1..417

09639930.10300

(D) OTHER INFORMATION: / Ceres Seq. ID 1599393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1877:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| accactccca  | gtccagttct | cccaccgtcc | cacgaaacac | actcaactct | gccccgaagc | 60  |
| ggagaaccgc  | cagccagaca | tgaaggagaa | ccagagcgca | gcagcccaag | gtcgaggagc | 120 |
| cgcaggacct  | cgccgccaac | ctaaagccgc | agcgccggga | caaacagccg | aggcagccca | 180 |
| agtcaggcgc  | caaagcgaag | cccgcggcgg | gcccgcgcgt | cgcgggcgcc | acgaccctcg | 240 |
| ccgcgcgcgc  | cgccgcagca | gcagcagcag | caaatgccgc | ctcgggcgcg | tcgtcgcccg | 300 |
| ggccggaaac  | ggctccgacc | gtgccggacg | tgtgcgtcgg | cggggacaag | gacggggacg | 360 |
| cggaacgcgga | cgcgagcgcg | tggactggga | cctcgacgcc | gggctgagcg | cggcgcgc   |     |

(2) INFORMATION FOR SEQ ID NO:1878:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1599394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1878:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Leu | Pro | Val | Pro | Val | Ser | His | Arg | Pro | Thr | Lys | His | Thr | Gln | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Pro | Glu | Ala | Glu | Asn | Arg | Gln | Pro | Asp | Met | Lys | Glu | Asn | Gln | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ala | Ala | Ala | Gln | Gly | Arg | Gly | Ala | Ala | Gly | Pro | Arg | Arg | Gln | Pro | Lys |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Ala | Ala | Ala | Pro | Gly | Gln | Thr | Ala | Glu | Ala | Ala | Gln | Val | Arg | Arg | Gln |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Ser | Glu | Ala | Arg | Gly | Gly | Pro | Ala | Arg | Arg | Gly | Gly | His | Asp | Pro | Arg |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Arg | Arg | Arg | Arg | Ser | Ser | Ser | Ser | Ser | Lys | Cys | Arg | Leu | Gly | Arg |
|     |     |     |     |     |     | 85  |     |     |     | 90  |     |     |     | 95  |     |
| Val | Val | Ala | Arg | Ala | Gly | Asn | Gly | Ser | Asp | Arg | Ala | Gly | Arg | Val | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Arg | Arg | Gly | Gln | Gly | Arg | Gly | Arg | Gly | Arg | Gly | Arg | Glu | Arg | Val | Asp |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Trp | Asp | Leu | Asp | Ala | Gly | Leu | Ser | Ala | Ala |     |     |     |     |     |     |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1879:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1599395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1879:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Glu | Asn | Gln | Ser | Ala | Ala | Ala | Gln | Gly | Arg | Gly | Ala | Ala | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Arg | Arg | Gln | Pro | Lys | Ala | Ala | Ala | Pro | Gly | Gln | Thr | Ala | Glu | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ala | Gln | Val | Arg | Arg | Gln | Ser | Glu | Ala | Arg | Gly | Gly | Pro | Ala | Arg | Arg |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Gly | Gly | His | Asp | Pro | Arg | Arg | Arg | Arg | Arg | Arg | Ser | Ser | Ser | Ser | Ser |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Lys | Cys | Arg | Leu | Gly | Arg | Val | Val | Ala | Arg | Ala | Gly | Asn | Gly | Ser | Asp |
| 65  |     |     |     |     |     | 70  |     |     |     |     |     | 75  |     |     | 80  |



(2) INFORMATION FOR SEQ ID NO:1883:

(A) LENGTH: 369 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (q

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..369

(D) OTHER INFORMATION: / Ceres Seq. ID 1599403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1883:

|            |            |             |            |             |            |     |
|------------|------------|-------------|------------|-------------|------------|-----|
| accatcgcaa | ttcacaagca | aagcaatcag  | agccaagcac | ccaccgtcct  | cctttttttt | 60  |
| cttcgactca | tcaaagcatg | totttgetgcg | gcggcaactg | cgcgtgcacc  | tccgggtgca | 120 |
| actgcggcag | cggatgcggc | gactgcaaca  | cctgcaactg | cggcaccagc  | tgcgggtgct | 180 |
| cctgctgcag | ctgcaactga | gccacccgcg  | atgacgagac | aaccacccgg  | cctccccccc | 240 |
| atcgtactac | aactatgtag | cggcgtctaa  | ataagatccc | tccaccggcc  | accgccattg | 300 |
| ttccttctcg | tcgctgcatg | gttgccctgcc | tcgtgcccg  | gctaataatac | atatacgggg | 360 |
| gtgttttgg  |            |             |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:1884:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1599404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1884:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1885:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1599405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1885:

Pro Ser Gln Phe Thr Ser Lys Ala Ile Arg Ala Lys His Pro Pro Ser

1 5 10 15  
Ser Phe Leu Ser Phe Asp Ser Ser Lys His Val Leu Leu Arg Arg Gln  
20 25 30  
Leu Arg Val His Leu Arg Leu Gln Leu Arg Gln Arg Met Arg Arg Leu  
35 40 45  
Gln His Leu Gln Leu Arg His Gln Leu Arg Leu Leu Leu Leu Gln Leu  
50 55 60  
Gln Leu Ser His Pro Arg  
65 70

(2) INFORMATION FOR SEQ ID NO:1886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1599406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1886:

His Arg Asn Ser Gln Ala Lys Gln Ser Glu Pro Ser Thr His Arg Pro  
1 5 10 15  
Pro Phe Phe Pro Ser Thr His Gln Ser Met Ser Cys Cys Gly Gly Asn  
20 25 30  
Cys Ala Cys Thr Ser Gly Cys Asn Cys Gly Ser Gly Cys Gly Asp Cys  
35 40 45  
Asn Thr Cys Asn Cys Gly Thr Ser Cys Gly Cys Ser Cys Cys Ser Cys  
50 55 60

Asn

65

(2) INFORMATION FOR SEQ ID NO:1887:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..508

(D) OTHER INFORMATION: / Ceres Seq. ID 1599416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1887:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aagcccactt tccccagtac tctactcacc caccactca cggactcatc tactgagcag  | 60  |
| cgcggtgggc atccgagcga gagggcgagc gcggaaggat cggaattccg aaggttgggc | 120 |
| atggaggcga gcggcgagaa ggctgcggtg gtgacgagc tgatggaggc gaaggaggtg  | 180 |
| tccgggaaga ccttctcggg aatcgccgcc gagacgggtc tcaccaacgt ctacgtggcg | 240 |
| cagctgctgc ggcgccaggc gcagctcaag gccgacacgg tgcccgcgct gagggcgggc | 300 |
| ctgcccacgc tcacggacga cctcatcgaa ctcatgatgc agccgccctt ccggtcctac | 360 |
| cacccaaca tcgtccacga gcccgccatt tacagattga atgaagctgt tatgcatttt  | 420 |
| ggagagagca tcaaggaaat catcaatgag gagtttggtg atggaatcat gtcagccata | 480 |
| gacttctatt gttcagttga caaggttg                                    |     |

(2) INFORMATION FOR SEQ ID NO:1888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

DOCKET# 08663360

(B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1599417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1888:

Lys Pro Thr Phe Pro Ser Thr Leu Leu Thr His Pro Leu Thr Asp Ser  
1 5 10 15  
Ser Thr Glu Gln Arg Gly Gly His Pro Ser Glu Arg Ala Ser Ala Glu  
20 25 30  
Gly Ser Glu Phe Arg Arg Leu Gly Met Glu Ala Ser Gly Glu Lys Ala  
35 40 45  
Ala Val Val Arg Arg Leu Met Glu Ala Lys Glu Val Ser Gly Lys Thr  
50 55 60  
Phe Ser Gly Ile Ala Ala Glu Thr Gly Leu Thr Asn Val Tyr Val Ala  
65 70 75 80  
Gln Leu Leu Arg Arg Gln Ala Gln Leu Lys Ala Asp Thr Val Pro Ala  
85 90 95  
Leu Arg Ala Ala Leu Pro Thr Leu Thr Asp Asp Leu Ile Glu Leu Met  
100 105 110  
Met Gln Pro Pro Phe Arg Ser Tyr His Pro Asn Ile Val His Glu Pro  
115 120 125  
Ala Ile Tyr Arg Leu Asn Glu Ala Val Met His Phe Gly Glu Ser Ile  
130 135 140  
Lys Glu Ile Ile Asn Glu Glu Phe Gly Asp Gly Ile Met Ser Ala Ile  
145 150 155 160  
Asp Phe Tyr Cys Ser Val Asp Lys Val  
165

(2) INFORMATION FOR SEQ ID NO:1889:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1599418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1889:

Met Glu Ala Ser Gly Glu Lys Ala Ala Val Val Arg Arg Leu Met Glu  
1 5 10 15  
Ala Lys Glu Val Ser Gly Lys Thr Phe Ser Gly Ile Ala Ala Glu Thr  
20 25 30  
Gly Leu Thr Asn Val Tyr Val Ala Gln Leu Leu Arg Arg Gln Ala Gln  
35 40 45  
Leu Lys Ala Asp Thr Val Pro Ala Leu Arg Ala Ala Leu Pro Thr Leu  
50 55 60  
Thr Asp Asp Leu Ile Glu Leu Met Met Gln Pro Pro Phe Arg Ser Tyr  
65 70 75 80  
His Pro Asn Ile Val His Glu Pro Ala Ile Tyr Arg Leu Asn Glu Ala  
85 90 95  
Val Met His Phe Gly Glu Ser Ile Lys Glu Ile Ile Asn Glu Glu Phe  
100 105 110  
Gly Asp Gly Ile Met Ser Ala Ile Asp Phe Tyr Cys Ser Val Asp Lys  
115 120 125  
Val

(2) INFORMATION FOR SEQ ID NO:1890:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..115  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599419  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1890:

Met Glu Ala Lys Glu Val Ser Gly Lys Thr Phe Ser Gly Ile Ala Ala  
1                    5                    10                    15  
Glu Thr Gly Leu Thr Asn Val Tyr Val Ala Gln Leu Leu Arg Arg Gln  
                    20                    25                    30  
Ala Gln Leu Lys Ala Asp Thr Val Pro Ala Leu Arg Ala Ala Leu Pro  
                    35                    40                    45  
Thr Leu Thr Asp Asp Leu Ile Glu Leu Met Met Gln Pro Pro Phe Arg  
                    50                    55                    60  
Ser Tyr His Pro Asn Ile Val His Glu Pro Ala Ile Tyr Arg Leu Asn  
65                    70                    75                    80  
Glu Ala Val Met His Phe Gly Glu Ser Ile Lys Glu Ile Ile Asn Glu  
                    85                    90                    95  
Glu Phe Gly Asp Gly Ile Met Ser Ala Ile Asp Phe Tyr Cys Ser Val  
                    100                    105                    110  
Asp Lys Val  
                    115

(2) INFORMATION FOR SEQ ID NO:1891:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 485 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..485  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1891:

ggcagtagaa gccgagaagg taggcccgcgt cgttccaaca tcacaaactc cacacggctc                    60  
tcctgtctcc gctgcccgcgt ccacctccct ccatgccgtc ggcttccctc cgcctcgccg                    120  
tcgtcggcgc gggcgcgccg gccctggttg ccgccgcga gctacgccgc gagggccatg                    180  
cgcccgctcgt cttcgagcgc gccgcgcgcg ttgggggcac ttggctctac acgcctcccg                    240  
ccacgtcctc cgaccgcgtc ggcgccgcgg cgacgcattc cagcctctac gcatcgctcc                    300  
gcaccaacct gccacgcgag accatgggct tcctcgactt ccccttcgcc gctggcgccg                    360  
cgggctcccg agacccccgc cggtttcccg ggcacgagga ggtgctccgc tacctggagg                    420  
cgttcgcgcg cgggttcgac ctgctccggc tcgtccgctt cgagacggag gtgctcagtg                    480  
tgagg

(2) INFORMATION FOR SEQ ID NO:1892:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 160 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..160  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1892:

Gly Ser Arg Ser Arg Glu Gly Arg Pro Ala Arg Ser Asn Ile Thr Asn  
1                    5                    10                    15  
Ser Thr Arg Leu Ser Cys Leu Arg Cys Pro Leu His Leu Pro Pro Cys  
                    20                    25                    30  
Arg Arg Leu Pro Ser Ala Ser Pro Ser Ser Ala Arg Ala Arg Arg Ala  
                    35                    40                    45

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(2) INFORMATION FOR SEQ ID NO:1893:

(A) LENGTH: 161 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..161  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599426

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..131  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599427

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1894:

Met Pro Ser Ala Ser Leu Arg Leu Ala Val Val Gly Ala Gly Ala Ala  
1 5 10 15  
Gly Leu Val Ala Ala Arg Glu Leu Arg Arg Glu Gly His Ala Pro Val  
20 25 30  
Val Phe Glu Arg Ala Ala Ala Val Gly Gly Thr Trp Leu Tyr Thr Pro  
35 40 45  
Pro Ala Thr Ser Ser Asp Pro Leu Gly Ala Ala Ala Thr His Ser Ser  
50 55 60  
Leu Tyr Ala Ser Leu Arg Thr Asn Leu Pro Arg Glu Thr Met Gly Phe  
65 70 75 80  
Leu Asp Phe Pro Phe Ala Ala Gly Ala Ala Gly Ser Arg Asp Pro Arg  
85 90 95  
Arg Phe Pro Gly His Glu Glu Val Leu Arg Tyr Leu Glu Ala Phe Ala  
100 105 110  
Arg Arg Phe Asp Leu Leu Arg Leu Val Arg Phe Glu Thr Glu Val Leu  
115 120 125  
Ser Val Arg  
130

(2) INFORMATION FOR SEQ ID NO:1895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..500
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1895:

atcacccct accagtttca attttcaaaa gggcgtggag gcgccgcacc accgccgccg 60  
ccaccactga cgagggagga aacgccacct ccccgagcca gtccgatgtt gtccgaccag 120  
gagctggccc agtacgtgga gtccctcgtc cagcacaccg ctgcgcaggg tggcaccggg 180  
atatcggcgg atgccgtggt gcgccagctc ggggcgcagc tcggcggttg cctctcccc 240  
aaggcgcagc tcatccgcag cgtcctcgtc gcgctcctcg gccccgcggc cgcgcggcg 300  
ccggaccccc cgggttcgcg taaggatccc ttcgaccccc caaccgctgc cgcgcggcg 360  
gggccccgcg ccgagactcc tccacagcag atgcacttct ctaccgcccgc cgcgtcgtcg 420  
gccccgccc cttctccagc cggtccccac ttcttcccgc agcagcacca gcaccagatg 480  
cagtacttcc tgtccgcccc

(2) INFORMATION FOR SEQ ID NO:1896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..166
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1896:

Ile Thr Pro Tyr Gln Phe Gln Phe Ser Lys Gly Arg Gly Gly Ala Ala  
1 5 10 15  
Pro Pro Pro Pro Pro Pro Leu Thr Arg Glu Glu Thr Pro Pro Pro Arg  
20 25 30  
Ala Ser Pro Met Leu Ser Asp Gln Glu Leu Ala Gln Tyr Val Glu Ser  
35 40 45  
Leu Val Gln His Thr Ala Ala Gln Gly Gly Thr Gly Ile Ser Ala Asp  
50 55 60  
Ala Val Val Arg Gln Leu Gly Ala Gln Leu Gly Val Asp Leu Ser Pro

0969990300

| (X1) SEQUENCE DESCRIPTION: Seq 1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|----------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met                              | Pro | Trp | Cys | Ala | Ser | Ser | Gly | Arg | Ser | Ser | Ala | Leu | Thr | Ser | Pro |  |
| 1                                |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Pro                              | Arg | Arg | Ser | Ser | Ser | Ala | Ala | Ser | Ser | Ser | Arg | Ser | Ser | Ala | Pro |  |
|                                  |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg                              | Pro | Arg | Arg | Arg | Arg | Thr | Pro | Arg | Val | Arg | Val | Arg | Ile | Pro | Ser |  |
|                                  |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1899:

(A) LENGTH: 414 base pairs

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..414

(D) OTHER INFORMATION: / Ceres Seq. ID 1599438

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:1055 |            |            |            |            |            |  |     |  |
|-------------------------------------------|------------|------------|------------|------------|------------|--|-----|--|
| gctccaccac                                | cacctcacca | tctccactcc | aaacaaggcg | aaggcgagcg | acagacaaac |  | 60  |  |
| ccaccccatc                                | gccctctctc | tgtctctctc | cttgcccacg | cccgcccca  | tgtgcgcgcc |  | 120 |  |
| cctcgagccc                                | cacgactaca | tggcctctc  | cgccgcggcc | gcggccgcgc | cgcgaccccc |  | 180 |  |
| gacctctctc                                | tctcttctc  | ctctctcgcc | ggccccccgc | ctcacccttc | gctctggcct |  | 240 |  |
| gccgggctcc                                | gagtccccc  | accgcgaccg | ggactgctgc | gaggactctc | cgccacagct |  | 300 |  |
| ctccctcgcc                                | ccgctgcggg | cgcgcagcgc | cgtctctgcc | aagcgcgcct | tcccggaccc |  | 360 |  |
| cgcccaqcg                                 | cccggcctt  | cgaaggctag | cgacgccaa  | cagcagctt  | cccc       |  |     |  |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1599439

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1903:

(2) INFORMATION FOR SEQ ID NO:1904:

(ii) MOLECULE TYPE: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1599444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1904:

(2) INFORMATION FOR SEQ ID NO:1905:

(ii) MOLECULE TYPE: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1599445

| (X1) SEQUENCE DESCRIPTION: SEQ ID NUMBER |            |            |            |            |            |  |     |
|------------------------------------------|------------|------------|------------|------------|------------|--|-----|
| gaaaaataaa                               | gaagagagag | aaaaagaaaa | aggagaggcc | cgcgactgta | gtgggattgt |  | 60  |
| gggaagatgc                               | ctcgggatgg | cgcgcaggcg | gcgcgcaccg | gagcgcggcg | agatggacga |  | 120 |
| ggtggtagag                               | gcggaccocg | atacggaggc | ggaggatcag | gaggagaggt | gggcgaggct |  | 180 |
| gctgcggagc                               | tgctctccga | cgtggtgcgg | cgcgtcgagg | cgtccggcgg | cgagcgggtg |  | 240 |
| cgggcgcgga                               | aggacgtcgt | ctctctgcgc | tgcgtgtgcc | gccggtggcg | ggacgcgcgc |  | 300 |
| gtctccgtcg                               | tgctgcgcgc | ggcggagtc  | ggcaagatca | cct        |            |  |     |

(2) INFORMATION FOR SEQ ID NO:1908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1908:

Met Pro Arg Asp Gly Ala Gln Ala Ala Arg Thr Gly Ala Arg Arg Asp  
1 5 10 15  
Gly Arg Gly Gly Arg Gly Gly Pro Gly Tyr Gly Gly Gly Gly Ser Gly  
20 25 30  
Gly Glu Val Gly Glu Ala Ala Ala Glu Leu Leu Ser Asp Val Val Arg  
35 40 45  
Arg Val Glu Ala Ser Gly Gly Glu Arg Trp Pro Ala Arg Lys Asp Val  
50 55 60  
Val Ser Cys Ala Cys Val Cys Arg Arg Trp Arg Asp Ala Ala Val Ser  
65 70 75 80  
Val Val Arg Pro Pro Ala Glu Ser Gly Lys Ile Thr  
85 90

(2) INFORMATION FOR SEQ ID NO:1909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1909:

Met Ala Arg Arg Arg Arg Ala Pro Glu Arg Gly Glu Met Asp Glu Val  
1 5 10 15  
Val Glu Ala Asp Pro Asp Thr Glu Ala Glu Asp Gln Glu Glu Arg Trp  
20 25 30  
Ala Arg Leu Leu Arg Ser Cys Ser Pro Thr Trp Cys Gly Ala Ser Arg  
35 40 45  
Arg Pro Ala Ala Ser Gly Gly Arg Arg Gly Arg Thr Ser Ser Pro Ala  
50 55 60  
Pro Ala Cys Ala Ala Gly Gly Gly Thr Pro Pro Ser Pro Ser Cys Val  
65 70 75 80  
Arg Arg Arg Ser Pro Ala Arg Ser Pro  
85

(2) INFORMATION FOR SEQ ID NO:1910:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1910:

Met Asp Glu Val Val Glu Ala Asp Pro Asp Thr Glu Ala Glu Asp Gln

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(2) INFORMATION FOR SEQ ID NO:1911:

(A) LENGTH: 450 base pairs

(C) STRANDEDNESS: sing

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (a

(A) NAME/KEY: -

(B) LOCATION: 1..450

(D) OTHER INFORMATION: / Ceres Seq. ID 1599454

| (X1) SEQUENCE DESCRIPTION: S12 T1 AATCTG                           |     |
|--------------------------------------------------------------------|-----|
| accgtgcagc ggcaagggtg tccaggtccc gtaaaatctg gctttttctcc ctccccatac | 60  |
| cccgcacaca cactcgcttt cttcggttct tctctctcga gcagccactt cgtctcttaa  | 120 |
| ccctacagcg acgacgagag cgaggctatg aaggggaaga agccgggtcaa ggagctcaag | 180 |
| ctcaccgctgc cggcgcagga gaccccggtg gacaagttcc tgacggcaag tggcacgttc | 240 |
| aaggatggtg agctgaggct caatcacagc ggcttcggcg ttatctctga ggaaaacggg  | 300 |
| gatgaagatg aatctacaaa cctgaagggt gaagatgtcg agtatctaat ggatgatctt  | 360 |
| gagatgattc aagtcatgtg caaaggaagc ggtggtgttg tccagctagt gaggcacaaa  | 420 |
| tgggtgggca cattgtttgc cttaaagggt                                   |     |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1599455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1912:

(2) INFORMATION FOR SEQ ID NO:1913:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1913:

(2) INFORMATION FOR SEQ ID NO:1914:

(A) LENGTH: 500 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..500

(D) OTHER INFORMATION: / Ceres Seq. ID 1599461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1914:

(2) INFORMATION FOR SEQ ID NO:1915:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1599462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1915:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Gln | Ile | Pro |     | His | Ala | Ser | Ala | Ala | Asp | Asp | Asp | His | Arg | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Arg | Leu | Pro | Pro | Leu | Arg | Arg | Ile | Arg | His | Ala | Arg | Arg | Pro | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Gly | Pro | Gly | Gly | Leu | Leu | Gln | Gly | Thr | Gly | Cys | Leu | Leu | Arg | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Arg | Glu | Ala | Arg | Gly | Gln | Lys | Ala | His | Arg | Asp | Arg | His | His | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Pro | Leu | Pro | Arg | Arg | Leu | Gln | Lys | Val | Pro | Arg | Arg | Leu | Arg | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

Gln Leu Pro Pro His Leu Gly Gln Ala Leu Arg Pro Ala Val Leu Arg  
85 90 95  
Gln Glu Ala Gly Ala Glu Ala Ala Arg Arg Arg Trp Gly Pro Pro Gly  
100 105 110  
Pro His Val Ala Ala Pro Ala Leu His Leu Gln Ala Ile Gly Ser Leu  
115 120 125  
Pro Val Val Gln Ile Leu Val Leu Ser Ser Ile Gly Ser Val Leu Arg  
130 135 140  
Trp Cys Leu Asp Ala Ile Val Leu Val Ser Gly Phe Val Ser Phe Ser  
145 150 155 160  
Trp Met His Met

(2) INFORMATION FOR SEQ ID NO:1916:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1599463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1916:

Asn Lys Ser Pro Arg Thr Pro Pro Gln Pro Thr Met Thr Thr Ala Ala  
1 5 10 15  
Asp Asp Tyr His His Ser Asp Gly Phe Val Met Pro Asp Val Leu Ala  
20 25 30  
Lys Gly Arg Glu Ala Cys Tyr Lys Ala Arg Asp Ala Phe Tyr Ala Cys  
35 40 45  
Ile Glu Lys His Ala Asp Lys Lys Pro Thr Glu Ile Ala Thr Met Gly  
50 55 60  
Leu Leu Tyr Pro Ala Asp Cys Lys Lys Ser Arg Ala Asp Phe Val Ser  
65 70 75 80  
Asn Cys Arg Pro Thr Trp Val Lys His Phe Asp Arg Gln Tyr Ser Ala  
85 90 95  
Lys Lys Arg Val Gln Arg Leu Leu Asp Gly Asp Gly Asp Arg Arg Gly  
100 105 110  
Pro Met Ser Leu Pro Gln Pro Tyr Thr Phe Lys Gln  
115 120

(2) INFORMATION FOR SEQ ID NO:1917:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1599464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1917:

Met Thr Thr Ala Ala Asp Asp Tyr His His Ser Asp Gly Phe Val Met  
1 5 10 15  
Pro Asp Val Leu Ala Lys Gly Arg Glu Ala Cys Tyr Lys Ala Arg Asp  
20 25 30  
Ala Phe Tyr Ala Cys Ile Glu Lys His Ala Asp Lys Lys Pro Thr Glu  
35 40 45  
Ile Ala Thr Met Gly Leu Leu Tyr Pro Ala Asp Cys Lys Lys Ser Arg  
50 55 60  
Ala Asp Phe Val Ser Asn Cys Arg Pro Thr Trp Val Lys His Phe Asp

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(2) INFORMATION FOR SEQ ID NO:1918:

| (X1) SEQUENCE DESCRIPTION |             |            |            |            |            | 60  |
|---------------------------|-------------|------------|------------|------------|------------|-----|
| gcgcaagcgc                | aagaaagggg  | gagcgcaaca | ttcgcgcgcg | cggggagggg | gagagacaag | 60  |
| gggggcgctg                | acacacacgc  | ggaccgcgcg | agctagcgag | cgagcgagat | ccccctctcg | 120 |
| cgctgctgga                | tccgatctga  | cctgacctta | cctcgtcgcc | gccagccgtg | agagagagaa | 180 |
| gaggaagagg                | aggaggaggc  | ggagatggca | ccggtgtcgg | cgctcgccaa | gtacaagctc | 240 |
| gtcttcctgg                | gggaccagtc  | cgtcggcaag | accagcatca | tcaccgcgtt | catgtacgat | 300 |
| aagttcgaca                | acacttacca  | ggctacaatt | ggtattgatt | tcctgtcaaa | gacaatgtac | 360 |
| cttgaagata                | gaactgtgag  | actocaactc | tgggatacag | ctggtcagga | aaggttcagg | 420 |
| agtttaattc                | caaagctatat | cagagactct | tcagttgctg | tcatt      |            |     |

| (X1) SEQUENCE DESCRIPTION: 322 18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------------------------------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg                                                                         | Lys | Arg | Lys | Lys | Gly | Gly | Ala | Gln | His | Ser | Arg | Pro | Arg | Gly | Gly |
| 1                                                                           |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg                                                                         | Glu | Thr | Arg | Gly | Ala | Val | Thr | His | Thr | Arg | Thr | Ala | Arg | Ala | Ser |
|                                                                             |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu                                                                         | Arg | Ala | Arg | Ser | Pro | Ser | Arg | Ala | Ala | Gly | Ser | Asp | Leu | Thr |     |
|                                                                             |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Pro | Val | Ser | Ala | Leu | Ala | Lys | Tyr | Lys | Leu | Val | Phe | Leu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Gln | Ser | Val | Gly | Lys | Thr | Ser | Ile | Ile | Thr | Arg | Phe | Met | Tyr | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

Lys Phe Asp Asn Thr Tyr Gln Ala Thr Ile Gly Ile Asp Phe Leu Ser  
35 40 45  
Lys Thr Met Tyr Leu Glu Asp Arg Thr Val Arg Leu Gln Leu Trp Asp  
50 55 60  
Thr Ala Gly Gln Glu Arg Phe Arg Ser Leu Ile Pro Ser Tyr Ile Arg  
65 70 75 80  
Asp Ser Ser Val Ala Val Ile  
85

(2) INFORMATION FOR SEQ ID NO:1921:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1599477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1921:

Met Tyr Asp Lys Phe Asp Asn Thr Tyr Gln Ala Thr Ile Gly Ile Asp  
1 5 10 15  
Phe Leu Ser Lys Thr Met Tyr Leu Glu Asp Arg Thr Val Arg Leu Gln  
20 25 30  
Leu Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Ser Leu Ile Pro Ser  
35 40 45  
Tyr Ile Arg Asp Ser Ser Val Ala Val Ile  
50 55

(2) INFORMATION FOR SEQ ID NO:1922:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 498 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..498

(D) OTHER INFORMATION: / Ceres Seq. ID 1599487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1922:

aataaatccc ccgcctccct gctctcctcc gtaaatcaca aaacttygcc caattcccca 60  
ctagcaaccg tccccacaat cctccgacga tgcctgccgc gccgacgctg ttgccccctt 120  
gcgacgcgga ggagccgctg ctggcggagt cctccgaccg cttctccatg ttcccgatcc 180  
gtttcccgca gatctgggag ttctacaaga aggcggtggc ctcttcttgg acggcggagg 240  
aggttggcct ctctgccgac gcccggcact gggacgaggc tctgtcccc gacgagcggc 300  
actttatctc ccacgtgctc gccttcttcg ctgcctccga cggcatcgtg ctcgagaacc 360  
tcgcttcccg cttcatgacc gacgtgcagg tcgcccaggc gcgggccttc tacggcttcc 420  
agatcgccat cgagaacatc cactcggaga tgtattcgct gctgctcgag acttacatcc 480  
gcgaccacgt cgagaagg

(2) INFORMATION FOR SEQ ID NO:1923:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1599488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1923:

CONFIDENTIAL

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Pro | Ile | Arg | Phe | Pro | Gln | Ile | Trp | Glu | Phe | Tyr | Lys | Lys | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Ala | Ser | Phe | Trp | Thr | Ala | Glu | Glu | Val | Gly | Leu | Ser | Ala | Asp | Ala |

| High temperature (°C) |      |
|-----------------------|------|
| High temp. (°C) 100   | 100  |
| High temp. (°C) 150   | 150  |
| High temp. (°C) 200   | 200  |
| High temp. (°C) 250   | 250  |
| High temp. (°C) 300   | 300  |
| High temp. (°C) 350   | 350  |
| High temp. (°C) 400   | 400  |
| High temp. (°C) 450   | 450  |
| High temp. (°C) 500   | 500  |
| High temp. (°C) 550   | 550  |
| High temp. (°C) 600   | 600  |
| High temp. (°C) 650   | 650  |
| High temp. (°C) 700   | 700  |
| High temp. (°C) 750   | 750  |
| High temp. (°C) 800   | 800  |
| High temp. (°C) 850   | 850  |
| High temp. (°C) 900   | 900  |
| High temp. (°C) 950   | 950  |
| High temp. (°C) 1000  | 1000 |
| High temp. (°C) 1050  | 1050 |
| High temp. (°C) 1100  | 1100 |
| High temp. (°C) 1150  | 1150 |
| High temp. (°C) 1200  | 1200 |
| High temp. (°C) 1250  | 1250 |
| High temp. (°C) 1300  | 1300 |
| High temp. (°C) 1350  | 1350 |
| High temp. (°C) 1400  | 1400 |
| High temp. (°C) 1450  | 1450 |
| High temp. (°C) 1500  | 1500 |
| High temp. (°C) 1550  | 1550 |
| High temp. (°C) 1600  | 1600 |
| High temp. (°C) 1650  | 1650 |
| High temp. (°C) 1700  | 1700 |
| High temp. (°C) 1750  | 1750 |
| High temp. (°C) 1800  | 1800 |
| High temp. (°C) 1850  | 1850 |
| High temp. (°C) 1900  | 1900 |
| High temp. (°C) 1950  | 1950 |
| High temp. (°C) 2000  | 2000 |
| High temp. (°C) 2050  | 2050 |
| High temp. (°C) 2100  | 2100 |
| High temp. (°C) 2150  | 2150 |
| High temp. (°C) 2200  | 2200 |
| High temp. (°C) 2250  | 2250 |
| High temp. (°C) 2300  | 2300 |
| High temp. (°C) 2350  | 2350 |
| High temp. (°C) 2400  | 2400 |
| High temp. (°C) 2450  | 2450 |
| High temp. (°C) 2500  | 2500 |
| High temp. (°C) 2550  | 2550 |
| High temp. (°C) 2600  | 2600 |
| High temp. (°C) 2650  | 2650 |
| High temp. (°C) 2700  | 2700 |
| High temp. (°C) 2750  | 2750 |
| High temp. (°C) 2800  | 2800 |
| High temp. (°C) 2850  | 2850 |
| High temp. (°C) 2900  | 2900 |
| High temp. (°C) 2950  | 2950 |
| High temp. (°C) 3000  | 3000 |
| High temp. (°C) 3050  | 3050 |
| High temp. (°C) 3100  | 3100 |
| High temp. (°C) 3150  | 3150 |
| High temp. (°C) 3200  | 3200 |
| High temp. (°C) 3250  | 3250 |
| High temp. (°C) 3300  | 3300 |
| High temp. (°C) 3350  | 3350 |
| High temp. (°C) 3400  | 3400 |
| High temp. (°C) 3450  | 3450 |
| High temp. (°C) 3500  | 3500 |
| High temp. (°C) 3550  | 3550 |
| High temp. (°C) 3600  | 3600 |
| High temp. (°C) 3650  | 3650 |
| High temp. (°C) 3700  | 3700 |
| High temp. (°C) 3750  | 3750 |
| High temp. (°C) 3800  | 3800 |
| High temp. (°C) 3850  | 3850 |
| High temp. (°C) 3900  | 3900 |
| High temp. (°C) 3950  | 3950 |
| High temp. (°C) 4000  | 4000 |
| High temp. (°C) 4050  | 4050 |
| High temp. (°C) 4100  | 4100 |
| High temp. (°C) 4150  | 4150 |
| High temp. (°C) 4200  | 4200 |
| High temp. (°C) 4250  | 4250 |
| High temp. (°C) 4300  | 4300 |
| High temp. (°C) 4350  | 4350 |
| High temp. (°C) 4400  | 4400 |
| High temp. (°C) 4450  | 4450 |
| High temp. (°C) 4500  | 4500 |
| High temp. (°C) 4550  | 4550 |
| High temp. (°C) 4600  | 4600 |
| High temp. (°C) 4650  | 4650 |
| High temp. (°C) 4700  | 4700 |
| High temp. (°C) 4750  | 4750 |
| High temp. (°C) 4800  | 4800 |
| High temp. (°C) 4850  | 4850 |
| High temp. (°C) 4900  | 4900 |
| High temp. (°C) 4950  | 4950 |
| High temp. (°C) 5000  | 5000 |
| High temp. (°C) 5050  | 5050 |
| High temp. (°C) 5100  | 5100 |
| High temp. (°C) 5150  | 5150 |
| High temp. (°C) 5200  | 5200 |
| High temp. (°C) 5250  | 5250 |
| High temp. (°C) 5300  | 5300 |
| High temp. (°C) 5350  | 5350 |
| High temp. (°C) 5400  | 5400 |
| High temp. (°C) 5450  | 5450 |
| High temp. (°C) 5500  | 5500 |
| High temp. (°C) 5550  | 5550 |
| High temp. (°C) 5600  | 5600 |
| High temp. (°C) 5650  | 5650 |
| High temp. (°C) 5700  | 5700 |
| High temp. (°C) 5750  | 5750 |
| High temp. (°C) 5800  | 5800 |
| High temp. (°C) 5850  | 5850 |
| High temp. (°C) 5900  | 5900 |

20 25 30  
Arg His Trp Asp Glu Ala Leu Ser Pro Asp Glu Arg His Phe Ile Ser  
35 40 45  
His Val Leu Ala Phe Phe Ala Ala Ser Asp Gly Ile Val Leu Glu Asn  
50 55 60  
Leu Ala Ser Arg Phe Met Thr Asp Val Gln Val Ala Glu Ala Arg Ala  
65 70 75 80  
Phe Tyr Gly Phe Gln Ile Ala Ile Glu Asn Ile His Ser Glu Met Tyr  
85 90 95  
Ser Leu Leu Leu Glu Thr Tyr Ile Arg Asp His Val Glu Lys  
100 105 110

(2) INFORMATION FOR SEQ ID NO:1926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..542
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1926:

gcccacgctg cataaacaac tctatctcaa cggcgacgac gctcccatct taacagccag 60  
gaagctggcg tcttgcttgt ccttggttctt ttcccacccg gctacccccg tcgtgcgcgc 120  
cgctttcccc gtggtttcag agctcaagtc ggctagctag gccgcctggc taatctccct 180  
gcctttctata agtacagaga tcagggaagc ggcactccat cactgactg accgctcatg 240  
gogaaggtcc acctctacgt cgccgcggcc tgcgcgctcg tcctcgcgct cgccaccccc 300  
gccctgcgcg gtgaccccg catgctgcag gacgtctgcc cggctgacta cgccctcccc 360  
gtgaagctga acgggttcgc gtgcaaggcg aacttttcgg cggacgactt cttcttcgac 420  
gggctgagga acccgggcaa caccaacaac ccggcgggct ccgtggtgac ggcggccaac 480  
gtggagaagt tcctggggcg tgaacacgct gggcgtctcc atggccgcgc atcgactacg 540  
cg

(2) INFORMATION FOR SEQ ID NO:1927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1927:

Pro Thr Leu His Lys Gln Leu Tyr Leu Asn Gly Asp Asp Ala Pro Ile  
1 5 10 15  
Leu Thr Ala Arg Lys Leu Ala Ser Cys Leu Ser Leu Phe Phe Ser His  
20 25 30  
Pro Ala Thr Pro Val Val Ala Ala Ala Phe Pro Val Val Ser Glu Leu  
35 40 45  
Lys Ser Ala Ser  
50

(2) INFORMATION FOR SEQ ID NO:1928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

09639301 "08653360"

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1928:

Met Ala Lys Val His Leu Tyr Val Ala Ala Ala Cys Ala Val Val Leu  
1 5 10 15  
Ala Leu Ala Thr Pro Ala Leu Ala Gly Asp Pro Asp Met Leu Gln Asp  
20 25 30  
Val Cys Pro Ala Asp Tyr Ala Ser Pro Val Lys Leu Asn Gly Phe Ala  
35 40 45  
Cys Lys Ala Asn Phe Ser Ala Asp Asp Phe Phe Phe Asp Gly Leu Arg  
50 55 60  
Asn Pro Gly Asn Thr Asn Asn Pro Ala Gly Ser Val Val Thr Ala Ala  
65 70 75 80  
Asn Val Glu Lys Phe Leu Gly Arg Glu His Ala Gly Arg Leu His Gly  
85 90 95  
Arg Ala Ser Thr Thr  
100

(2) INFORMATION FOR SEQ ID NO:1929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1929:

Met Leu Gln Asp Val Cys Pro Ala Asp Tyr Ala Ser Pro Val Lys Leu  
1 5 10 15  
Asn Gly Phe Ala Cys Lys Ala Asn Phe Ser Ala Asp Asp Phe Phe Phe  
20 25 30  
Asp Gly Leu Arg Asn Pro Gly Asn Thr Asn Asn Pro Ala Gly Ser Val  
35 40 45  
Val Thr Ala Ala Asn Val Glu Lys Phe Leu Gly Arg Glu His Ala Gly  
50 55 60  
Arg Leu His Gly Arg Ala Ser Thr Thr  
65 70

(2) INFORMATION FOR SEQ ID NO:1930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..512
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1930:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| acagcaccgc accgcactgc atcggtcgcc agccgagccg agccgagccc tgctctctcc  | 60  |
| tccagctccc caaatcacac tccgccatgg ccggcacgtg cgctcacgtc gaggctctcc  | 120 |
| gcgcgcagcc ggcgtgggcg ctggcgctgg ccgcggtggg cctgctcggt gccgtgcgcg  | 180 |
| ccgcgcggcg cttcgcgctc tgggtctacg ccgcgttcct ccgcccgggc aagcccctgc  | 240 |
| gccgcgcgta cggcgccctg gccgtcggtg cgggcgccac cgacggcatc ggccgcgcgcg | 300 |
| tcgccttcgc cctcgccgcg tccgggctcg ggctcgctct cgtcggccgc aaccaggaga  | 360 |
| agctggccgc cgtcgccgcc gagatcaagg ccaggcacc caaggtcccc gaggtgcgga   | 420 |
| ctttcgtgct cgacttcgcc ggcgaggggc tggccgccc cgtcgaggcg ctcaaggact   | 480 |
| ccatccgggg cctcgacgtc ggcgtgctcg tc                                |     |



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1931:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | His | Arg | Thr | Ala | Leu | His | Arg | Ser | Pro | Ala | Glu | Pro | Ser | Arg | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Leu | Ser | Pro | Pro | Ala | Pro | Gln | Ile | Thr | Leu | Arg | His | Gly | Arg | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Arg | Ser | Arg | Arg | Val | Pro | Pro | Arg | Ala | Ala | Gly | Val | Gly | Ala | Gly |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ala | Gly | Arg | Gly | Gly | Pro | Ala | Arg | Gly | Arg | Ala | Arg | Arg | Arg | Pro | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |
| Arg | Ala | Leu | Gly | Leu | Arg | Arg | Val | Pro | Pro | Pro | Gly | Gln | Ala | Pro | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |
| Pro | Pro | Leu | Arg | Arg | Leu | Gly | Arg | Arg | Asp | Gly | Arg | His | Arg | Arg | His |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Pro | Arg | Arg | Arg | Leu | Pro | Pro | Arg | Arg | Val | Arg | Ala | Arg | Ala | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Pro | Arg | Arg | Pro | Gln | Pro | Gly | Glu | Ala | Gly | Arg | Arg | Arg | Arg | Arg | Asp |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Gln | Gly | Gln | Ala | Pro | Gln | Gly | Pro | Arg | Gly | Ala | Asp | Phe | Arg | Ala | Arg |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Leu | Arg | Arg | Arg | Gly | Ala | Gly | Arg | Arg | Arg | Arg | Gly | Ala | Gln | Gly | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |
| His | Pro | Gly | Pro | Arg | Arg | Arg | Arg | Ala | Arg |     |     |     |     |     |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

```
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..170
 (D) OTHER INFORMATION: / Ceres Seq. ID 1599497
```

| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1932: |        |        |         |        |        |        |        |         |        |        |        |        |         |        |        |
|--------------------------------------------|--------|--------|---------|--------|--------|--------|--------|---------|--------|--------|--------|--------|---------|--------|--------|
| Ser 1                                      | Thr    | Ala    | Pro     | His 5  | Cys    | Ile    | Gly    | Arg     | Gln 10 | Pro    | Ser    | Arg    | Ala     | Glu 15 | Pro    |
| Cys                                        | Ser    | Leu    | Leu 20  | Gln    | Leu    | Pro    | Lys    | Ser 25  | His    | Ser    | Ala    | Met    | Ala 30  | Gly    | Thr    |
| Cys                                        | Ala    | His 35 | Val     | Glu    | Phe    | Leu    | Arg 40 | Ala     | Gln    | Pro    | Ala    | Trp 45 | Ala     | Leu    | Ala    |
| Leu                                        | Ala 50 | Ala    | Val     | Gly    | Leu    | Leu 55 | Val    | Ala     | Val    | Arg    | Ala 60 | Ala    | Ala     | Arg    | Phe    |
| Ala 65                                     | Leu    | Trp    | Val     | Tyr    | Ala 70 | Ala    | Phe    | Leu     | Arg    | Pro 75 | Gly    | Lys    | Pro     | Leu    | Arg 80 |
| Arg                                        | Arg    | Tyr    | Gly     | Ala 85 | Trp    | Ala    | Val    | Thr     | Val 90 | Gly    | Ala    | Thr    | Asp     | Gly 95 | Ile    |
| Gly                                        | Arg    | Ala    | Val 100 | Ala    | Phe    | Arg    | Leu    | Ala 105 | Ala    | Ser    | Gly    | Leu    | Gly 110 | Leu    | Val    |
| Leu                                        | Val    | Gly    | Arg     | Asn    | Gln    | Glu    | Lys    | Leu     | Ala    | Ala    | Val    | Ala    | Ala     | Glu    | Ile    |

(A) LENGTH: 95 amino acids

| Table 1. Demographic characteristics of the study population |                |
|--------------------------------------------------------------|----------------|
| Age (years)                                                  | 65.0 ± 10.0    |
| Gender                                                       |                |
| Male                                                         | 50 (50.0%)     |
| Female                                                       | 50 (50.0%)     |
| Education (years)                                            | 12.0 ± 2.0     |
| Marital status                                               |                |
| Married                                                      | 40 (80.0%)     |
| Single                                                       | 10 (20.0%)     |
| Occupation                                                   |                |
| Retired                                                      | 30 (60.0%)     |
| Unemployed                                                   | 20 (40.0%)     |
| Income (USD/month)                                           | 1000.0 ± 500.0 |
| Health status                                                |                |
| Good                                                         | 30 (60.0%)     |
| Poor                                                         | 20 (40.0%)     |
| Comorbidities                                                |                |
| Hypertension                                                 | 15 (30.0%)     |
| Diabetes                                                     | 10 (20.0%)     |
| Cholesterol                                                  | 12 (24.0%)     |
| Arthritis                                                    | 8 (16.0%)      |
| Other                                                        | 5 (10.0%)      |
| Medication                                                   |                |
| Yes                                                          | 25 (50.0%)     |
| No                                                           | 25 (50.0%)     |
| Smoking status                                               |                |
| Smoker                                                       | 10 (20.0%)     |
| Non-smoker                                                   | 40 (80.0%)     |
| Alcohol consumption                                          |                |
| Yes                                                          | 5 (10.0%)      |
| No                                                           | 45 (90.0%)     |

| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1935: |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|--------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu                                        | Glu | Asn | Leu | Thr | Val | Cys | Pro | Val | Cys | Arg | His | Ser | Ser | Ser | Ser |
| 1                                          |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Xaa                                        | Arg | Glu | Lys | Ala | Glu | Asp | Asn | Thr | Lys | Met | Ser | Lys | Met | Ala | Glu |
|                                            |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu                                        | Lys | Ala | Ala | Ala | Val | Gly | Gly | Leu | Gly | Gly | Ala | Gly | Ala | Ala | Asp |
|                                            |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala                                        | Ala | Gln | Gln | Gln | Pro | His | Pro | Gln | Asp | Phe | Arg | Pro | Ser | Leu | Ser |
|                                            | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser                                        | Ser | Pro | Arg | Ala | Ala | Ala | Ala | Ala | Ala | Ala | Ala | Arg | Arg | Pro | Pro |
| 65                                         |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg                                        | Ser | His | Gly | Gly | Thr | Asp | Arg | Glu | Gly | Phe | Ser | Gln | Ala | Ala |     |
|                                            |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

(i) SEQUENCE CHARACTERISTICS:

```
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1599509

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

| Table 1. Demographic characteristics of the study population |             |
|--------------------------------------------------------------|-------------|
| Age (years)                                                  | 65.0 ± 10.0 |
| Gender                                                       |             |
| Male                                                         | 50.0%       |
| Female                                                       | 50.0%       |
| Education (years)                                            | 12.0 ± 2.0  |
| Marital status                                               |             |
| Married                                                      | 60.0%       |
| Single                                                       | 40.0%       |
| Occupation                                                   |             |
| Retired                                                      | 70.0%       |
| Unemployed                                                   | 30.0%       |
| Income (USD/month)                                           | 1,200 ± 300 |
| Health status                                                |             |
| Good                                                         | 60.0%       |
| Fair                                                         | 40.0%       |
| Poor                                                         | 0.0%        |
| Comorbidities                                                |             |
| Hypertension                                                 | 30.0%       |
| Diabetes                                                     | 20.0%       |
| Cholesterol                                                  | 10.0%       |
| Arthritis                                                    | 15.0%       |
| Depression                                                   | 5.0%        |
| Other                                                        | 10.0%       |

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1599510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1937:

Met Ala Glu Gln Thr Glu Lys Ala Phe Leu Lys Gln Pro Lys Val Phe  
1 5 10 15  
Leu Ser Ser Lys Lys Ser Gly Lys Gly Lys Lys Pro Gly Lys Gly Gly  
20 25 30  
Asn Arg Phe Trp Lys Ser Ile Gly Leu Gly Phe Lys Thr Pro Arg Glu  
35 40 45  
Ala Ile Glu Gly Thr Tyr Ile Asp Lys Lys Cys Pro Phe Thr Gly Thr  
50 55 60  
Val Ser Ile Arg Gly Arg Ile Ile Ala Gly Thr Cys His Ser Ala Lys  
65 70 75 80  
Met Asn Arg Thr Ile Ile Val Arg Arg  
85

(2) INFORMATION FOR SEQ ID NO:1938:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..401

(D) OTHER INFORMATION: / Ceres Seq. ID 1599520

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1938:

caaggatcag gactctgtgt ctaaagccct tgagctcagt ggctctgaca ttggtggtgg 60  
ctatgagctt tatgttgatg aagccaaacc aagaggcgat ggccagcgtg gtggtggtag 120  
atctggtggc cgttctggtg ggagatttgg tgaccgttct ggtggccggc gtggtggtgg 180  
tagatttggg gaaagatctg ggggcaggga tgggtggcggc agattcgtg gccgacgtgg 240  
tggtagggat ggcgcccgag gacgtggtgg ccgtggcttt ggtaacaagc acagcgctgg 300  
cactcccagt gcaggaaaga agactacttt tggatgatg tgatgatgaa cgcggaggat 360  
gcggcaaaag gatccaatga aattgtgttt ttttggcttt g

(2) INFORMATION FOR SEQ ID NO:1939:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1599521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1939:

Lys Asp Gln Asp Ser Val Ser Lys Ala Leu Glu Leu Ser Gly Ser Asp  
1 5 10 15  
Ile Gly Gly Gly Tyr Glu Leu Tyr Val Asp Glu Ala Lys Pro Arg Gly  
20 25 30  
Asp Gly Gln Arg Gly Gly Gly Arg Ser Gly Gly Arg Ser Gly Gly Arg  
35 40 45  
Phe Gly Asp Arg Ser Gly Gly Arg Arg Gly Gly Gly Arg Phe Gly Glu  
50 55 60  
Arg Ser Gly Gly Arg Asp Gly Gly Gly Arg Phe Gly Gly Arg Arg Gly  
65 70 75 80  
Gly Arg Asp Gly Gly Arg Gly Arg Gly Gly Arg Gly Phe Gly Asn Lys  
85 90 95

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(2) INFORMATION FOR SEQ ID NO:1940:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1940:

(2) INFORMATION FOR SEQ ID NO:1941:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1941:

(2) INFORMATION FOR SEQ ID NO:1942:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 459 base pairs

[illegible]

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..459
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1599524
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1942:

|            |            |             |             |            |            |     |
|------------|------------|-------------|-------------|------------|------------|-----|
| acagcttgcg | tggctgtgg  | tctcatctca  | ctcacactct  | ctctctctct | cggcgacgtc | 60  |
| tacgccgagt | gccagggcat | tcttcaggcg  | caggctcgctg | gctcgctgcc | gccctacacc | 120 |
| aggtgccccg | gtcttcttcc | gtcccttcgc  | cggcgacgag  | cactgccagc | gtgatccttt | 180 |
| ccgacaggac | agtatagcgg | atggcttcgt  | cgggtgcgggc | gccatcgggg | tcggtgatcg | 240 |
| ccgtggcatc | gtcctcttcc | tcagcagccg  | cggccggggg  | gtgcggcacg | ggctcgccgt | 300 |
| gcgcgcgctg | caagttcctg | cgctcgcaagt | gccagccgga  | ctgcgtgttc | gcgccctact | 360 |
| tcccaccgga | caaccgcag  | aagttcgtgc  | gcgtgcacgg  | cgtcttcggc | gcgagcaacg | 420 |
| tgaccaagct | gatgaacgaa | atccacccgt  | tgcagcgcg   |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1943:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 152 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..152
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1599525
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1943:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Leu | Ala | Trp | Ser | Val | Val | Ser | Ser | His | Ser | His | Ser | Leu | Ser | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ala | Thr | Ser | Thr | Pro | Ser | Ala | Gln | Ala | Phe | Phe | Arg | Arg | Arg | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ala | Arg | Cys | Arg | Pro | Thr | Pro | Gly | Ala | Pro | Val | Phe | Phe | Arg | Pro |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Phe | Ala | Gly | Asp | Glu | His | Cys | Gln | Arg | Asp | Pro | Phe | Arg | Gln | Asp | Ser |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Ala | Asp | Gly | Phe | Val | Gly | Ala | Gly | Ala | Ile | Gly | Val | Gly | Asp | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Gly | Ile | Val | Leu | Phe | Leu | Ser | Ser | Arg | Gly | Arg | Gly | Val | Arg | His |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Leu | Ala | Val | Arg | Arg | Val | Gln | Val | Pro | Ala | Ser | Gln | Val | Pro | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Leu | Arg | Val | Arg | Ala | Leu | Leu | Pro | Thr | Gly | Gln | Pro | Ala | Glu | Val |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Ala | Arg | Ala | Arg | Arg | Leu | Arg | Arg | Glu | Gln | Arg | Asp | Gln | Ala | Asp |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Arg | Asn | Pro | Pro | Val | Ala | Ala |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1944:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 86 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..86
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1599526
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1944:

09609900 101000

(2) INFORMATION FOR SEQ ID NO:1945:

(A) LENGTH: 452 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
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(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

(A) NAME/KEY: -

(B) LOCATION: 1..452

(D) OTHER INFORMATION: / Ceres Seq. ID 1599530

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| acgcacgccc | agacagacga | gaccagatcg | gggaccctcg  | cggcgcccag | ttcccgagcg | 60  |
| aacccaaccc | actaccacac | kyccagaagc | aaaagcccct  | cgccttttcc | gcgcccttgg | 120 |
| tctcctcccg | tccatccgcg | gcgagaacga | ccgacgacka  | caggccgaga | tgtgctgctg | 180 |
| cccagacaag | gcgtgctgca | tctgcacgct | catcgctgctg | gtgctggtgg | ccgtcgccct | 240 |
| cgtcttcggc | ttcggcgtct | acaccgcggg | cttcacacaag | ctcaccagca | acatgcacct | 300 |
| gcaggacgat | gcatacggcc | gcgggtggcg | cggcggtctcc | ttccgcgcct | acggccactt | 360 |
| tgccccgcgc | ccgtactaga | aggaccgcgc | ccccttctcc  | gagatctagg | gcctggatgc | 420 |
| tgggcgattc | gagccccgct | ccgctctcgg | tg          |            |            |     |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1599531

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | His | Ala | Gln | Thr | Asp | Glu | Thr | Arg | Ser | Gly | Thr | Leu | Ala | Ala | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ser | Arg | Ala | Asn | Pro | Thr | His | Tyr | Pro | Xaa | Xaa | Arg | Ser | Lys | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ser | Pro | Phe | Pro | Arg | Leu | Gly | Ser | Pro | Pro | Val | His | Pro | Arg | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Arg | Pro | Thr | Xaa | Thr | Gly | Arg | Asp | Val | Leu | Leu | Pro | Glu | Gln | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Leu | His | Leu | His | Ala | His | Arg | Ala | Gly | Ala | Gly | Gly | Arg | Arg | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Leu | Arg | Leu | Arg | Arg | Leu | His | Pro | Arg | Leu | Pro | Gln | Ala | His | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | His | Ala | Pro | Ala | Gly | Arg | Cys | Ile | Arg | Pro | Arg | Trp | Arg | Arg | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Leu | Pro | Arg | Leu | Arg | Pro | Leu | Cys | Pro | Ala | Ala | Val | Leu | Glu | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Pro | Pro | Leu | Leu | Arg | Asp | Leu | Gly | Pro | Gly | Cys | Trp | Ala | Ile | Arg |







- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..118  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599546  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1951:

Met Ala Pro Ala Val Glu Ala Val Lys Glu Thr Gly Thr Phe Gln Lys  
1                    5                    10                    15  
Val Pro Ala Leu Asn Glu Arg Ile Leu Ser Ser Met Ser Arg Arg Ser  
                    20                    25                    30  
Val Ala Ala His Pro Trp His Asp Leu Glu Ile Gly Pro Gly Ala Pro  
                    35                    40                    45  
Thr Ile Phe Asn Cys Val Ile Glu Ile Pro Arg Gly Ser Lys Val Lys  
50                    55                    60  
Tyr Glu Leu Asp Lys Lys Thr Gly Leu Ile Lys Val Asp Arg Val Leu  
65                    70                    75                    80  
Tyr Ser Ser Val Val Tyr Pro His Asn Tyr Gly Phe Ile Pro Arg Thr  
                    85                    90                    95  
Leu Cys Glu Asp Ser Asp Pro Leu Asp Val Leu Val Ile Met Gln Glu  
100                    105                    110  
Pro Val Ile Pro Gly Cys  
115

(2) INFORMATION FOR SEQ ID NO:1952:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 91 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..91  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599547  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1952:

Met Ser Arg Arg Ser Val Ala Ala His Pro Trp His Asp Leu Glu Ile  
1                    5                    10                    15  
Gly Pro Gly Ala Pro Thr Ile Phe Asn Cys Val Ile Glu Ile Pro Arg  
20                    25                    30  
Gly Ser Lys Val Lys Tyr Glu Leu Asp Lys Lys Thr Gly Leu Ile Lys  
35                    40                    45  
Val Asp Arg Val Leu Tyr Ser Ser Val Val Tyr Pro His Asn Tyr Gly  
50                    55                    60  
Phe Ile Pro Arg Thr Leu Cys Glu Asp Ser Asp Pro Leu Asp Val Leu  
65                    70                    75                    80  
Val Ile Met Gln Glu Pro Val Ile Pro Gly Cys  
85                    90

(2) INFORMATION FOR SEQ ID NO:1953:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 512 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..512  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599548  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1953:

gcagaagaag ccggcggcga agaaggtggc ggaggaggag ccctcggaga aggcggctcc 60  
ggcggagaag gccccgcgg ggaagaaggc caaggcggag aagcggctac ctgcgggcaa 120  
gtccgcccgc aaggagggcg gcgacaagaa ggggaggaag aaggcgaaga agagcgtgga 180

096698010300

gacctacaag atctacatct tcaaggtcct gaagcaggtg caccocgaca tcggcatctc 240  
ctccaaggcc atgtccatca tgaactcctt catcaacgac atcttcgaga agctcgccgc 300  
ggaggccgcc aagctcgccc ggtacaacaa gaagcccacc atcacctccc gcgagatcca 360  
gacctccgtc cgcctcgtcc tcccggcgga gctcgccaag cagcccgctc cggagggtac 420  
caaggccgtc accaagtcca cctcgtctta gccgccttgt agtagtggtg gttggctggt 480  
gtgtgtaagt ggtgcagtgg cttttgcttg tg

(2) INFORMATION FOR SEQ ID NO:1954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1599549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1954:

Ala Glu Glu Ala Gly Gly Glu Glu Gly Gly Gly Gly Ala Leu Gly  
1 5 10 15  
Glu Gly Gly Ser Gly Gly Glu Gly Pro Arg Gly Glu Glu Gly Gln Gly  
20 25 30  
Gly Glu Ala Ala Thr Cys Gly Gln Val Arg Arg Gln Gly Gly Arg Arg  
35 40 45  
Gln Glu Gly Glu Glu Glu Gly Glu Glu Glu Arg Gly Asp Leu Gln Asp  
50 55 60  
Leu His Leu Gln Gly Pro Glu Ala Gly Ala Pro Arg His Arg His Leu  
65 70 75 80  
Leu Gln Gly His Val His His Glu Leu Leu His Gln Arg His Leu Arg  
85 90 95  
Glu Ala Arg Arg Gly Gly Arg Gln Ala Arg Pro Val Gln Gln Glu Ala  
100 105 110  
His His His Leu Pro Arg Asp Pro Asp Leu Arg Pro Pro Arg Pro Pro  
115 120 125  
Arg Arg Ala Arg Gln Ala Arg Arg Leu Gly Gly Tyr Gln Gly Arg His  
130 135 140  
Gln Val His Leu Val Leu Ala Ala Leu  
145 150

(2) INFORMATION FOR SEQ ID NO:1955:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1599550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1955:

Gln Lys Lys Pro Ala Ala Lys Lys Val Ala Glu Glu Glu Pro Ser Glu  
1 5 10 15  
Lys Ala Ala Pro Ala Glu Lys Ala Pro Ala Gly Lys Lys Ala Lys Ala  
20 25 30  
Glu Lys Arg Leu Pro Ala Gly Lys Ser Ala Gly Lys Glu Gly Gly Asp  
35 40 45  
Lys Lys Gly Arg Lys Lys Ala Lys Lys Ser Val Glu Thr Tyr Lys Ile  
50 55 60  
Tyr Ile Phe Lys Val Leu Lys Gln Val His Pro Asp Ile Gly Ile Ser  
65 70 75 80  
Ser Lys Ala Met Ser Ile Met Asn Ser Phe Ile Asn Asp Ile Phe Glu

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1599553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1958:

Met Ile Ile Met Val Val Val Val Gly Ile Ser Gln Pro Val Phe Trp  
1 5 10 15  
Ser Gly Ile Ser Val Gly Thr Ala Gly Gln Lys Thr Ser Val Ala His  
20 25 30  
Leu Asp Ser Leu Val Glu Leu Lys Ile Tyr Ile Phe Gln Glu Ile Ile  
35 40 45  
Thr Leu Gly Ile Pro Glu Gly Leu Gly Leu Ser Ser Ile Met Ile Leu  
50 55 60  
Leu Met Leu Leu Met Arg Ser Thr Ile Trp Met Gly Arg  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1959:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1599554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1959:

Met Val Val Val Val Gly Ile Ser Gln Pro Val Phe Trp Ser Gly Ile  
1 5 10 15  
Ser Val Gly Thr Ala Gly Gln Lys Thr Ser Val Ala His Leu Asp Ser  
20 25 30  
Leu Val Glu Leu Lys Ile Tyr Ile Phe Gln Glu Ile Ile Thr Leu Gly  
35 40 45  
Ile Pro Glu Gly Leu Gly Leu Ser Ser Ile Met Ile Leu Leu Met Leu  
50 55 60  
Leu Met Arg Ser Thr Ile Trp Met Gly Arg  
65 70

(2) INFORMATION FOR SEQ ID NO:1960:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 455 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..455

(D) OTHER INFORMATION: / Ceres Seq. ID 1599555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1960:

gttatccggt tcaaagccga gcggcggtctc ctctctccag cggtccagc caatccggca 60  
atcccgcctc ccagctcgc tgctcgccc ctctcctccg cctccgccca tggcggcctt 120  
cccctccgcc tccccgtcgc cggcgatctc cgctcgcacc tggagcatgg ctccctccg 180  
tacgtccctc ccgcactcc gcccctcccc cgcgggcagg ctccgttcgt cgttctcgcc 240  
cgcgggcgcg gccacggctg catcggtcgg ctgcctcggg tccttctccg gcctcgcgcc 300  
cgtctcgaat ctctctccc tcggcgctga gaactcaagc tttgagcatc ggttgtytgg 360  
tattgatgcc cgtggaanga tagttgcgat gcgacatggg agacgcgttt cctaaaytta 420  
acaggcctcc cggatcaagg atagcactgc tgcgt

(2) INFORMATION FOR SEQ ID NO:1961:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

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(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..109  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599556  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1961:  
Val Ile Arg Phe Lys Ala Glu Arg Arg Leu Leu Ser Pro Ala Ala Pro  
1                  5                  10                  15  
Ala Asn Pro Ala Ile Pro Leu Pro Gln Leu Ala Ala Arg Pro Leu Ser  
                  20                  25                  30  
Ser Ala Leu Arg His Gly Gly Leu Pro Leu Arg Leu Pro Val Ala Gly  
                  35                  40                  45  
Asp Leu Arg Leu Asp Leu Glu His Gly Phe Pro Pro Tyr Val Pro Pro  
                  50                  55                  60  
Arg Thr Pro Pro Leu Pro Arg Gly Gln Ala Pro Phe Val Val Leu Ala  
65                  70                  75                  80  
Arg Gly Gly Gly His Gly Cys Ile Gly Arg Leu Pro Arg Val Leu Leu  
                  85                  90                  95  
Arg Pro Arg Ala Arg Leu Glu Ser Pro Leu Pro Arg Arg  
                  100                  105

(2) INFORMATION FOR SEQ ID NO:1962:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 137 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..137  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1962:

Leu Ser Gly Ser Lys Pro Ser Gly Val Ser Ser Leu Gln Arg Leu Gln  
1                  5                  10                  15  
Pro Ile Arg Gln Ser Arg Ser Pro Ser Ser Leu Leu Ala Arg Ser Pro  
                  20                  25                  30  
Pro Pro Ser Ala Met Ala Ala Phe Pro Ser Ala Ser Pro Ser Pro Ala  
                  35                  40                  45  
Ile Ser Ala Ser Thr Trp Ser Met Ala Ser Leu Arg Thr Ser Leu Pro  
                  50                  55                  60  
Ala Leu Arg Pro Ser Pro Ala Gly Arg Leu Arg Ser Ser Phe Ser Pro  
65                  70                  75                  80  
Ala Ala Ala Ala Thr Ala Ala Ser Val Gly Cys Leu Gly Ser Phe Ser  
                  85                  90                  95  
Gly Leu Ala Pro Val Ser Asn Leu Leu Ser Leu Gly Ala Glu Asn Ser  
                  100                  105                  110  
Ser Phe Glu His Arg Leu Xaa Gly Ile Asp Ala Arg Gly Xaa Ile Val  
                  115                  120                  125  
Ala Met Arg His Gly Arg Arg Val Ser  
                  130                  135

(2) INFORMATION FOR SEQ ID NO:1963:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 126 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

09669960-101300

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1963:

Tyr Pro Val Gln Ser Arg Ala Ala Ser Pro Leu Ser Ser Gly Ser Ser  
1 5 10 15  
Gln Ser Gly Asn Pro Ala Pro Pro Ala Arg Cys Ser Pro Ala Leu Leu  
20 25 30  
Arg Pro Pro Pro Trp Arg Pro Ser Pro Pro Pro Arg Arg Arg Arg  
35 40 45  
Ser Pro Pro Arg Pro Gly Ala Trp Leu Pro Ser Val Arg Pro Ser Pro  
50 55 60  
His Ser Ala Pro Pro Pro Arg Ala Gly Ser Val Arg Arg Ser Arg Pro  
65 70 75 80  
Arg Arg Arg Pro Arg Leu His Arg Ser Ala Ala Ser Gly Pro Ser Pro  
85 90 95  
Ala Ser Arg Pro Ser Arg Ile Ser Ser Pro Ser Ala Leu Arg Thr Gln  
100 105 110  
Ala Leu Ser Ile Gly Cys Xaa Val Leu Met Pro Val Glu Xaa  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1964:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1964:

agtattacca ggatgtcttt cagccgcaga ttagcaggcc gcctgcgctc cttgcccccta 60  
agcctcgttt ccggtgtacg actccaacga cgacgagatg gcctccccgc tccgtcgagg 120  
cttccccctcc ctccggccgcg cgcttctcac gccggcgccg gcgcgggatgc tctccgcgga 180  
ggcctccgat gccctcgttg agatcaagcc cagggagatt gggatgggtct ccggcatccc 240  
cgaggagcac ctccgccgta aggttgtaat ttattcacca gctaggactg catctcagca 300  
aggttcaggc aaagttggga ggtggaaaat taactttttg tcaacccaaa agtgggagaa 360  
cccattgatg ggatggacat ctactgggga tccatatgct aatgtcggtg aagcaggact 420  
tacattcaac agtcgggagt cagcaaaagc atttgctgaa aaacatggat ggaatttatg 480  
tggtacggaa acggcataca cctcttctga agcct

(2) INFORMATION FOR SEQ ID NO:1965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1965:

Met Ala Ser Pro Leu Arg Arg Ser Phe Pro Ser Leu Gly Arg Ala Leu  
1 5 10 15  
Leu Thr Pro Ala Pro Ala Arg Met Leu Ser Ala Glu Ala Ser Asp Ala  
20 25 30  
Leu Val Glu Ile Lys Pro Arg Glu Ile Gly Met Val Ser Gly Ile Pro  
35 40 45  
Glu Glu His Leu Arg Arg Lys Val Val Ile Tyr Ser Pro Ala Arg Thr  
50 55 60

00652950





Ala 85 90 95

(2) INFORMATION FOR SEQ ID NO:1968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..327
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1968:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| atcagccatc | ccctccgcgc | gcaagtctct | ctgaattgtg | ggctctccggc | gnatggcggc | 60  |
| tctagctcca | tccaagnatt | ctgggcacca | agctcaactt | cgccgggtcc  | tcccgtacg  | 120 |
| ccacggcagc | gcccaccgcg | ggggctcaga | agatcgtctc | cctcttcagc  | aagaagcctg | 180 |
| cccagaagcc | caagccctct | gcggtgtcgt | cctcttctcc | ggacatcagc  | gacgagctcg | 240 |
| ccaagtggta | cggtcctgac | aggaggatct | acctgcggga | tgggctcttg  | gaccgctcgg | 300 |
| aggtaccgga | gtacctcacc | ggagagg    |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:1969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1969:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Ser | His | Pro | Leu | Pro | Arg | Gln | Val | Ser | Leu | Asn | Cys | Gly | Ser | Pro |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Ala | Xaa | Gly | Gly | Ser | Ser | Ser | Ile | Gln | Xaa | Phe | Trp | Ala | Pro | Ser | Ser |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Thr | Ser | Pro | Ala | Pro | Pro | Ala | Thr | Pro | Arg | Gln | Arg | Pro | Pro | Arg | Gly |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Leu | Arg | Arg | Ser | Ser | Pro | Ser | Ser | Ala | Arg | Ser | Leu | Pro | Arg | Ser | Pro |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ser | Pro | Leu | Arg | Cys | Arg | Pro | Leu | Leu | Arg | Thr | Ser | Ala | Thr | Ser | Ser |  |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Pro | Ser | Gly | Thr | Val | Leu | Thr | Gly | Gly | Ser | Thr | Cys | Arg | Met | Gly | Ser |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Trp | Thr | Ala | Arg | Arg | Tyr | Arg | Ser | Thr | Ser | Pro | Glu | Arg |     |     |     |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1970:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Ala | Leu | Ala | Pro | Ser | Lys | Xaa | Ser | Gly | His | Gln | Ala | Gln | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |

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(A) NAME/KEY: peptide

| Table 1. Demographic characteristics of the study population |                 |
|--------------------------------------------------------------|-----------------|
| Age (years)                                                  | 65.0 ± 1.5      |
| Gender                                                       |                 |
| Male                                                         | 50.0%           |
| Female                                                       | 50.0%           |
| Education (years)                                            | 12.0 ± 1.0      |
| Marital status                                               |                 |
| Married                                                      | 60.0%           |
| Single                                                       | 40.0%           |
| Occupation                                                   |                 |
| Retired                                                      | 70.0%           |
| Unemployed                                                   | 30.0%           |
| Income (USD/month)                                           | 1,200.0 ± 200.0 |
| Health status                                                |                 |
| Good                                                         | 60.0%           |
| Fair                                                         | 40.0%           |
| Poor                                                         | 0.0%            |
| Comorbidities                                                |                 |
| Hypertension                                                 | 30.0%           |
| Diabetes                                                     | 20.0%           |
| Cholesterol                                                  | 10.0%           |
| Smoking status                                               |                 |
| Smoker                                                       | 10.0%           |
| Non-smoker                                                   | 90.0%           |
| Alcohol consumption                                          |                 |
| Regular                                                      | 5.0%            |
| Occasional                                                   | 15.0%           |
| Never                                                        | 80.0%           |

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1599590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1973:

Glu Thr His Ser Pro Ser Pro Gly Ile Ala Gly Ile Xaa His Lys Arg  
1 5 10 15  
Asn Leu Gln Pro Trp His Arg Ser Ser Arg His Arg Arg Arg Arg Ser  
20 25 30  
Ser Ser Ser Cys Trp Arg Ser Pro Cys Arg Pro Pro Arg Arg Thr Ala  
35 40 45  
Gly Ala Arg Arg Ala Cys Ala Ala Ala Gly Ser Gly Thr Ala Gly Arg  
50 55 60  
Ala Arg Thr Thr Ala Ala Pro Gly Ala Ser Arg Ala Pro Ala Thr Cys  
65 70 75 80  
Arg Arg Pro Thr Thr Arg Pro Trp Pro Ala Ser  
85 90

(2) INFORMATION FOR SEQ ID NO:1974:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1599591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1974:

Lys Leu Thr Arg His Arg Arg Ala Ser Arg Ala Ser Xaa Thr Asn Ala  
1 5 10 15  
Thr Cys Ser His Gly Thr Glu Ala Arg Ala Thr Asp Gly Gly Gly Arg  
20 25 30  
Arg Arg Pro Ala Gly Ala Arg Leu Val Gly Arg Arg Ala Glu Leu Arg  
35 40 45  
Val Arg Val Gly Pro Val Leu Gln Pro Val Arg Val Leu Arg Asp Gly  
50 55 60  
Arg Gly Leu Leu Arg Arg Arg Val Pro Val Gly Pro Leu Arg Arg Ala  
65 70 75 80  
Gly Asp Gln Gln Arg Val Arg Gly Gln His Arg Asp Ala Gly Leu Leu  
85 90 95  
Arg Arg Ala Pro Arg Ala Gly Arg Arg Leu Val  
100 105

(2) INFORMATION FOR SEQ ID NO:1975:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..350

(D) OTHER INFORMATION: / Ceres Seq. ID 1599617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1975:

acaattccac ataacctcgc ccgcgcccgc tcnnccacga gacgccttct tgctctcgss 60  
ttccggtgac gcccgccact tctccccga cgagatgacg aaacgcacca agaaggcagg 120  
aatcgttggc aaatatggta ccaggtatgg tgccagttta cgtaaacaga tcaagaagat 180  
ggaggtctcg cagcactcca aatacttctg tgagttctgt ggcaagtttg ccgtgaagag 240  
gaaagcagtt ngatatctggg gatgcaagga ctgtgggaan gttaacgccg gtngcgccta 300  
cacaatgaac actgctagtg cggtcactss tgagaagcac aatccggcgc

(2) INFORMATION FOR SEQ ID NO:1976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..116
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1599618
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1976:

Gln Phe His Ile Thr Ser Pro Ala Pro Pro Xaa Pro Arg Asp Ala Phe  
1 5 10 15  
Leu Leu Ser Xaa Ser Gly Asp Ala Arg His Phe Leu Pro Asp Glu Met  
20 25 30  
Thr Lys Arg Thr Lys Lys Ala Gly Ile Val Gly Lys Tyr Gly Thr Arg  
35 40 45  
Tyr Gly Ala Ser Leu Arg Lys Gln Ile Lys Lys Met Glu Val Ser Gln  
50 55 60  
His Ser Lys Tyr Phe Cys Glu Phe Cys Gly Lys Phe Ala Val Lys Arg  
65 70 75 80  
Lys Ala Val Xaa Ile Trp Gly Cys Lys Asp Cys Gly Xaa Val Asn Ala  
85 90 95  
Gly Xaa Ala Tyr Thr Met Asn Thr Ala Ser Ala Val Thr Xaa Glu Lys  
100 105 110  
His Asn Pro Ala  
115

(2) INFORMATION FOR SEQ ID NO:1977:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 85 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1977:

Met Thr Lys Arg Thr Lys Lys Ala Gly Ile Val Gly Lys Tyr Gly Thr  
1 5 10 15  
Arg Tyr Gly Ala Ser Leu Arg Lys Gln Ile Lys Lys Met Glu Val Ser  
20 25 30  
Gln His Ser Lys Tyr Phe Cys Glu Phe Cys Gly Lys Phe Ala Val Lys  
35 40 45  
Arg Lys Ala Val Xaa Ile Trp Gly Cys Lys Asp Cys Gly Xaa Val Asn  
50 55 60  
Ala Gly Xaa Ala Tyr Thr Met Asn Thr Ala Ser Ala Val Thr Xaa Glu  
65 70 75 80  
Lys His Asn Pro Ala  
85

(2) INFORMATION FOR SEQ ID NO:1978:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 276 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..276
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599628

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(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1599631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1981:

```
Val Ser Ile Ser Pro Ile Arg Val Ser Pro Pro Pro Pro Pro Pro Pro
1 5 10 15
Pro Leu Pro Ser Ser Pro Pro Ala Glu Ala Met Pro Ser His Lys Thr
 20 25 30
Phe Arg Ile Lys Lys Lys Leu Ala Lys Lys Met Arg Gln Asn Arg Pro
 35 40 45
Ile Pro Tyr Trp Ile Arg Met Arg Thr Asp Asn Thr Ile Arg Tyr Asn
 50 55 60
Ala Lys Arg Arg His Trp Arg Arg Thr Lys Leu Gly Phe
65 70 75
```

(2) INFORMATION FOR SEQ ID NO:1982:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 371 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..371

(D) OTHER INFORMATION: / Ceres Seq. ID 1599638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1982:

```
accaaggaaa ttcacaaaga gatactagtc cctaccaaag catacttcct gaaacactct 60
tgcaatccac tgagtcctgt ttgttgagac ttgagacgca tagagctagc gtcgacaatg 120
tcgctcgtga ggcgcmsaac gtgttcgacc cttctcgat ggacctctgg gacccttcg 180
acaccatggt ccgctccatc gtcccgtcgg cggcctccac caactccgag accgccgtct 240
tcgccagcgc ccgcatcgac tggaaggaga cgcccagggc gcacgtgttc aaggccgacc 300
tccccggcgt caagaaggag gagatcaagg tcgaggtcga ggacggcaac gtgctggtca 360
tcagcggcca g
```

(2) INFORMATION FOR SEQ ID NO:1983:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1599639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1983:

```
Gln Gly Asn Ser Gln Arg Asp Thr Ser Pro Tyr Gln Ser Ile Leu Pro
1 5 10 15
Glu Thr Leu Leu Gln Ser Thr Glu Ser Cys Leu Leu Arg Leu Glu Thr
 20 25 30
His Arg Ala Ser Val Asp Asn Val Ala Arg Glu Ala Xaa Asn Val Phe
 35 40 45
Asp Pro Phe Ser Met Asp Leu Trp Asp Pro Phe Asp Thr Met Phe Arg
 50 55 60
Ser Ile Val Pro Ser Ala Ala Ser Thr Asn Ser Glu Thr Ala Val Phe
 65 70 75 80
Ala Ser Ala Arg Ile Asp Trp Lys Glu Thr Pro Glu Ala His Val Phe
 85 90 95
Lys Ala Asp Leu Pro Gly Val Lys Lys Glu Glu Ile Lys Val Glu Val
 100 105 110
Glu Asp Gly Asn Val Leu Val Ile Ser Gly Gln
```

09689960 104600



gggcatgatg acaagatacg catagtcttc aacaaggccg accaagttga tgcacagcag 180  
ctgatgagag tgtacggagc

(2) INFORMATION FOR SEQ ID NO:1987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1987:

Asn Asp Phe Thr Gly Val Thr Ser Trp Phe Ala Ala Lys Cys Asp Leu  
1 5 10 15  
Ile Leu Xaa Leu Phe Asp Pro His Lys Leu Asp Ile Ser Asp Glu Phe  
20 25 30  
Lys Arg Val Ile Gly Ser Leu Arg Gly His Asp Asp Lys Ile Arg Ile  
35 40 45  
Val Leu Asn Lys Ala Asp Gln Val Asp Ala Gln Gln Leu Met Arg Val  
50 55 60  
Tyr Gly  
65

(2) INFORMATION FOR SEQ ID NO:1988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1988:

Thr Ile Ser Pro Glu Ser Arg Arg Gly Leu Arg Pro Ser Ala Thr Ser  
1 5 10 15  
Ser Phe Xaa Cys Leu Ile Arg Ile Ser Leu Thr Ser Ala Met Ser Ser  
20 25 30  
Ser Val

(2) INFORMATION FOR SEQ ID NO:1989:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..423
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1989:

cacaatttgt tcaggttttc aataacagtc cagatgagac agcttatttc aggatgttac 60  
tcaatcgtga gagtatcact aactcggttg ccatgatcca gccttccttg atatcatttt 120  
cttttgattc acctccatct ccggtatttc tagatgtggc atcaatagca gcagatcgta 180  
tactgctact tgatgcgtac tttagtgttg tcatttttss atggaatgac aattgctcag 240  
tgagaaaca tgggttatca gaaccaacct gagcatgagc aatttgcaca actattacaa 300  
gcaccacatg aggaggcaca gatgataata aagggtcgat ttccagttcc aagactagtg 360  
gtctgcgaca acatggctcg caggcratgt ttttgtingc taagctgaat ccatcggcc 420

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(2) INFORMATION FOR SEQ ID NO:1990:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1990:

(2) INFORMATION FOR SEQ ID NO:1991:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1991:

(2) INFORMATION FOR SEQ ID NO:1992:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1992:

Met Arg Thr Leu Val Leu Ser Phe Xaa Xaa Gly Met Thr Ile Ala Gln  
1 5 10 15

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..71  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599680  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1995:  
Ser Xaa Xaa Gly Phe Xaa Arg Arg Arg Arg Arg Phe Val Val  
1 5 10 15  
Ser Ala Ala Ala Met Pro Ser His Lys Thr Phe Arg Ile Lys Lys Lys  
20 25 30  
Leu Ala Lys Lys Met Arg Gln Xaa Arg Pro Ile Pro Tyr Trp Ile Arg  
35 40 45  
Met Arg Thr Asp Asn Thr Ile Arg Tyr Asn Ala Lys Arg Arg His Trp  
50 55 60  
Arg Arg Thr Lys Leu Gly Phe  
65 70

(2) INFORMATION FOR SEQ ID NO:1996:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..51  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1996:

Met Pro Ser His Lys Thr Phe Arg Ile Lys Lys Lys Leu Ala Lys Lys  
1 5 10 15  
Met Arg Gln Xaa Arg Pro Ile Pro Tyr Trp Ile Arg Met Arg Thr Asp  
20 25 30  
Asn Thr Ile Arg Tyr Asn Ala Lys Arg Arg His Trp Arg Arg Thr Lys  
35 40 45  
Leu Gly Phe  
50

(2) INFORMATION FOR SEQ ID NO:1997:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..336  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1997:

aatctgaccc actctcgtcg caccgaacgc aagtagcaaa gcaggaccca tcctctccca 60  
tctctcggtc tccccatccc aaccgcgcgc cgccgcgcc gcttctcccg tctccagcgc 120  
ccacagcgca ttgtatccgc ggggcgagct gagtcaccaa gctgggtctag ggcccatcca 180  
tttgaaccc tcgcgagaag caaagcgnac ggagcgccab sntcttagat cgattgctcg 240  
ccaggtgtt ggcgaggagt cgtcaaccct cacggcrgcc atgtctgtgg agckcatcct 300  
gtggcttttc tccttcgtct ccgtcatggt cctcat

(2) INFORMATION FOR SEQ ID NO:1998:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

DOCKET# 08663960

(B) LOCATION: 1..49

(D) OTHER INFORMATION: / Ceres Seq. ID 1599687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1998:

```
Ser Asp Pro Leu Ser Ser His Ala Thr Gln Val Ala Lys Gln Asp Pro
1 5 10 15
Ser Ser Pro Ile Ser Arg Ser Pro His Pro Asn Pro Pro Pro Pro Pro
20 25 30
Pro Leu Leu Pro Ser Pro Ala Pro Thr Ala His Cys Ile Arg Gly Ala
35 40 45
Ser
```

(2) INFORMATION FOR SEQ ID NO:1999:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 396 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..396

(D) OTHER INFORMATION: / Ceres Seq. ID 1599692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1999:

```
ctccgatctc cctctctctc gttctgctca catcgacgcg gttcggttcc agtttcactc 60
ccactgccgt ctcgssaacc tccccgtgtc cacgcttcgt cctcgcgttc ccaaccaagc 120
tctccgcgct gcnatkgccg cgacctcccc cttcgaactgc gtcctcctag acctcgacga 180
caccctgtac ccggggcgaca cgggcatcgg cgcgggccctg agggcgcaaca tcgacgagtt 240
cctccaggcc aagctcggcg tgctcgccga cgaggcccg cagcgcgccc gagctcttc 300
gcgcgcacgg cagctccctc gccgggctca tcgcgctcgg ctacgacgtg caccgcggacg 360
agtaccacag ctacgtgcac ggcaggctac cgtaacg
```

(2) INFORMATION FOR SEQ ID NO:2000:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1599693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2000:

```
Leu Arg Ser Pro Ser Leu Ser Phe Cys Ser His Arg Arg Gly Ser Val
1 5 10 15
Pro Val Ser Leu Pro Leu Pro Ser Xaa Xaa Pro Pro Leu Phe His Ala
20 25 30
Ser Ser Ser Arg Ser Gln Pro Ser Ser Pro Ala Cys Xaa Xaa Arg Asp
35 40 45
Leu Pro Leu Arg Leu Arg Pro Pro Arg Pro Arg Arg His Pro Val Pro
50 55 60
Gly Arg His Gly His Arg Arg Gly Pro Glu Ala Gln His Arg Arg Val
65 70 75 80
Pro Pro Gly Gln Ala Arg Arg Val Gly Arg Arg Gly Pro Pro Arg Ala
85 90 95
Pro Ser Ser Ser Ala Arg Thr Ala Ala Pro Ser Pro Gly Ser Ser Arg
100 105 110
Ser Ala Thr Thr Cys Thr Arg Thr Ser Thr Thr Ala Thr Cys Thr Ala
115 120 125
Gly Tyr Arg Thr
130
```

(2) INFORMATION FOR SEQ ID NO:2001:

0963980-101300

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..433

(D) OTHER INFORMATION: / Ceres Seq. ID 1599697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2002:

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:1001 |            |            |            |            |            |     |
|-------------------------------------------|------------|------------|------------|------------|------------|-----|
| tcagagtcaa                                | cgggcccaac | cctctcagtc | tgggctctc  | gggtgcgcag | tctctgcta  | 60  |
| ggtttaggtc                                | tccaccggcc | gcagcctcca | caccaagagc | ggnncgagat | cgccggaaga | 120 |
| gggggggaggc                               | gcggagatga | gcgggasssn | gttcaacgct | tcaagtgcgc | tgtgcgggtg | 180 |
| gcgtggagtc                                | ccggctgta  | catcacgctg | gtgcggggcc | taccgggcac | gcgcgcctc  | 240 |
| caccgccgca                                | cgtcgaggc  | catgcgcctc | cgccgctgcc | accgcaccgt | cgagcaccgc | 300 |
| accacgcctg                                | cgtcgtcgg  | gatgctcacc | caggtgaagc | gcctcgtcgc | cgtcgagacc | 360 |
| gaggagatcg                                | tacaacgcgc | gcaasagggc | cgaggcggag | aggcgcgcgc | cagacccccg | 420 |
| ctcgatcgtct                               | ccc        |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2003:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1599698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2003:

| Descriptive statistics         |       |
|--------------------------------|-------|
| Number of respondents          | 100   |
| Age (mean)                     | 35.5  |
| Gender (male/female)           | 50/50 |
| Education (mean)               | 12.5  |
| Occupation (mean)              | 1.5   |
| Income (mean)                  | 1.5   |
| Marital status (mean)          | 1.5   |
| Religious affiliation (mean)   | 1.5   |
| Political affiliation (mean)   | 1.5   |
| Health status (mean)           | 1.5   |
| Stress level (mean)            | 1.5   |
| Life satisfaction (mean)       | 1.5   |
| Work-life balance (mean)       | 1.5   |
| Family support (mean)          | 1.5   |
| Community support (mean)       | 1.5   |
| Healthcare access (mean)       | 1.5   |
| Financial stability (mean)     | 1.5   |
| Emotional well-being (mean)    | 1.5   |
| Social support (mean)          | 1.5   |
| Physical health (mean)         | 1.5   |
| Mental health (mean)           | 1.5   |
| Overall quality of life (mean) | 1.5   |

| (X1) SEQUENCE DESCRIPTION: 221 |     |     |     |        |     |     |     |     |        |     |     |     |     |        |        |
|--------------------------------|-----|-----|-----|--------|-----|-----|-----|-----|--------|-----|-----|-----|-----|--------|--------|
| Ser 1                          | Glu | Glu | Arg | Leu 5  | Pro | Ser | Pro | Ser | Arg 10 | Ser | Ser | Leu | Pro | Pro 15 | Arg    |
| Ala                            | Ala | Met | Asp | Ala 20 | Val | Asp | Ser | Val | Val 25 | Asp | Pro | Leu | Arg | Ser    | Ser    |
| Pro                            | Arg | Thr | Ala | Ser 35 | Ala | Ser | Ser | Ser | Ala 40 | Ala | Thr | Ser | Pro | Thr    | Ala    |
| Xaa                            | Ser | Ser | Pro | Arg    | Ser | Pro | Arg | Ala | Leu    | Arg | Ser | Ala | Ser | Ser    | Ser    |
| Trp 65                         | Asp | Ser | Ser | Ala    | Ser | Leu | Ser | Ser | Ser    | Ser | Ser | Ser | Pro | Ser    | Thr 80 |

(2) INFORMATION FOR SEQ ID NO:2008:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 440 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..440  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599724

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2008:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| tctatttgaa agttcaggtg aaagatacag gctgtggaat tgggtccacag gatctacctc  | 60  |
| atgtattttac aaagtttgct catcctcaaaa gcggaggaaa ccgagggttt aatggtagtg | 120 |
| gtcttggcct tgccatatgc aagagggtttg ttagtctcat gggagggcac atctggattg  | 180 |
| acagcgaagg aaccggaaga ggttgccaccg caacattcgt cgtcaagctc ggcgtgtgtg  | 240 |
| acaacacaaa cacctaccag cagcagctga tccctctagt atggccaagc agcgcagact   | 300 |
| ccgatttgcg tgctccgaaa cctcttcgag acgggagagg atctactccc ttganatctc   | 360 |
| ggtaccaaag gagcgtatga gcctagtgtg aatgattgag ggcatagtgc caagtagggg   | 420 |
| accgattagt gccaccgtct                                               |     |

(2) INFORMATION FOR SEQ ID NO:2009:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 125 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..125  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2009:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Tyr | Leu | Lys | Val | Gln | Val | Lys | Asp | Thr | Gly | Cys | Gly | Ile | Gly | Pro | Gln |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asp | Leu | Pro | His | Val | Phe | Thr | Lys | Phe | Ala | His | Pro | Gln | Ser | Gly | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asn | Arg | Gly | Phe | Asn | Gly | Ser | Gly | Leu | Gly | Leu | Ala | Ile | Cys | Lys | Arg |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Phe | Val | Ser | Leu | Met | Gly | Gly | His | Ile | Trp | Ile | Asp | Ser | Glu | Gly | Thr |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gly | Arg | Gly | Cys | Thr | Ala | Thr | Phe | Val | Val | Lys | Leu | Gly | Val | Cys | Asp |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Asn | Thr | Asn | Thr | Tyr | Gln | Gln | Gln | Leu | Ile | Pro | Leu | Val | Trp | Pro | Ser |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ser | Ala | Asp | Ser | Asp | Leu | Arg | Ala | Pro | Lys | Pro | Leu | Pro | Asp | Gly | Arg |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |
| Gly | Ser | Thr | Pro | Leu | Xaa | Ser | Arg | Tyr | Gln | Arg | Ser | Val |     |     |     |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2010:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 69 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..69  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2010:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Tyr | Leu | Gln | Ser | Leu | Leu | Ile | Leu | Lys | Ala | Glu | Glu | Thr | Glu | Gly |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |

036988010300



(2) INFORMATION FOR SEQ ID NO:2011:

- (2) INFORMATION FOR SEQ ID NO:2012:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2012:

(2) INFORMATION FOR SEQ ID NO:2013:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2013:

(21) SEQUENCE DESCRIPTION: SEQ ID: 1

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Pro | Ser | Thr | Arg | Ala | Ala | Glu | Leu | Arg | Val | Thr | Ala | Ala | Xaa | Xaa |
| 1   |     |     |     | 5   |     |     | 10  |     |     |     |     |     |     | 15  |     |
| Asn | Gly | Ala | Asp | Ala | Pro | Pro | Pro | Pro | Pro | Pro | Cys | Arg | Thr | His | Ser |

(x1) SEQUENCE DESCRIPTION: SEQ ID: 101

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gaacaaacgca gagaaaagaa aaccgctcca atccggaagc tgaaaatagc agaagaatcc | 60  |
| agaggcgact ccagggtttgt cggcgatgct gcgagcggga ggcaggcggc tmctcgcccc | 120 |

(2) INFORMATION FOR SEQ ID NO:2017:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2017:

(2) INFORMATION FOR SEQ ID NO:2018:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2018:

(2) INFORMATION FOR SEQ ID NO:2019:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2019:

(2) INFORMATION FOR SEQ ID NO:2020:





- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..458
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1599770
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2025:

|              |             |            |            |            |            |     |
|--------------|-------------|------------|------------|------------|------------|-----|
| aggggaacccat | cttctctcttc | cccgcgctgc | ctgctgcctg | ctcgagcttg | gagatggcgt | 60  |
| tggtgcggcg   | atgcctctgt  | ggatccgagg | aagactgcag | agcgcttttg | ggcatggaaa | 120 |
| atctccggct   | gttctcctac  | agagagatca | gagcaggcac | aaacaacttc | gatcagagta | 180 |
| acaagcttgg   | acgagggtgt  | tttggaactg | tctacaaggg | agttctaaga | gacggcactg | 240 |
| aatttgccgc   | gaaggttctg  | tcctcggaat | ccgagcaggg | gatcaaggag | ttcctagctg | 300 |
| agatcgagag   | catctcccag  | gtgaagcacg | cgaacctcgt | caggctgctg | ggctgctgcg | 360 |
| tgcagaggaa   | aaaaaggatc  | ctggtgtacg | agtacottgc | gaacaacagc | ctcgatcatg | 420 |
| cgctcaaagg   | agcagcagca  | gatctaccct | ggagcacg   |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2026:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 152 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..152
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1599771
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2026:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Thr | Ile | Phe | Phe | Pro | Ala | Leu | Pro | Ala | Ala | Cys | Ser | Ser | Leu |     |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Glu | Met | Ala | Leu | Val | Arg | Arg | Cys | Leu | Cys | Gly | Ser | Glu | Glu | Asp | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Arg | Ala | Leu | Leu | Gly | Met | Glu | Asn | Leu | Arg | Leu | Phe | Ser | Tyr | Arg | Glu |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Ile | Arg | Ala | Gly | Thr | Asn | Asn | Phe | Asp | Gln | Ser | Asn | Lys | Leu | Gly | Arg |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Gly | Phe | Gly | Thr | Val | Tyr | Lys | Gly | Val | Leu | Arg | Asp | Gly | Thr | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Phe | Ala | Ala | Lys | Val | Leu | Ser | Ser | Glu | Ser | Glu | Gln | Gly | Ile | Lys | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Phe | Leu | Ala | Glu | Ile | Glu | Ser | Ile | Ser | Gln | Val | Lys | His | Ala | Asn | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Val | Arg | Leu | Leu | Gly | Cys | Cys | Val | Gln | Arg | Lys | Lys | Arg | Ile | Leu | Val |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Tyr | Glu | Tyr | Leu | Ala | Asn | Asn | Ser | Leu | Asp | His | Ala | Leu | Lys | Gly | Ala |
|     |     |     | 130 |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Ala | Ala | Asp | Leu | Pro | Trp | Ser | Thr |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2027:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 135 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..135
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1599772
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2027:

0968980-10130



gcacctggat gtggcgagtg gaagaggcca atgaagcaga atcctgctta caagggcaag 240  
tggcatgcac ctatgattga caaccccaac tacaagggaa tctggaagcc tcaggagatc 300  
cccaaccctg agtactttga gcttgacaag cctgactttg atccaattgc tgctattggg 360  
attgagatct ggacaatgca ggatggcatc ctgtttgaca atatcttgat tgctgacgat 420  
nagaaggttg c

(2) INFORMATION FOR SEQ ID NO:2030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2030:

Asp Trp Asp Val Asp Ala Pro Met Glu Ile Val Asp Asp Glu Ala Thr  
1 5 10 15  
Lys Pro Glu Gly Trp Leu Asp Asp Glu Pro Glu Glu Ile Asp Asp Pro  
20 25 30  
Glu Ala Ala Asn Pro Glu Asp Trp Asp Asp Glu Glu Asp Gly Glu Trp  
35 40 45  
Glu Ala Pro Lys Ile Asp Asn Pro Lys Cys Glu Glu Ala Pro Gly Cys  
50 55 60  
Gly Glu Trp Lys Arg Pro Met Lys Gln Asn Pro Ala Tyr Lys Gly Lys  
65 70 75 80  
Trp His Ala Pro Met Ile Asp Asn Pro Asn Tyr Lys Gly Ile Trp Lys  
85 90 95  
Pro Gln Glu Ile Pro Asn Pro Glu Tyr Phe Glu Leu Asp Lys Pro Asp  
100 105 110  
Phe Asp Pro Ile Ala Ala Ile Gly Ile Glu Ile Trp Thr Met Gln Asp  
115 120 125  
Gly Ile Leu Phe Asp Asn Ile Leu Ile Ala Asp Asp Xaa Lys Val  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2031:

Met Glu Ile Val Asp Asp Glu Ala Thr Lys Pro Glu Gly Trp Leu Asp  
1 5 10 15  
Asp Glu Pro Glu Glu Ile Asp Asp Pro Glu Ala Ala Asn Pro Glu Asp  
20 25 30  
Trp Asp Asp Glu Glu Asp Gly Glu Trp Glu Ala Pro Lys Ile Asp Asn  
35 40 45  
Pro Lys Cys Glu Glu Ala Pro Gly Cys Gly Glu Trp Lys Arg Pro Met  
50 55 60  
Lys Gln Asn Pro Ala Tyr Lys Gly Lys Trp His Ala Pro Met Ile Asp  
65 70 75 80  
Asn Pro Asn Tyr Lys Gly Ile Trp Lys Pro Gln Glu Ile Pro Asn Pro  
85 90 95  
Glu Tyr Phe Glu Leu Asp Lys Pro Asp Phe Asp Pro Ile Ala Ala Ile  
100 105 110

006555960







gaactccacc tccccgtgct actacgacgg ccgctactgg accatctsga agctgccccat 420  
gttcggtgc aacgacgccca cccaggtgta caaggatct

(2) INFORMATION FOR SEQ ID NO:2038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2038:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gln | Asp | Asp | Pro | Ser | Lys | Gln | Ala | Ser | Ser | Glu | Tyr | Ile | His | Thr | Arg |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Gln | Pro | Gly | Ser | His | Gly | Ala | His | Arg | Asp | Asp | Gly | Leu | Val | Gly | His |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg | Arg | Arg | Ser | Val | Pro | Gly | Ala | Gln | Val | His | Arg | Gln | Pro | Pro | His |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Pro | Pro | Leu | Leu | Gln | Lys | Pro | Arg | Gln | Arg | Gln | Gln | Arg | Arg | Lys |  |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Asp | Pro | Val | His | Ala | Gly | Val | Ala | Gly | Leu | Arg | Xaa | Gln | Glu | Val | Arg |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Asp | Ala | Val | Val | Pro | Ala | Ala | Ala | Val | Asp | Gly | Arg | Pro | Ala | Glu | Ala |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Val | Asp | Tyr | Leu | Leu | Arg | Asn | Gly | Trp | Ile | Pro | Cys | Leu | Glu | Phe | Ser |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Xaa | Val | Gly | Phe | Val | Tyr | Arg | Glu | Asn | Ser | Thr | Ser | Pro | Cys | Tyr | Tyr |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Asp | Gly | Arg | Tyr | Trp | Thr | Ile | Xaa | Lys | Leu | Pro | Met | Phe | Gly | Cys | Asn |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Asp | Ala | Thr | Gln | Val | Tyr | Lys | Asp |     |     |     |     |     |     |     |     |  |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2039:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2039:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Thr | Thr | Gln | Ala | Ser | Lys | Gln | Ala | Ser | Thr | Tyr | Ile | Leu | Gly |     |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |
| Ser | Gln | Ala | Ala | Met | Ala | Pro | Thr | Val | Met | Met | Ala | Ser | Ser | Ala | Thr |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ala | Val | Ala | Pro | Phe | Gln | Gly | Leu | Lys | Ser | Thr | Ala | Ser | Leu | Pro | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Arg | Arg | Ser | Ser | Arg | Ser | Leu | Gly | Asn | Val | Ser | Asn | Gly | Gly | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ile | Arg | Cys | Met | Gln | Val | Trp | Pro | Ala | Tyr | Xaa | Asn | Lys | Lys | Phe | Glu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Leu | Ser | Tyr | Leu | Pro | Pro | Leu | Ser | Thr | Asp | Asp | Leu | Leu | Lys | Gln |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Trp | Thr | Thr | Cys | Cys | Ala | Thr | Ala | Gly | Tyr | Pro | Ala | Ser | Ser | Ser | Ala |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Xaa | Ser | Ala | Ser | Cys | Thr | Ala | Arg | Thr | Pro | Pro | Pro | Arg | Ala | Thr | Thr |

03669980 03669980

115 120 125  
Thr Ala Ala Thr Gly Pro Ser Xaa Ser Cys Pro Cys Ser Ala Ala Thr  
130 135 140  
Thr Pro Pro Arg Cys Thr Arg Ile  
145 150

(2) INFORMATION FOR SEQ ID NO:2040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599832

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2040:

Met Ala Pro Thr Val Met Met Ala Ser Ser Ala Thr Ala Val Ala Pro  
1 5 10 15  
Phe Gln Gly Leu Lys Ser Thr Ala Ser Leu Pro Ile Ala Arg Arg Ser  
20 25 30  
Ser Arg Ser Leu Gly Asn Val Ser Asn Gly Gly Arg Ile Arg Cys Met  
35 40 45  
Gln Val Trp Pro Ala Tyr Xaa Asn Lys Lys Phe Glu Thr Leu Ser Tyr  
50 55 60  
Leu Pro Pro Leu Ser Thr Asp Asp Leu Leu Lys Gln Trp Thr Thr Cys  
65 70 75 80  
Cys Ala Thr Ala Gly Tyr Pro Ala Ser Ser Ala Xaa Ser Ala Ser  
85 90 95  
Cys Thr Ala Arg Thr Pro Pro Pro Arg Ala Thr Thr Thr Ala Ala Thr  
100 105 110  
Gly Pro Ser Xaa Ser Cys Pro Cys Ser Ala Ala Thr Thr Pro Pro Arg  
115 120 125  
Cys Thr Arg Ile  
130

(2) INFORMATION FOR SEQ ID NO:2041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..350
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2041:

gcgagcaacc cggcgaaasc ccccaaacc tcgcacccta aaacagcggc gcacaagatg 60  
tccgacgacc ccaccaacgg cggcggcggg gatcgctgg aggacgtcgt cgcgccgagg 120  
gtgaaacaca acctcgtgat gatggcttsn tcgaaatcca aggataggga caaagataga 180  
gaaarggaca aggacagaga tcgtcgccga gaccgtgaca gagatcgagg gagagacagg 240  
gaccgtgata gggataggga caggacagg gatcgggaca gagacaagga tcgccaaagt 300  
aggcatcacc gtnaaanacg ggaacagcga gaccgtccts atgatcacag

(2) INFORMATION FOR SEQ ID NO:2042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

09633360

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..116  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2042:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ser | Asn | Pro | Ala | Lys | Xaa | Pro | Lys | Pro | Ser | His | Pro | Lys | Thr | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | His | Lys | Met | Ser | Asp | Asp | Pro | Thr | Asn | Gly | Gly | Gly | Gly | Asp | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Glu | Asp | Val | Val | Ala | Pro | Arg | Val | Lys | His | Asn | Leu | Val | Met | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Xaa | Ser | Lys | Ser | Lys | Asp | Arg | Asp | Lys | Asp | Arg | Glu | Xaa | Asp | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asp | Arg | Asp | Arg | Arg | Arg | Asp | Arg | Asp | Arg | Asp | Arg | Gly | Arg | Asp | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Arg | Asp | Arg | Asp | Arg | Asp | Arg | Asp | Arg | Asp | Arg | Asp | Arg | Asp | Lys |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asp | Arg | Gln | Ser | Arg | His | His | Arg | Xaa | Xaa | Arg | Glu | Gln | Arg | Asp | Arg |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Pro | Xaa | Asp | His |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..97  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2043:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Asp | Asp | Pro | Thr | Asn | Gly | Gly | Gly | Gly | Asp | Arg | Val | Glu | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Val | Ala | Pro | Arg | Val | Lys | His | Asn | Leu | Val | Met | Met | Ala | Xaa | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Ser | Lys | Asp | Arg | Asp | Lys | Asp | Arg | Glu | Xaa | Asp | Lys | Asp | Arg | Asp |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Arg | Arg | Arg | Asp | Arg | Asp | Arg | Asp | Arg | Gly | Arg | Asp | Arg | Asp | Arg | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Asp | Arg | Asp | Arg | Asp | Arg | Asp | Arg | Asp | Arg | Asp | Lys | Asp | Arg | Gln |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Arg | His | His | Arg | Xaa | Xaa | Arg | Glu | Gln | Arg | Asp | Arg | Pro | Xaa | Asp |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |

His

(2) INFORMATION FOR SEQ ID NO:2044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..70  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2044:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Ala | Xaa | Ser | Lys | Ser | Lys | Asp | Arg | Asp | Lys | Asp | Arg | Glu | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Lys | Asp | Arg | Asp | Arg | Arg | Arg | Asp | Arg | Asp | Arg | Asp | Arg | Gly | Arg |



- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..136  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599855  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2047:

Lys Ala Thr Ala Ser Ala Arg Ser Ser Ser Leu Gly Gly Gly Pro Thr  
1                    5                    10                    15  
Asp Gln Pro Ala Arg Trp Arg Ala Gly Arg Ser Ala Phe Ser Trp Pro  
                    20                    25                    30  
Trp Arg Ala Leu Arg Xaa Ala Ala Arg Ala Ala Asp Asp Asp Asp Lys  
                    35                    40                    45  
Thr Gln Pro Trp Gln Cys Phe Arg Ser Cys Ser Arg Gly Cys His His  
50                    55                    60  
His His Asp His Asp His Asp Asn Gly Ala Ala Ala Val Ala Asp Phe  
65                    70                    75                    80  
Leu Ser Gly Ala Ala Ala Lys Val Ser Ala Ala Val Thr Arg Glu Cys  
                    85                    90                    95  
Lys Asn Asn Ser Cys His Asp Asn Ala Cys Phe Lys Asp Xaa Pro Ala  
                    100                    105                    110  
Ile Thr Tyr Pro Gln Cys Ala Ile Ala Thr Cys Leu Ser Leu Pro His  
115                    120                    125  
His Ser Lys Xaa Asn Gly Val Leu  
130                    135

(2) INFORMATION FOR SEQ ID NO:2048:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 81 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..81  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2048:

Met Ala Arg Arg Ala Val Gly Val Leu Ala Val Ala Arg Ser Ser  
1                    5                    10                    15  
Xaa Gly Arg Glu Gly Ser Arg Arg Arg Arg Gln Asp Ala Ala Leu Ala  
                    20                    25                    30  
Val Leu Gln Val Met Leu Gln Arg Leu Pro Pro Pro Pro Arg Pro Arg  
35                    40                    45  
Pro Arg Gln Arg Arg Cys Cys Arg Gly Gly Leu Pro Leu Arg Gly Arg  
50                    55                    60  
Arg Gln Gly Leu Arg Arg Arg His Pro Arg Val Gln Glu Gln Gln Leu  
65                    70                    75                    80  
Pro

(2) INFORMATION FOR SEQ ID NO:2049:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 457 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
    (B) LOCATION: 1..457  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2049:

09639800 103000

acacaccacc accgctgctg ctgcacctca tacatatata accggagcta gaagctcgtc 60  
tctgccacca aggagggcct gaagctggac gagagtgagg atgagaagaa gcgcaaggag 120  
gagctcaagg agaagtttga gggcctctgc aaggctcatca aggaggtgct gggcgacaag 180  
gtggagaagg tgggtggtctc cgacgogtgg tggactcccc ctgctgcctg gtgaccggcg 240  
agtacggttg gaccgccaac atggagcgga tcatgaaagc ccaggcgctg agggactcca 300  
gcatgtctgg gtacatgtcc tccaagaaga cgatggagat caaccccgag aacgccatca 360  
tggaggagct ccgcaagcgt gccgaggctg acaagaacga caagtccgtt aaggaccttn 420  
tcatgctgct gttcgagacg gcgctgctca cttctgg

(2) INFORMATION FOR SEQ ID NO:2050:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1599862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2050:

Met Arg Arg Ser Ala Arg Arg Ser Ser Arg Ser Leu Arg Ala Ser  
1 5 10 15  
Ala Arg Ser Ser Arg Arg Cys Trp Ala Thr Arg Trp Arg Arg Trp Trp  
20 25 30  
Ser Pro Thr Arg Gly Gly Leu Pro Leu Leu Pro Gly Asp Arg Arg Val  
35 40 45  
Arg Leu Asp Arg Gln His Gly Ala Asp His Glu Ser Pro Gly Ala Glu  
50 55 60  
Gly Leu Gln His Val Trp Val His Val Leu Gln Asp Asp Gly Asp  
65 70 75 80  
Gln Pro Arg Glu Arg His His Gly Gly Ala Pro Gln Ala Cys Arg Gly  
85 90 95

(2) INFORMATION FOR SEQ ID NO:2051:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1599863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2051:

Met Glu Arg Ile Met Lys Ala Gln Ala Leu Arg Asp Ser Ser Met Ser  
1 5 10 15  
Gly Tyr Met Ser Ser Lys Lys Thr Met Glu Ile Asn Pro Glu Asn Ala  
20 25 30  
Ile Met Glu Glu Leu Arg Lys Arg Ala Glu Ala Asp Lys Asn Asp Lys  
35 40 45  
Ser Val Lys Asp Leu Xaa Met Leu Leu Phe Glu Thr Ala Leu Leu Thr  
50 55 60  
Ser  
65

(2) INFORMATION FOR SEQ ID NO:2052:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:



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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2052:
Met Lys Ala Gln Ala Leu Arg Asp Ser Ser Met Ser Gly Tyr Met Ser
1 5 10 15
Ser Lys Lys Thr Met Glu Ile Asn Pro Glu Asn Ala Ile Met Glu Glu
 20 25 30
Leu Arg Lys Arg Ala Glu Ala Asp Lys Asn Asp Lys Ser Val Lys Asp
 35 40 45
Leu Xaa Met Leu Leu Phe Glu Thr Ala Leu Leu Thr Ser
 50 55 60

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2053:

(2) INFORMATION FOR SEQ ID NO:2054:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2054:

(2) INFORMATION FOR SEQ ID NO:2055:

(A) LENGTH: 332 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

| Lactose       |      |
|---------------|------|
| Concentration | Time |
| 0.1           | 0.1  |
| 0.2           | 0.2  |
| 0.3           | 0.3  |
| 0.4           | 0.4  |
| 0.5           | 0.5  |
| 0.6           | 0.6  |
| 0.7           | 0.7  |
| 0.8           | 0.8  |
| 0.9           | 0.9  |
| 1.0           | 1.0  |
| 1.1           | 1.1  |
| 1.2           | 1.2  |
| 1.3           | 1.3  |
| 1.4           | 1.4  |
| 1.5           | 1.5  |
| 1.6           | 1.6  |
| 1.7           | 1.7  |
| 1.8           | 1.8  |
| 1.9           | 1.9  |
| 2.0           | 2.0  |
| 2.1           | 2.1  |
| 2.2           | 2.2  |
| 2.3           | 2.3  |
| 2.4           | 2.4  |
| 2.5           | 2.5  |
| 2.6           | 2.6  |
| 2.7           | 2.7  |
| 2.8           | 2.8  |
| 2.9           | 2.9  |
| 3.0           | 3.0  |
| 3.1           | 3.1  |
| 3.2           | 3.2  |
| 3.3           | 3.3  |
| 3.4           | 3.4  |
| 3.5           | 3.5  |
| 3.6           | 3.6  |
| 3.7           | 3.7  |
| 3.8           | 3.8  |
| 3.9           | 3.9  |
| 4.0           | 4.0  |
| 4.1           | 4.1  |
| 4.2           | 4.2  |
| 4.3           | 4.3  |
| 4.4           | 4.4  |
| 4.5           | 4.5  |
| 4.6           | 4.6  |
| 4.7           | 4.7  |
| 4.8           | 4.8  |
| 4.9           | 4.9  |
| 5.0           | 5.0  |
| 5.1           | 5.1  |
| 5.2           | 5.2  |
| 5.3           | 5.3  |
| 5.4           | 5.4  |
| 5.5           | 5.5  |
| 5.6           | 5.6  |
| 5.7           | 5.7  |
| 5.8           | 5.8  |
| 5.9           | 5.9  |
| 6.0           | 6.0  |
| 6.1           | 6.1  |
| 6.2           | 6.2  |
| 6.3           | 6.3  |
| 6.4           | 6.4  |
| 6.5           | 6.5  |
| 6.6           | 6.6  |
| 6.7           | 6.7  |
| 6.8           | 6.8  |
| 6.9           | 6.9  |
| 7.0           | 7.0  |
| 7.1           | 7.1  |
| 7.2           | 7.2  |
| 7.3           | 7.3  |
| 7.4           | 7.4  |
| 7.5           | 7.5  |
| 7.6           | 7.6  |
| 7.7           | 7.7  |
| 7.8           | 7.8  |
| 7.9           | 7.9  |
| 8.0           | 8.0  |
| 8.1           | 8.1  |
| 8.2           | 8.2  |
| 8.3           | 8.3  |
| 8.4           | 8.4  |
| 8.5           | 8.5  |
| 8.6           | 8.6  |
| 8.7           | 8.7  |
| 8.8           | 8.8  |
| 8.9           | 8.9  |
| 9.0           | 9.0  |
| 9.1           | 9.1  |
| 9.2           | 9.2  |
| 9.3           | 9.3  |
| 9.4           | 9.4  |
| 9.5           | 9.5  |
| 9.6           | 9.6  |
| 9.7           | 9.7  |
| 9.8           | 9.8  |
| 9.9           | 9.9  |
| 10.0          | 10.0 |

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..332  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2055:  
taacagtact tgtggtggca tttatgttac aggatggcac tgcgaactac ttgaaaggac 60  
ttatgctgat cctatgttat ctaatagttg ctgccagttt ctttgttcac gttgatccac 120  
aatcaagtga aggetgaagc catatatacct gtaagtaacg cgccaaatac cttttgagac 180  
ttaataatct tgttttgttc cgcctgtctc aagccgggtt ccttcatacgtg ctgcagaagg 240  
aatttttgta ttttgttttg tggatactga tgtgtactag ggtantctcg atgtatacag 300  
aaacaagaag tggcagcatg ttatattcga tt

(2) INFORMATION FOR SEQ ID NO:2056:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 37 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..37  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599892

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2056:  
Asn Ser Thr Cys Gly Gly Ile Tyr Val Thr Gly Trp His Cys Glu Leu  
1                   5                   10                   15  
Leu Glu Arg Thr Tyr Ala Asp Pro Met Leu Ser Asn Ser Cys Cys Gln  
                  20                   25                   30  
Phe Leu Cys Ser Arg  
                  35

(2) INFORMATION FOR SEQ ID NO:2057:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 44 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..44  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599893

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2057:  
Thr Val Leu Val Val Ala Phe Met Leu Gln Asp Gly Thr Ala Asn Tyr  
1                   5                   10                   15  
Leu Lys Gly Leu Met Leu Ile Leu Cys Tyr Leu Ile Val Ala Ala Ser  
                  20                   25                   30  
Phe Phe Val His Val Asp Pro Gln Ser Ser Glu Gly  
                  35                   40

(2) INFORMATION FOR SEQ ID NO:2058:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 37 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..37  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1599894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2058:

DOCKET "08562950"

Met Leu Gln Asp Gly Thr Ala Asn Tyr Leu Lys Gly Leu Met Leu Ile  
1 5 10 15  
Leu Cys Tyr Leu Ile Val Ala Ala Ser Phe Phe Val His Val Asp Pro  
20 25 30  
Gln Ser Ser Glu Gly  
35

(2) INFORMATION FOR SEQ ID NO:2059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..354
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2059:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| gcggaasstg tccagatcgc gtgattccgc atcccgttcg ckakcgcgac acacgctgac | 60  |
| agctcacggc tgaccttccc gagtcccgc gccctccagc tccatcttga ttcttgaggc  | 120 |
| gavscgggtg cgtaagagtc tgccatggcc agcgagaata aggtctttgg gttcgaggaa | 180 |
| gtcgccaagc acaacgtcac caaggactnc tggatcatca tcgccggcaa ggtgtatgac | 240 |
| gtcactccgt ttatggatga gcactctggt ggagacgagg ttttgctagc tgtaactggg | 300 |
| aaagatgcta cagctgattt cgaagatatt ggccacagtg attccrcaaw ggac       |     |

(2) INFORMATION FOR SEQ ID NO:2060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2060:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ala Ser Glu Asn Lys Val Phe Gly Phe Glu Glu Val Ala Lys His |  |
| 1 5 10 15                                                       |  |
| Asn Val Thr Lys Asp Xaa Trp Ile Ile Ala Gly Lys Val Tyr Asp     |  |
| 20 25 30                                                        |  |
| Val Thr Pro Phe Met Asp Glu His Pro Gly Gly Asp Glu Val Leu Leu |  |
| 35 40 45                                                        |  |
| Ala Val Thr Gly Lys Asp Ala Thr Ala Asp Phe Glu Asp Ile Gly His |  |
| 50 55 60                                                        |  |
| Ser Asp Ser Xaa Xaa Asp                                         |  |
| 65 70                                                           |  |

(2) INFORMATION FOR SEQ ID NO:2061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..385
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2061:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gggccccctcc gcacgcctgc acacattccg cgcacacccc ggcagccgca aacgccttcg | 60  |
| ccgtcgcgtc ccgtcctcc gcccgcccga cgcgaccctt aggacctgga gagagaggtc   | 120 |
| ggcatggctg ccgcagtggc gcacgacgct ggtatggacg ccgtccagaa ggcgcctcatg | 180 |

DOCKET "08669950"

(2) INFORMATION FOR SEQ ID NO:2062:

(D) OTHER INFORMATION: / Ceres Seq. ID 1599915

[illegible]

(ix) FEATURE:

(2) INFORMATION FOR SEQ ID NO:2068:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1599945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2068:

(2) INFORMATION FOR SEQ ID NO:2069:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 428 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..428

(D) OTHER INFORMATION: / Ceres Seq. ID 1599954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2069:

cttccaccac gcagtcactc ccgggccgcc gccgccgccg cctccgcgaa aaaccctagc

[illegible]

(2) INFORMATION FOR SEQ ID NO:2070:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

```
(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1599955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2070:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Pro | Pro | Arg | Ser | His | Ser | Arg | Ala | Ala | Ala | Ala | Ser | Ala |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |

Lys Asn Pro Ser Arg Leu Arg Ala Ile Thr Pro Arg Gly Ala Thr Met  
20 25 30

Val Ala Thr Lys Lys Thr Lys Lys Ser Thr Asp Asn Ile Asn Asn Lys

Leu Gln Leu Val Met Lys Ser Gly Lys Tyr Thr Leu Gly Tyr Lys Thr

Val Leu Arg Thr Leu Arg Asn Ser Lys Ser Lys Leu Val Ile Ile Ala  
65 70 75 80

Asn Asn Cys Pro Pro Leu Arg Lys Xaa  
85

(2) INFORMATION FOR SEQ ID NO:2071:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..52

(D) OTHER INFORMATION: / Ceres Seq. ID 1599956

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2071:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10

|   | Phe | His | His | Ala | Val | Thr | Pro | Gly | Pro | Pro | Pro | Pro | Pro | Arg |
|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1 |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |

Lys Thr Leu Ala Gly Phe Ala Leu Ser Leu Gln Gly Ala Arg Pro Trp  
20 25 30

Trp Pro Gln Arg Arg Arg Arg Asn Pro Arg Thr Thr Ser Ile Thr Ser

Cys Ser Leu Leu  
50

(2) INFORMATION FOR SEQ ID NO:2072:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..58

(2) INFORMATION FOR SEQ ID NO:2073:

(A) LENGTH: 315 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..315

(D) OTHER INFORMATION: / Ceres Seq. ID 1599969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2073:

|            |            |             |            |             |             |     |
|------------|------------|-------------|------------|-------------|-------------|-----|
| gcagtgcttc | acacccacgc | cttcacacc   | caccaccacc | accacccggac | agggacacgc  | 60  |
| acggcactag | ctcgaggagg | gtcggcaagc  | cagagtcaca | gcagaaggtg  | aaagggagcg  | 120 |
| gacatggggg | cggatcggtt | cctgagcgtg  | gcgnagggcg | gcctcggcgg  | cgaggcgcctc | 180 |
| tacttcgcgg | tcatcctgtg | gctgtccgtc  | atgtcgtgga | tcattctcac  | ctgggtcggc  | 240 |
| gacggcgggg | aggacgggag | gcggggggagg | aagcgccggg | gcagccgcgg  | cacccggtgt  | 300 |
| tcgtccgcac | atcga      |             |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2074:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1599970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2074:

[illegible]

(2) INFORMATION FOR SEO ID NO:2075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

[illegible]



(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2075:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ala | Asp | Arg | Phe | Leu | Ser | Val | Ala | Xaa | Gly | Gly | Leu | Gly | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Ala | Leu | Tyr | Phe | Ala | Val | Ile | Leu | Trp | Leu | Ser | Val | Met | Ser | Trp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ile | Phe | Thr | Trp | Val | Gly | Asp | Gly | Gly | Glu | Asp | Gly | Arg | Arg | Gly |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Arg | Lys | Arg | Arg | Gly | Ser | Arg | Gly | Thr | Arg | Cys | Ser | Ser | Ala | Arg | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2076:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..314
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2076:

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| ccgccccgct | ccttgccctcc | gatccccaat | tcctccttcg  | gatctcgcat | tcagcgcann | 60  |
| aggtgtgaag | gaagggggac  | gcggaggaag | atgggggctcg | cgttcgggaa | gctcttcakc | 120 |
| cggctcttcg | ccaagaagga  | gatgcggatc | ctcatggctcg | gcctcgacgc | cgccggtaaa | 180 |
| accaccatcc | tctacaagct  | caagctcggc | gagatcgta   | ccaccatccc | caccatcggt | 240 |
| ttcaatgttg | aaactgttga  | gtacaagarc | attagcttca  | ctgtctngga | tgctgggggt | 300 |
| caggacaaga | tcag        |            |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2077:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Pro | Arg | Ser | Leu | Pro | Pro | Ile | Pro | Asn | Ser | Ser | Phe | Gly | Ser | Arg |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | Gln | Arg | Xaa | Arg | Cys | Glu | Gly | Arg | Gly | Thr | Arg | Arg | Lys | Met | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ala | Phe | Gly | Lys | Leu | Phe | Xaa | Arg | Leu | Phe | Ala | Lys | Lys | Glu | Met |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Arg | Ile | Leu | Met | Val | Gly | Leu | Asp | Ala | Ala | Gly | Lys | Thr | Thr | Ile | Leu |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Tyr | Lys | Leu | Lys | Leu | Gly | Glu | Ile | Val | Thr | Thr | Ile | Pro | Thr | Ile | Gly |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Phe | Asn | Val | Glu | Thr | Val | Glu | Tyr | Lys | Xaa | Ile | Ser | Phe | Thr | Val | Xaa |
|     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Asp | Val | Gly | Gly | Gln | Asp | Lys | Ile |     |     |     |     |     |     |     |     |
|     |     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..104  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599978  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2078:

Arg Pro Ala Pro Cys Leu Arg Ser Pro Ile Pro Pro Ser Asp Leu Ala  
1 5 10 15  
Phe Ser Ala Xaa Gly Val Lys Glu Gly Arg Gly Gly Arg Trp Gly  
20 25 30  
Ser Arg Ser Gly Ser Ser Ser Xaa Gly Ser Ser Pro Arg Arg Arg Cys  
35 40 45  
Gly Ser Ser Trp Ser Ala Ser Thr Pro Pro Val Lys Pro Pro Ser Ser  
50 55 60  
Thr Ser Ser Ser Ser Ala Arg Ser Ser Pro Pro Ser Pro Pro Ser Val  
65 70 75 80  
Ser Met Leu Lys Leu Leu Ser Thr Arg Xaa Leu Ala Ser Leu Ser Xaa  
85 90 95  
Met Ser Gly Val Arg Thr Arg Ser  
100

(2) INFORMATION FOR SEQ ID NO:2079:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 74 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..74  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599979  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2079:

Met Gly Leu Ala Phe Gly Lys Leu Phe Xaa Arg Leu Phe Ala Lys Lys  
1 5 10 15  
Glu Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr  
20 25 30  
Ile Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr  
35 40 45  
Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Xaa Ile Ser Phe Thr  
50 55 60  
Val Xaa Asp Val Gly Gly Gln Asp Lys Ile  
65 70

(2) INFORMATION FOR SEQ ID NO:2080:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 389 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..389  
(D) OTHER INFORMATION: / Ceres Seq. ID 1599983  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2080:

acagttccac gccgccactc cccccaaccc gaccacgctg cgcctccgct tgatccccag 60  
ccgaggggagg aatgggtaag ggtacgggca gcttcggcaa gcgccggaac aagacgcaca 120  
cgctctgcat cgcgtgcggc cgccgcasst tccacctcca gaagagtacc tgctcctcct 180

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gcggttaccc cgccgcccgc atccgcaagt ataactggag tgtgaaggcc atcaggcgca 240  
agacaaccgg taccgaaagg atnaggtaca tgcgccacgt gcctcgccgt ttcaagagca 300  
acttcagaga agggactssa ggctgctccc aagaagagtg ctgccgctgc caactaagts 360  
stggatcttg ctatcaagaa tctgataag

(2) INFORMATION FOR SEQ ID NO:2081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2081:

Thr Val Pro Arg Arg His Ser Pro Gln Pro Asp His Ala Ala Pro Pro  
1 5 10 15  
Leu Asp Pro Gln Pro Arg Glu Glu Trp Val Arg Val Arg Ala Ala Ser  
20 25 30  
Ala Ser Ala Gly Thr Arg Arg Thr Arg Ser Ala Ser Ala Ala Ala  
35 40 45  
Ala Xaa Ser Thr Ser Arg Arg Val Pro Ala Pro Pro Ala Val Thr Pro  
50 55 60  
Pro Pro Ala Ser Ala Ser Ile Thr Gly Val  
65 70

(2) INFORMATION FOR SEQ ID NO:2082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1599985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2082:

Met Gly Lys Gly Thr Gly Ser Phe Gly Lys Arg Arg Asn Lys Thr His  
1 5 10 15  
Thr Leu Cys Ile Arg Cys Gly Arg Arg Xaa Phe His Leu Gln Lys Ser  
20 25 30  
Thr Cys Ser Ser Cys Gly Tyr Pro Ala Ala Arg Ile Arg Lys Tyr Asn  
35 40 45  
Trp Ser Val Lys Ala Ile Arg Arg Lys Thr Thr Gly Thr Glu Arg Xaa  
50 55 60  
Arg Tyr Met Arg His Val Pro Arg Arg Phe Lys Ser Asn Phe Arg Glu  
65 70 75 80  
Gly Thr Xaa Gly Cys Ser Gln Glu Glu Cys Cys Arg Cys Gln Leu Ser  
85 90 95  
Xaa Gly Ser Cys Tyr Gln Glu Ser Asp Lys  
100 105

(2) INFORMATION FOR SEQ ID NO:2083:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

00669980-1013100

(B) LOCATION: 1..408

(D) OTHER INFORMATION: / Ceres Seq. ID 1599992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2083:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ctccactcgc cctccabnsn cagaaaaccc tagccgcccgc caccgaagcg gcctcccagg | 60  |
| taagcaggag cgtccacccc gccgcgctca tgaagcgcaa tccccgcgtc acgagctccc  | 120 |
| gccggaagtg ccgcaasgca cttttacggc cccgtcctcc gtccgcccgc ttctcatgtc  | 180 |
| cgccgggcts tcgacggagc tccgccacaa gtacaacgtg cgctccatcc cgatccgcaa  | 240 |
| gacgacgagg tgcaggctgt gcgoggcaca gacttcgtca atccatcgcr gctggacaag  | 300 |
| cgtccgctcg tanaggtgat cgttgagatg accggcgggc gcgtggacta cagcttcgag  | 360 |
| tgcacggcgc tgcstcggg gatgaccgac gccttcagat gcaccaag                |     |

(2) INFORMATION FOR SEQ ID NO:2084:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1599993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2084:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ser Thr Arg Pro Pro Xaa Xaa Glu Asn Pro Ser Arg Arg His Arg Ser |  |
| 1 5 10 15                                                       |  |
| Gly Leu Pro Gly Lys Gln Glu Arg Pro Pro Arg Arg Arg His Glu Ala |  |
| 20 25 30                                                        |  |
| Gln Ser Pro Arg His Glu Leu Pro Glu Val Pro Gln Xaa Thr Phe     |  |
| 35 40 45                                                        |  |
| Thr Ala Pro Ser Ser Val Arg Arg Val Leu Met Ser Ala Gly Xaa Ser |  |
| 50 55 60                                                        |  |
| Thr Glu Leu Arg His Lys Tyr Asn Val Arg Ser Ile Pro Ile Arg Lys |  |
| 65 70 75 80                                                     |  |
| Thr Thr Arg Cys Arg Ser Cys Ala Ala Gln Thr Ser Ser Ile His Arg |  |
| 85 90 95                                                        |  |
| Xaa Trp Thr Ser Val Pro Ser Xaa Arg                             |  |
| 100 105                                                         |  |

(2) INFORMATION FOR SEQ ID NO:2085:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1599994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2085:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Pro Leu Ala Leu Pro Xaa Gln Lys Thr Leu Ala Ala Ala Thr Glu Ala |  |
| 1 5 10 15                                                       |  |
| Ala Ser Gln Val Ser Arg Ser Val His Pro Ala Ala Val Met Lys Arg |  |
| 20 25 30                                                        |  |
| Asn Pro Arg Val Thr Ser Ser Arg Arg Lys Cys Arg Xaa Ala Leu Leu |  |
| 35 40 45                                                        |  |
| Arg Pro Arg Pro Pro Ser Ala Ala Phe Ser Cys Pro Pro Gly Xaa Arg |  |
| 50 55 60                                                        |  |
| Arg Ser Ser Ala Thr Ser Thr Thr Cys Ala Pro Ser Arg Ser Ala Arg |  |
| 65 70 75 80                                                     |  |
| Arg Arg Gly Ala Gly Arg Ala Arg His Arg Leu Arg Gln Ser Ile Xaa |  |
| 85 90 95                                                        |  |
| Ala Gly Gln Ala Phe Arg Arg Xaa Gly Asp Arg                     |  |

DOCKET# 09668960



[illegible]

(2) INFORMATION FOR SEQ ID NO:2092:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51

(D) OTHER INFORMATION: / Ceres Seq. ID 1600041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2092:

Met His Leu Asp Ala Gln His Trp Leu Cys Ser Asp Lys Ser Thr Arg  
1 5 10 15  
His Tyr Xaa Pro Ser Lys Phe Lys Lys Phe Xaa Val His Asn Val Ser  
20 25 30  
Glu Leu Glu Leu Leu Met Met His Asn Arg Thr Tyr Cys Ala Glu Ile  
35 40 45  
Ala His Asn  
50

(2) INFORMATION FOR SEQ ID NO:2093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..415

(D) OTHER INFORMATION: / Ceres Seq. ID 1600059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2093:

gaccgagcta ggagaagcgc gaacncgtgc atgcgcagac gttgaggtcg agggacacgg 60  
tatctctgag cttcatcgga gagcgacccg ccaccgccac gcttgggcgc aagccgagaa 120  
gagtgccggg ccgggagacc ggacgattat tgatccgtag cagattcgct aatggcggag 180  
acggcggaca tggagcggat cttcaagcgg ttcgacacca acggcgacgg taagatctcg 240  
ctgtcggagc tgacggaggc gctacggacg ctggggtcca cctctgccga cgaggtgcag 300  
cgcgatgatg ccgagatcga caccgacggc gacggctgta togacttcaa cgagttcatc 360  
accttctgca acgccaaccc ggggctcatg aaggacgtcg caaaggtcct ctgat

(2) INFORMATION FOR SEQ ID NO:2094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52

(D) OTHER INFORMATION: / Ceres Seq. ID 1600060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2094:

Thr Glu Leu Gly Glu Ala Arg Xaa Arg Ala Cys Ala Asp Val Glu Val  
1 5 10 15  
Glu Gly His Gly Ile Ser Glu Leu His Arg Arg Ala Thr Arg His Arg  
20 25 30  
His Ala Trp Pro Gln Ala Glu Lys Ser Ala Gly Pro Gly Asp Arg Thr  
35 40 45  
Ile Ile Asp Pro  
50

(2) INFORMATION FOR SEQ ID NO:2095:

(i) SEQUENCE CHARACTERISTICS:

00000000 00000000





gccggactcn gaaattncca tcaggtctgct agagcccatc aaggagcagt tccccatcct 360  
atcctacgct gactttctacc agcttinctgg agtcgtsssc agtcgaggta acggcgacc 420  
tgatgtccct tccacccc

(2) INFORMATION FOR SEQ ID NO:2098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2098:

Gly Trp Leu Pro Pro Asn Ser Phe His Pro Arg Leu Leu Arg Ser Asp  
1 5 10 15  
His Arg Ala Ser Ser Gly Ala Xaa Arg Asp Val Ser Arg His Gly Glu  
20 25 30  
Gly Leu Pro His Gly Glu Arg Gly Leu Pro Gln Gly Gly Arg Gln Gly  
35 40 45  
Gln Ala Gln Xaa Pro Arg Pro His Arg Arg Glu Glu Leu Arg Pro Ala  
50 55 60  
His Ala Pro Pro Arg Met Ala Leu Arg Gly His Leu Arg Cys Gly His  
65 70 75 80  
Gln Asn Arg Gly Pro Leu Arg His His Glu Glu Pro Arg Arg Ala Xaa  
85 90 95  
His Gly Ala Asn Ala Gly Leu Xaa Asn Xaa His Gln Ala Ala Arg Ala  
100 105 110  
His Gln Gly Ala Val Pro His Pro Ile Leu Arg  
115 120

(2) INFORMATION FOR SEQ ID NO:2099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2099:

Ala Gly Ser His Arg Ile His Ser Thr Pro Val Ser Ser Asp Arg Thr  
1 5 10 15  
Thr Gly Pro Ala Ala Gly Xaa Ile Val Thr Ser Ala Gly Met Val Lys  
20 25 30  
Ala Tyr Pro Thr Val Asn Glu Asp Tyr Leu Lys Ala Val Asp Lys Ala  
35 40 45  
Lys Arg Xaa Xaa Arg Gly Leu Ile Ala Glu Lys Asn Cys Ala Pro Leu  
50 55 60  
Met Leu Arg Leu Ala Trp His Ser Ala Gly Thr Phe Asp Val Ala Thr  
65 70 75 80  
Lys Thr Gly Gly Pro Phe Gly Thr Met Lys Asn Pro Ala Glu Gln Xaa  
85 90 95  
Thr Glu Pro Thr Pro Asp Xaa Glu Ile Xaa Ile Arg Leu Leu Glu Pro  
100 105 110  
Ile Lys Glu Gln Phe Pro Ile Leu Ser Tyr Ala Asp Phe Tyr Gln Leu  
115 120 125  
Xaa Gly Val Xaa Xaa Ser Arg Gly Asn Gly Gly Pro Asp Val Pro Ser  
130 135 140

096555950

Thr  
145

(2) INFORMATION FOR SEQ ID NO:2100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2100:

```
Met Val Lys Ala Tyr Pro Thr Val Asn Glu Asp Tyr Leu Lys Ala Val
1 5 10 15
Asp Lys Ala Lys Arg Xaa Xaa Arg Gly Leu Ile Ala Glu Lys Asn Cys
20 25 30
Ala Pro Leu Met Leu Arg Leu Ala Trp His Ser Ala Gly Thr Phe Asp
35 40 45
Val Ala Thr Lys Thr Gly Gly Pro Phe Gly Thr Met Lys Asn Pro Ala
50 55 60
Glu Gln Xaa Thr Glu Pro Thr Pro Asp Xaa Glu Ile Xaa Ile Arg Leu
65 70 75 80
Leu Glu Pro Ile Lys Glu Gln Phe Pro Ile Leu Ser Tyr Ala Asp Phe
85 90 95
Tyr Gln Leu Xaa Gly Val Xaa Xaa Ser Arg Gly Asn Gly Gly Pro Asp
100 105 110
Val Pro Ser Thr
115
```

(2) INFORMATION FOR SEQ ID NO:2101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..416
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2101:

```
aagtaaacct cgtttccgca tgccgaccgt aaacgtgaaa tggcagaagg aggtctttcc 60
aggcatagag attgacacta gccagcctcc gattgktttg aagagtcagc tatacacact 120
aactggtgtg ccacctgaac gccaaaaaat tatggtgaag ggtggattat tgaaggatga 180
tgcagattgg tctactttgg gagtgaaaga tggccaaaag ttaatgatga taggcacagc 240
tgatgagatt gttaaagctc cagagaragg tccactgttt gttgaggatc taccagaaga 300
agagcaagtg gttgcactgg gtcacagtct ggtctttaca atcttnggaa tacatgctat 360
atgadttcca cattgcratg tttgcrttca gttccagagc tgaagtcagc gctgct
```

(2) INFORMATION FOR SEQ ID NO:2102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2102:

0956960 0956960

| Met | Val | Lys | Gly | Gly | Leu | Leu | Lys | Asp | Asp | Ala | Asp | Trp | Ser | Thr | Leu |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Val | Lys | Asp | Gly | Gln | Lys | Leu | Met | Met | Ile | Gly | Thr | Ala | Asp | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Val | Lys | Ala | Pro | Glu | Xaa | Gly | Pro | Leu | Phe | Val | Glu | Asp | Leu | Pro |

[illegible]

35 40 45  
Glu Glu Glu Gln Val Val Ala Leu Gly His Ser Leu Val Phe Thr Ile  
50 55 60  
Xaa Gly Ile His Ala Ile  
65 70

(2) INFORMATION FOR SEQ ID NO:2105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..309
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2105:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| gctatacatc ccgaatccga cgctccatcg agtgtgtgcg gcggcgggag gagacggaag   | 60  |
| agaacgatgc aggcggtggc acgggcgcgt gggcttgccg ctgcggctgt ggctgcgcgg   | 120 |
| ccgtcggcga tggaggcagg gcaccgcggg caggtgcagc aagcccgggg cattgtggtg   | 180 |
| caggtgaggg acgggaacct ggagcgggcg ctggcggtca tggagcgcaa gatgaggtcc   | 240 |
| agcggcatgg agcgcccttat ccgagcgcgcg acccactacc acgtgaaaga ctcggagaag | 300 |
| cgcggtgctc                                                          |     |

(2) INFORMATION FOR SEQ ID NO:2106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2106:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ala Ile His Pro Glu Ser Asp Ala Pro Ser Ser Val Cys Gly Gly Gly |  |
| 1 5 10 15                                                       |  |
| Arg Arg Arg Lys Arg Thr Met Gln Ala Val Ala Arg Ala Arg Gly Leu |  |
| 20 25 30                                                        |  |
| Ala Ala Ala Ala Val Ala Ala Arg Pro Ser Ala Met Glu Ala Gly His |  |
| 35 40 45                                                        |  |
| Arg Gly Gln Val Gln Gln Ala Arg Gly Ile Val Val Gln Val Arg Asp |  |
| 50 55 60                                                        |  |
| Gly Asn Leu Glu Arg Ala Leu Ala Val Met Glu Arg Lys Met Arg Ser |  |
| 65 70 75 80                                                     |  |
| Ser Gly Met Glu Arg Leu Ile Arg Ala Arg Thr His Tyr His Val Lys |  |
| 85 90 95                                                        |  |
| Asp Ser Glu Lys Arg Val Leu                                     |  |
| 100                                                             |  |

(2) INFORMATION FOR SEQ ID NO:2107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2107:

00559301-01300

Tyr Thr Ser Arg Ile Arg Arg Ser Ile Glu Cys Val Arg Arg Arg Glu  
1 5 10 15  
Glu Thr Glu Glu Asn Asp Ala Gly Gly Thr Gly Ala Trp Ala Cys  
20 25 30  
Gly Cys Gly Cys Gly Cys Ala Ala Val Gly Asp Gly Gly Arg Ala Pro  
35 40 45  
Arg Ala Gly Ala Ala Ser Pro Gly His Cys Gly Ala Gly Glu Gly Arg  
50 55 60  
Glu Pro Gly Ala Gly Ala Gly Gly His Gly Ala Gln Asp Glu Val Gln  
65 70 75 80  
Arg His Gly Ala Pro Tyr Pro Ser Ala His Pro Leu Pro Arg Glu Arg  
85 90 95  
Leu Gly Glu Ala Arg Ala  
100

(2) INFORMATION FOR SEQ ID NO:2108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..81
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2108:

Met Gln Ala Val Ala Arg Ala Arg Gly Leu Ala Ala Ala Val Ala  
1 5 10 15  
Ala Arg Pro Ser Ala Met Glu Ala Gly His Arg Gly Gln Val Gln Gln  
20 25 30  
Ala Arg Gly Ile Val Val Gln Val Arg Asp Gly Asn Leu Glu Arg Ala  
35 40 45  
Leu Ala Val Met Glu Arg Lys Met Arg Ser Ser Gly Met Glu Arg Leu  
50 55 60  
Ile Arg Ala Arg Thr His Tyr His Val Lys Asp Ser Glu Lys Arg Val  
65 70 75 80  
Leu

(2) INFORMATION FOR SEQ ID NO:2109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..421
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2109:

cttggccttg gctggcgctc gcacctcaca gcagcagcag tcaacaacaa cctccactgc 60  
cgcaaccac cgagaggcga gaccggcggc ggcaaaagga cgatacaaaa gcagccaggg 120  
ttgctggcaa cassgtcggt cgcccgcccg ctgcgccatgg ggaggtcgcc gtgctgcgag 180  
aaggcgcaca ccaacaaggc cgcggtggacc aaggaggagg acgagcgccg gtcgcgcac 240  
atcaggggcg acggcgaggg gtgctggcgc tcgctgcccc aggcgcgcg ctctgcgct 300  
gcggcaagag ctgcgcctc cgtggatca actacctcg ccccgacctc aagcgcggca 360  
acttcacgga ggagaggacg agctcatcgt caagctgcac asgtccctcg gcaacaagtg 420  
g

(2) INFORMATION FOR SEQ ID NO:2110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO: 1<br>100 150 200 250 300 350 400 450 500 550 600 650 700 750 800 850 900 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|----------------------------------------------------------------------------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu                                                                                                            | Gly | Leu | Gly | Trp | Arg | Ser | His | Leu | Thr | Ala | Ala | Ala | Val | Asn | Asn |  |
| 1                                                                                                              |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Asn                                                                                                            | Leu | His | Cys | Arg | Asn | Pro | Pro | Arg | Gly | Glu | Thr | Gly | Gly | Gly | Lys |  |
|                                                                                                                |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg                                                                                                            | Thr | Ile | Gln | Lys | Gln | Pro | Gly | Leu | Leu | Ala | Thr | Xaa | Ser | Val | Ala |  |
|                                                                                                                |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg                                                                                                            | Pro | Leu | Ala | Met | Gly | Arg | Ser | Pro | Cys | Cys | Glu | Lys | Ala | His | Thr |  |
|                                                                                                                | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |  |
| Asn                                                                                                            | Lys | Gly | Ala | Trp | Thr | Lys | Glu | Glu | Asp | Glu | Arg | Leu | Val | Ala | His |  |
| 65                                                                                                             |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Ile                                                                                                            | Arg | Ala | His | Gly | Glu | Gly | Cys | Trp | Arg | Ser | Leu | Pro | Lys | Ala | Ala |  |
|                                                                                                                |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Gly                                                                                                            | Ser | Cys | Ala | Ala | Ala | Arg | Ala | Ala | Ala | Ser | Ala | Gly | Ser | Thr | Thr |  |
|                                                                                                                |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |
| Ser                                                                                                            | Ala | Pro | Thr | Ser | Ser | Ala | Ala | Thr | Ser | Arg | Arg | Arg | Gly | Arg | Ala |  |
|                                                                                                                |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| His                                                                                                            | Arg | Gln | Ala | Ala | Xaa | Val | Pro | Arg | Gln | Gln | Val |     |     |     |     |  |
|                                                                                                                | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |

(i) SEQUENCE CHARACTERISTICS:

```
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1600107

| SEQUENCE DESCRIPTION: SEQ ID NO: 1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu                                | Ala | Leu | Ala | Gly | Ala | Arg | Thr | Ser | Gln | Gln | Gln | Ser | Thr | Thr |     |  |
| 1                                  |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |  |
| Thr                                | Ser | Thr | Ala | Ala | Thr | His | Arg | Glu | Ala | Arg | Pro | Ala | Ala | Ala | Lys |  |
|                                    |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gly                                | Arg | Tyr | Lys | Ser | Ser | Gln | Gly | Cys | Trp | Gln | Xaa | Xaa | Arg | Ser | Pro |  |
|                                    |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ala                                | Arg | Ser | Pro | Trp | Gly | Gly | Arg | Arg | Ala | Ala | Arg | Arg | Arg | Thr | Pro |  |
|                                    |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Thr                                | Arg | Ala | Arg | Gly | Pro | Arg | Arg | Arg | Thr | Ser | Ala | Trp | Ser | Arg | Thr |  |
| 65                                 |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Ser                                | Gly | Arg | Thr | Ala | Arg | Gly | Ala | Gly | Ala | Arg | Cys | Pro | Arg | Pro | Pro |  |
|                                    |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Ala                                | Pro | Ala | Leu | Arg | Gln | Glu | Leu | Pro | Pro | Pro | Leu | Asp | Gln | Leu | Pro |  |
|                                    |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |
| Pro                                | Pro | Arg | Pro | Gln | Ala | Arg | Gln | Leu | His | Gly | Gly | Glu | Asp | Glu | Leu |  |
|                                    |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ile                                | Val | Lys | Leu | His | Xaa | Ser | Leu | Gly | Asn | Lys | Trp |     |     |     |     |  |
|                                    |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids  
(B) TYPE: amino acid

| Table 1. Demographic characteristics of the study population |             |
|--------------------------------------------------------------|-------------|
| Age (years)                                                  | 50.0 ± 10.0 |
| Gender                                                       |             |
| Male                                                         | 50.0%       |
| Female                                                       | 50.0%       |
| Marital status                                               |             |
| Married                                                      | 80.0%       |
| Single                                                       | 20.0%       |
| Education level                                              |             |
| High school or above                                         | 60.0%       |
| Below high school                                            | 40.0%       |
| Occupation                                                   |             |
| White collar                                                 | 30.0%       |
| Blue collar                                                  | 70.0%       |
| Income (USD/month)                                           |             |
| < 1000                                                       | 20.0%       |
| 1000-2000                                                    | 30.0%       |
| 2000-3000                                                    | 30.0%       |
| > 3000                                                       | 20.0%       |
| Health status                                                |             |
| Good                                                         | 70.0%       |
| Fair                                                         | 30.0%       |
| Bad                                                          | 0.0%        |
| Smoking status                                               |             |
| Smoker                                                       | 30.0%       |
| Non-smoker                                                   | 70.0%       |
| Alcohol consumption                                          |             |
| Regular                                                      | 10.0%       |
| Occasional                                                   | 20.0%       |
| Never                                                        | 70.0%       |
| Family size                                                  |             |
| 1-2                                                          | 30.0%       |
| 3-4                                                          | 40.0%       |
| 5-6                                                          | 20.0%       |
| > 6                                                          | 10.0%       |
| Health insurance                                             |             |
| Yes                                                          | 80.0%       |
| No                                                           | 20.0%       |
| Chronic diseases                                             |             |
| Hypertension                                                 | 10.0%       |
| Diabetes                                                     | 5.0%        |
| Heart disease                                                | 3.0%        |
| Other                                                        | 2.0%        |
| Medication use                                               |             |
| Regular                                                      | 15.0%       |
| Occasional                                                   | 10.0%       |
| Never                                                        | 75.0%       |

(X1) SEQUENCE DESCRIPTION: SEQ ID NUMBER: 1

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Gln | Leu | Arg | Ala | Leu | Pro | Ser | Pro | Ser | Thr | Cys | Val | Leu | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Thr | Phe | His | Ser | Ile | Pro | Ser | His | Arg | Ser | Val | His | Trp | Thr | Met | Ala |

20 25 30  
Ser Leu Leu Leu Phe Leu Arg Ala Ile Val Ile Ser Ala Asp Asp Glu  
35 40 45  
Glu Leu Thr Gly Ala Asp Glu Gly Arg Asp Ala Ala Arg Glu Arg  
50 55 60  
Arg Pro Glu Asn Cys Ala Phe Gly Pro Ala Ala Arg Asp Thr Glu  
65 70 75 80  
Glu Glu Glu Glu Glu Glu Glu Glu Arg Trp Leu Val Ser Cys Leu  
85 90 95  
Glu Trp Pro Arg Val Asp Arg Lys Ser Ala Trp Met Gln Met Val Xaa  
100 105 110  
Arg Pro Gly Gly Ala Lys Cys Phe Arg Arg Phe Ile Leu Leu Ala Val  
115 120 125  
Ala Ala Cys Xaa Xaa Ser Xaa Arg Xaa Ala Pro Gln Asp Xaa Gln  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2115:

Met Ala Ser Leu Leu Leu Phe Leu Arg Ala Ile Val Ile Ser Ala Asp  
1 5 10 15  
Asp Glu Glu Leu Thr Gly Ala Asp Glu Gly Arg Asp Ala Ala Arg  
20 25 30  
Glu Arg Arg Pro Glu Asn Cys Ala Phe Gly Pro Ala Ala Arg Asp  
35 40 45  
Thr Glu Glu Glu Glu Glu Glu Glu Glu Glu Arg Trp Leu Val Ser  
50 55 60  
Cys Leu Glu Trp Pro Arg Val Asp Arg Lys Ser Ala Trp Met Gln Met  
65 70 75 80  
Val Xaa Arg Pro Gly Gly Ala Lys Cys Phe Arg Arg Phe Ile Leu Leu  
85 90 95  
Ala Val Ala Ala Cys Xaa Xaa Ser Xaa Arg Xaa Ala Pro Gln Asp Xaa  
100 105 110  
Gln

(2) INFORMATION FOR SEQ ID NO:2116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2116:

Met Thr Arg Asn Ser Arg Ala Arg Thr Arg Asp Gly Met Arg Arg Arg  
1 5 10 15  
Val Asn Gly Asp Arg Arg Thr Ala Arg Ser Gly Arg Arg Arg Arg Ala  
20 25 30  
Thr Arg Arg Arg Arg Arg Arg Arg Arg Arg Lys Asn Gly Gly Trp Ser  
35 40 45

00559301 " 02559360







Asn Tyr Lys Xaa Glu Ala Gln Cys Lys Pro Glu Val Phe Leu Ser Ile  
35 40 45  
Tyr Ile Arg Ser Xaa Asn His Asn Xaa Val Leu Ile Ser Arg His Val  
50 55 60  
Asp Ile Ile Thr Phe Tyr Asn Glu Val Phe Val Pro Ala Ala Lys Pro  
65 70 75 80  
Xaa Pro Gly Val Ile Asn Ile Ile Trp Tyr Ser Ser Arg Arg Gln Glu  
85 90 95  
Glu Xaa

(2) INFORMATION FOR SEQ ID NO:2123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1600149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2123:

Met Leu Ile Ser Leu Leu Phe Thr Met Arg Ser Leu Phe Gln Gln Pro  
1 5 10 15  
Ser Leu Xaa Leu Val Ser Leu Ile Ser Ser Gly Thr Arg Pro Glu Asp  
20 25 30  
Lys Lys Asn Xaa Asn Gly Gln Val Pro Gly Ser Pro Lys Leu Ser Pro  
35 40 45  
Phe Pro Asn Xaa Pro Asp Met Ser Pro Lys Xaa Val Ser Ala Ser His  
50 55 60  
Asn Val Tyr Val  
65

(2) INFORMATION FOR SEQ ID NO:2124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..60

(D) OTHER INFORMATION: / Ceres Seq. ID 1600150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2124:

Met Arg Ser Leu Phe Gln Gln Pro Ser Leu Xaa Leu Val Ser Leu Ile  
1 5 10 15  
Ser Ser Gly Thr Arg Pro Glu Asp Lys Lys Asn Xaa Asn Gly Gln Val  
20 25 30  
Pro Gly Ser Pro Lys Leu Ser Pro Phe Pro Asn Xaa Pro Asp Met Ser  
35 40 45  
Pro Lys Xaa Val Ser Ala Ser His Asn Val Tyr Val  
50 55 60

(2) INFORMATION FOR SEQ ID NO:2125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 441 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

CONFIDENTIAL

(B) LOCATION: 1..441

(D) OTHER INFORMATION: / Ceres Seq. ID 1600160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2125:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| ggaacgggta  | gattgctgat | gagaaaaaca | agctggcata | aatgaataat | tcgcaattgg | 60  |
| catcttgacag | gtgaaaggac | tgttgaagga | gaagaaggtg | gagatgctgg | tggaaccaga | 120 |
| tctcagaaag  | cctacgagga | ggtcgaggtg | gagagccgtt | attcaggtgg | cactcctctg | 180 |
| cacgcagggc  | tcccccttg  | accgtccaaa | gatgtcggag | gtggtgagga | tgctcgaagg | 240 |
| tgacgggctg  | gcagagcgtt | gggacgaatg | gcagaaagta | gaggtggtga | ggcaggaggc | 300 |
| tgagtcggca  | ccgctccgca | atgactggat | cgtcgattcc | acgtacaacc | ttcgtgccgt | 360 |
| ggagctgtcc  | ggcccaagg  | agccactcca | cgactccgat | garagaraac | actgaattcg | 420 |
| ccaagattca  | ntctaattgc | t          |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1600161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2126:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Leu | Val | Asp | Pro | Asp | Leu | Arg | Lys | Pro | Thr | Arg | Arg | Ser | Arg | Trp |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Arg | Ala | Val | Ile | Gln | Val | Ala | Leu | Leu | Cys | Thr | Gln | Gly | Ser | Pro | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asp | Arg | Pro | Lys | Met | Ser | Glu | Val | Arg | Met | Leu | Glu | Gly | Asp | Gly |     |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Leu | Ala | Glu | Arg | Trp | Asp | Glu | Trp | Gln | Lys | Val | Glu | Val | Val | Arg | Gln |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Glu | Ala | Glu | Ser | Ala | Pro | Leu | Arg | Asn | Asp | Trp | Ile | Val | Asp | Ser | Thr |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |  |
| Tyr | Asn | Leu | Arg | Ala | Val | Glu | Leu | Ser | Gly | Pro | Arg |     |     |     |     |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..56

(D) OTHER INFORMATION: / Ceres Seq. ID 1600162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2127:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Glu | Val | Val | Arg | Met | Leu | Glu | Gly | Asp | Gly | Leu | Ala | Glu | Arg |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Trp | Asp | Glu | Trp | Gln | Lys | Val | Glu | Val | Val | Arg | Gln | Glu | Ala | Glu | Ser |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Ala | Pro | Leu | Arg | Asn | Asp | Trp | Ile | Val | Asp | Ser | Thr | Tyr | Asn | Leu | Arg |  |
|     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |     |  |
| Ala | Val | Glu | Leu | Ser | Gly | Pro | Arg |     |     |     |     |     |     |     |     |  |
|     | 50  |     |     |     | 55  |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

09589580 101300





|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Gln | Gln | Glu | Gly | Ser | Val | Arg | Lys | Thr | Ser | Cys | Tyr | Cys | Lys | Cys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

(2) INFORMATION FOR SEQ ID NO:2134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2134:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asn | Leu | Arg | Ser | Gln | Asn | Cys | His | Gln | Gly | Val | Ala | Met | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gly | Val | Lys | Phe | Ala | Pro | Glu | Lys | Ala | Asn | Thr | Asn | Arg | Arg | Ala | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Asp | Ile | Lys | Asn | Ile | Ile | Gly | Gly | Pro | His | Gln | His | Leu | Ala | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Lys | Arg | Ala | Leu | Ser | Glu | Lys | Pro | Ala | Ala | Thr | Ala | Asn | Ala | Lys |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Gln | Ala | Gly | Phe | Val | Gly | His | Arg | Gln | Xaa | Thr | Arg | Lys | Phe | Ala |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Thr | Xaa | Ala | Asn | Gln | Pro | Thr | Val | Ala | Leu | Leu | Asp | Pro | Ile | Xaa |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ser | Glu | Arg | Leu | Lys | Arg | Asn | Ala | Asp | Thr | Ala | Phe |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2135:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gly | Val | Lys | Phe | Ala | Pro | Glu | Lys | Ala | Asn | Thr | Asn | Arg | Arg |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Leu | Ser | Asp | Ile | Lys | Asn | Ile | Ile | Gly | Gly | Pro | His | Gln | His | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Val | Ser | Lys | Arg | Ala | Leu | Ser | Glu | Lys | Pro | Ala | Ala | Thr | Ala | Asn |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Lys | Asp | Gln | Ala | Gly | Phe | Val | Gly | His | Arg | Gln | Xaa | Thr | Arg | Lys |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Phe | Ala | Ala | Thr | Xaa | Ala | Asn | Gln | Pro | Thr | Val | Ala | Leu | Leu | Asp | Pro |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Xaa | Ser | Glu | Arg | Leu | Lys | Arg | Asn | Ala | Asp | Thr | Ala | Phe |     |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

09669980-101300





(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 392 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..392  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1600215  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2139:  
atagcttggc tcgcacggtg tcgctggctc ccctcccctt ccctcccac tgttacatcc 60  
agcgagctgt tcacggcgt gcssagctca gtgaggcagc gtttgcgagt ccgggacgag 120  
gggagcggcg ggcgacatgg ggaggggccc cagcgagata aagcggatcg agaaccacac 180  
gcagcggcag tccaccttct acaagcgag ggacggcctc ttcaagaagg ctagggagct 240  
ctccgttctg tgcgacgtgg acctgctgct gctcctcttc tccacctccg gcaagctcta 300  
ccactacctc tcgcccaccg tcccctccgt caaggacctg gtcgagaggt acgaggccac 360  
gacgcacacc aaggtctgga ccgacatccg cc  
(2) INFORMATION FOR SEQ ID NO:2140:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 77 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..77  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1600216  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2140:  
Ile Ala Trp Leu Ala Arg Cys Arg Trp Leu Pro Ser Pro Ser Leu Pro  
1                    5                    10                    15  
Thr Val Thr Ser Ser Glu Leu Phe Thr Ala Val Xaa Ser Ser Val Arg  
                    20                    25                    30  
Gln Arg Leu Arg Val Arg Asp Glu Gly Ser Gly Gly Arg His Gly Glu  
                    35                    40                    45  
Gly Pro Gln Arg Asp Lys Ala Asp Arg Glu Pro His Ala Ala Ala Val  
                    50                    55                    60  
His Leu Leu Gln Ala Gln Gly Arg Pro Leu Gln Glu Gly  
65                    70                    75  
(2) INFORMATION FOR SEQ ID NO:2141:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 52 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..52  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1600217  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2141:  
Ser Leu Ala Arg Thr Val Ser Leu Ala Pro Leu Pro Phe Pro Pro His  
1                    5                    10                    15  
Cys Tyr Ile Gln Arg Ala Val His Gly Arg Xaa Xaa Leu Ser Glu Ala  
                    20                    25                    30  
Ala Phe Ala Ser Pro Gly Arg Gly Glu Arg Arg Ala Thr Trp Gly Gly  
                    35                    40                    45  
Ala Ala Ala Arg  
50  
(2) INFORMATION FOR SEQ ID NO:2142:

09689980 104360

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 85 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..85  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1600218  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2142:  
Met Gly Arg Gly Arg Ser Glu Ile Lys Arg Ile Glu Asn Pro Thr Gln  
1                  5                  10                  15  
Arg Gln Ser Thr Phe Tyr Lys Arg Arg Asp Gly Leu Phe Lys Lys Ala  
                  20                  25                  30  
Arg Glu Leu Ser Val Leu Cys Asp Val Asp Leu Leu Leu Leu Phe  
                  35                  40                  45  
Ser Thr Ser Gly Lys Leu Tyr His Tyr Leu Ser Pro Thr Val Pro Ser  
50                  55                  60  
Val Lys Asp Leu Val Glu Arg Tyr Glu Ala Thr Thr His Thr Lys Val  
65                  70                  75                  80  
Trp Thr Asp Ile Arg  
                  85

(2) INFORMATION FOR SEQ ID NO:2143:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 466 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..466  
(D) OTHER INFORMATION: / Ceres Seq. ID 1600233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2143:

tgaagggtac gtcgacgagc aaccatacgg caacgatcgt gttcaacagc agtcgttggg          60  
gtgaagccgt cgccgatcgt ggcagccttc tcgtcgcgcg gncccagcgt cgccagcccc          120  
ggagtgtctga agcccagacat catggcgccg gggctcaaca tactgcgcgc gtggccgctcg          180  
gaggtgcccc tcggggggccc ccagtcgagc agcttcaacg tcgtctccgg caggtccatg          240  
gcgacgcgca taccaccggc gtcgggccct cgtcaagaag gtgcacccgg actggtccac          300  
cgccgcgata aagtcgcgca tcatgacacg tccagcgccg tcgacaacgc gggcaaccag          360  
atcatggacg aggagcaccg gaaggcgagc ttctactccg tcggcgccgg ccacgttgtc          420  
ccggcgaagg ccgtaagacc ccggcctggt gtacgacctc ggcgtc

(2) INFORMATION FOR SEQ ID NO:2144:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 107 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..107  
(D) OTHER INFORMATION: / Ceres Seq. ID 1600234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2144:

Lys Gly Thr Ser Thr Ser Asn His Thr Ala Thr Ile Val Phe Asn Ser  
1                  5                  10                  15  
Ser Arg Trp Gly Glu Ala Val Ala Asp Arg Gly Ser Leu Leu Val Ala  
                  20                  25                  30  
Arg Xaa Gln Arg Arg Gln Pro Arg Ser Ala Glu Ala Arg His His Gly  
35                  40                  45

Client "08060950"

(2) INFORMATION FOR SEQ ID NO:2145:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2145:

(2) INFORMATION FOR SEQ ID NO:2146:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2146:

(2) INFORMATION FOR SEQ ID NO:2147:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 446 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Arg | Phe | Ser | Ile | Met | Leu | Ala | Thr | Thr | Ala | Leu | Ala | Thr |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |
| Phe | Phe | Val | Ile | Gly | Ser | Cys | Thr | Thr | Pro | Leu | Thr | Phe | Lys | Val | Gly |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |

| (X1) SEQUENCE DESCRIPTION: SEQ ID NUMBER |            |            |            |             |            |     |
|------------------------------------------|------------|------------|------------|-------------|------------|-----|
| tctaggatga                               | atagattcaa | aagaagggt  | ctaagggtca | ttgctgatca  | tttghctgct | 60  |
| gaggaagtgt                               | aggatataaa | ggatatgttc | aagactatgg | atactgacaa  | tgatggaatt | 120 |
| gtatcttatg                               | aagaactgaa | gactggaata | gcaaaacttg | gttctcatct  | tgcggaatca | 180 |
| gaagtacaga                               | tgctcattga | agctgtggac | acaaacggga | ggggggcact  | agactacggg | 240 |
| gaatttctg                                | ccgtctcgct | ccacctgcag | aggatggcga | acgacgagca  | tctccggcgg | 300 |
| gccttctctgt                              | tcttcgacaa | ggacggcaac | ggtttcatcg | agcccagagga | gcttcgagag | 360 |
| gctctggtgg                               | acgacggggc | gtccgacdtc | atcgaggaag | tggtgaacga  | catactgcaa | 420 |
| gaagtcgcaca                              | ccgacaagga | cggcaagatc | agctacgagg | agtttgtggc  | gatgatgaag | 480 |
| accgcgc                                  |            |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2152:

Ser Arg Met Asn Arg Phe Lys Arg Arg Ala Leu Arg Val Ile Ala Asp  
1 5 10 15  
His Leu Xaa Ala Glu Glu Val Glu Asp Ile Lys Asp Met Phe Lys Thr  
20 25 30  
Met Asp Thr Asp Asn Asp Gly Ile Val Ser Tyr Glu Glu Leu Lys Thr  
35 40 45  
Gly Ile Ala Lys Leu Gly Ser His Leu Ala Glu Ser Glu Val Gln Met  
50 55 60  
Leu Ile Glu Ala Val Asp Thr Asn Gly Arg Gly Ala Leu Asp Tyr Gly  
65 70 75 80  
Glu Phe Leu Ala Val Ser Leu His Leu Gln Arg Met Ala Asn Asp Glu  
85 90 95  
His Leu Arg Arg Ala Phe Leu Phe Phe Asp Lys Asp Gly Asn Gly Phe  
100 105 110  
Ile Glu Pro Glu Glu Leu Arg Glu Ala Leu Val Asp Asp Gly Ala Ser  
115 120 125  
Asp Xaa Ile Glu Glu Val Val Asn Asp Ile Leu Gln Glu Val Asp Thr  
130 135 140  
Asp Lys Asp Gly Lys Ile Ser Tyr Glu Glu Phe Val Ala Met Met Lys  
145 150 155 160  
Thr Gly

(2) INFORMATION FOR SEQ ID NO:2153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2153:

Met Asn Arg Phe Lys Arg Arg Ala Leu Arg Val Ile Ala Asp His Leu  
1 5 10 15  
Xaa Ala Glu Glu Val Glu Asp Ile Lys Asp Met Phe Lys Thr Met Asp  
20 25 30  
Thr Asp Asn Asp Gly Ile Val Ser Tyr Glu Glu Leu Lys Thr Gly Ile  
35 40 45  
Ala Lys Leu Gly Ser His Leu Ala Glu Ser Glu Val Gln Met Leu Ile  
50 55 60  
Glu Ala Val Asp Thr Asn Gly Arg Gly Ala Leu Asp Tyr Gly Glu Phe  
65 70 75 80  
Leu Ala Val Ser Leu His Leu Gln Arg Met Ala Asn Asp Glu His Leu  
85 90 95  
Arg Arg Ala Phe Leu Phe Phe Asp Lys Asp Gly Asn Gly Phe Ile Glu  
100 105 110  
Pro Glu Glu Leu Arg Glu Ala Leu Val Asp Asp Gly Ala Ser Asp Xaa

09689801030

(2) INFORMATION FOR SEQ ID NO:2154:

(A) LENGTH: 134 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1600259

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..493

(D) OTHER INFORMATION: / Ceres Seq. ID 1600269

| (X1) SEQUENCE DESCRIPTION: SEQ ID NUMBER: |            |            |            |            |            |     |
|-------------------------------------------|------------|------------|------------|------------|------------|-----|
| tcgaaaaaac                                | cttactatgc | tgatctcctt | gatttggtca | atgaggttga | gttcaagaca | 60  |
| gcttcaggtc                                | agctgctgga | ccttatcact | acccatgagg | gagaaaaaga | tctaacaaag | 120 |
| tataacataa                                | cagttcacgg | tcgaattgtt | caatacaaga | cagcctatta | ttcattttat | 180 |
| ctgccggttg                                | catgtgcctt | gctgctctct | ggcgagaatt | tggacaatta | tggtgatgta | 240 |
| gagaacatcc                                | ttgttgaaat | gggaacatac | tttcaagtcc | aggatgacta | tctggattgt | 300 |
| tatggtgatc                                | ctgaatttat | cggcaagatt | ggaacggaca | ttgaagatta | caagtgtctc | 360 |
| tggctagttg                                | tgcaagccct | tgagcgtgct | gatgagagcc | aaaagcgcac | tctatttgaa | 420 |
| aattatggca                                | agaaagatca | gcctgtgtgg | caaaagtga  | gaacctctac | aaagaacttg | 480 |
| acctagagcc                                | ggt        |            |            |            |            |     |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

| Variable                        | Mean        | SD   | Min | Max    |
|---------------------------------|-------------|------|-----|--------|
| Age                             | 34.5        | 10.2 | 18  | 65     |
| Gender                          | Male        | 10.5 | 0   | 20     |
| Marital Status                  | Married     | 15.2 | 0   | 30     |
| Education                       | High School | 12.8 | 0   | 25     |
| Occupation                      | Unemployed  | 18.5 | 0   | 35     |
| Income                          | \$15,000    | 12.0 | 0   | 30,000 |
| Health Status                   | Good        | 10.0 | 0   | 20     |
| Smoking Status                  | Non-smoker  | 12.0 | 0   | 20     |
| Alcohol Consumption             | Low         | 10.0 | 0   | 20     |
| Exercise Frequency              | Low         | 10.0 | 0   | 20     |
| Stress Level                    | High        | 15.0 | 0   | 30     |
| Sleep Quality                   | Good        | 10.0 | 0   | 20     |
| Depression Score                | Low         | 10.0 | 0   | 20     |
| Anxiety Score                   | Low         | 10.0 | 0   | 20     |
| Life Satisfaction               | Low         | 10.0 | 0   | 20     |
| Overall Health                  | Good        | 10.0 | 0   | 20     |
| Physical Activity               | Low         | 10.0 | 0   | 20     |
| Dietary Habits                  | Unhealthy   | 10.0 | 0   | 20     |
| Social Support                  | Low         | 10.0 | 0   | 20     |
| Work-Life Balance               | Low         | 10.0 | 0   | 20     |
| Financial Stability             | Low         | 10.0 | 0   | 20     |
| Family Size                     | Small       | 10.0 | 0   | 20     |
| Home Ownership                  | Renter      | 10.0 | 0   | 20     |
| Commute Time                    | Long        | 10.0 | 0   | 20     |
| Neighborhood Safety             | Low         | 10.0 | 0   | 20     |
| Access to Healthcare            | Low         | 10.0 | 0   | 20     |
| Health Insurance                | Medicaid    | 10.0 | 0   | 20     |
| Chronic Conditions              | None        | 10.0 | 0   | 20     |
| Mental Health Services          | Low         | 10.0 | 0   | 20     |
| Substance Use                   | Low         | 10.0 | 0   | 20     |
| Self-Management                 | Low         | 10.0 | 0   | 20     |
| Health Literacy                 | Low         | 10.0 | 0   | 20     |
| Health Beliefs                  | Low         | 10.0 | 0   | 20     |
| Health Behavior                 | Low         | 10.0 | 0   | 20     |
| Health Outcomes                 | Low         | 10.0 | 0   | 20     |
| Health Equity                   | Low         | 10.0 | 0   | 20     |
| Health Disparities              | Low         | 10.0 | 0   | 20     |
| Health Promotion                | Low         | 10.0 | 0   | 20     |
| Health Policy                   | Low         | 10.0 | 0   | 20     |
| Health Research                 | Low         | 10.0 | 0   | 20     |
| Health Communication            | Low         | 10.0 | 0   | 20     |
| Health Education                | Low         | 10.0 | 0   | 20     |
| Health Training                 | Low         | 10.0 | 0   | 20     |
| Health Evaluation               | Low         | 10.0 | 0   | 20     |
| Health Monitoring               | Low         | 10.0 | 0   | 20     |
| Health Assessment               | Low         | 10.0 | 0   | 20     |
| Health Planning                 | Low         | 10.0 | 0   | 20     |
| Health Implementation           | Low         | 10.0 | 0   | 20     |
| Health Maintenance              | Low         | 10.0 | 0   | 20     |
| Health Improvement              | Low         | 10.0 | 0   | 20     |
| Health Innovation               | Low         | 10.0 | 0   | 20     |
| Health Leadership               | Low         | 10.0 | 0   | 20     |
| Health Governance               | Low         | 10.0 | 0   | 20     |
| Health Accountability           | Low         | 10.0 | 0   | 20     |
| Health Transparency             | Low         | 10.0 | 0   | 20     |
| Health Integrity                | Low         | 10.0 | 0   | 20     |
| Health Honesty                  | Low         | 10.0 | 0   | 20     |
| Health Fairness                 | Low         | 10.0 | 0   | 20     |
| Health Justice                  | Low         | 10.0 | 0   | 20     |
| Health Equality                 | Low         | 10.0 | 0   | 20     |
| Health Freedom                  | Low         | 10.0 | 0   | 20     |
| Health Security                 | Low         | 10.0 | 0   | 20     |
| Health Stability                | Low         | 10.0 | 0   | 20     |
| Health Prosperity               | Low         | 10.0 | 0   | 20     |
| Health Well-being               | Low         | 10.0 | 0   | 20     |
| Health Quality of Life          | Low         | 10.0 | 0   | 20     |
| Health Life Expectancy          | Low         | 10.0 | 0   | 20     |
| Health Disability               | Low         | 10.0 | 0   | 20     |
| Health Chronic Disease          | Low         | 10.0 | 0   | 20     |
| Health Infectious Disease       | Low         | 10.0 | 0   | 20     |
| Health Non-communicable Disease | Low         | 10.0 | 0   | 20     |
| Health Injury                   | Low         | 10.0 | 0   | 20     |
| Health Violence                 | Low         | 10.0 | 0   | 20     |
| Health Suicide                  | Low         | 10.0 | 0   | 20     |
| Health Mental Health            | Low         | 10.0 | 0   | 20     |
| Health Substance Use            | Low         | 10.0 | 0   | 20     |
| Health Addictive Behavior       | Low         | 10.0 | 0   | 20     |
| Health Risk Behavior            | Low         | 10.0 | 0   | 20     |
| Health Protective Behavior      | Low         | 10.0 | 0   | 20     |
| Health Resilience               | Low         | 10.0 | 0   | 20     |
| Health Coping                   | Low         | 10.0 | 0   | 20     |
| Health Adaptation               | Low         | 10.0 | 0   | 20     |
| Health Change                   | Low         | 10.0 | 0   | 20     |
| Health Development              | Low         | 10.0 | 0   | 20     |
| Health Growth                   | Low         | 10.0 |     |        |

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..152  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1600270  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2156:

Ser Lys Lys Pro Tyr Tyr Ala Asp Leu Leu Asp Leu Phe Asn Glu Val  
1                   5                   10                   15  
Glu Phe Lys Thr Ala Ser Gly Gln Leu Asp Leu Ile Thr Thr His  
                  20                   25                   30  
Glu Gly Glu Lys Asp Leu Thr Lys Tyr Asn Ile Thr Val His Gly Arg  
                  35                   40                   45  
Ile Val Gln Tyr Lys Thr Ala Tyr Tyr Ser Phe Tyr Leu Pro Val Ala  
                  50                   55                   60  
Cys Ala Leu Leu Leu Ser Gly Glu Asn Leu Asp Asn Tyr Gly Asp Val  
65                   70                   75                   80  
Glu Asn Ile Leu Val Glu Met Gly Thr Tyr Phe Gln Val Gln Asp Asp  
                  85                   90                   95  
Tyr Leu Asp Cys Tyr Gly Asp Pro Glu Phe Ile Gly Lys Ile Gly Thr  
                  100                   105                   110  
Asp Ile Glu Asp Tyr Lys Cys Ser Trp Leu Val Val Gln Ala Leu Glu  
                  115                   120                   125  
Arg Ala Asp Glu Ser Gln Lys Arg Ile Leu Phe Glu Asn Tyr Gly Lys  
                  130                   135                   140  
Lys Asp Gln Pro Val Trp Gln Lys  
145                   150

- (2) INFORMATION FOR SEQ ID NO:2157:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 383 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:

- (A) NAME/KEY: -  
    (B) LOCATION: 1..383  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1600285

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2157:

atcacaaatc tatctcgtc gctctccagg ctccagctag actgtcctgc tctgcttccg                   60  
tgctactcac tgtgcacagc cagccagctt cagcagagtc cggctcggct gtcgggtcgc                   120  
agtctgcag cgcaacaatg gacaggcctg cgcaggcgcc cagcagctg ccgccggggt                   180  
tccggttcca ccctaccgac gaggagctgg tcgtgctgta cctccgccg aagsscctgg                   240  
ctcgcgccgt gccggccgcc gtcattcccg tcgtccacga gtcgccaggc tcgatccgtg                   300  
ggacgtccct ggggcgagcg aaggggaggg ctacttcttc agcctgcggc gangcgcssg                   360  
gcgaccggcc gcagagggag ggc

- (2) INFORMATION FOR SEQ ID NO:2158:

- (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 127 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..127  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1600286

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2158:

Ile Thr Asn Leu Ser Arg Ser Leu Ser Arg Leu Gln Leu Asp Cys Pro

00669980-10430



1 5 10 15  
Ala Leu Leu Pro Cys Tyr Ser Leu Cys Thr Ala Ser Gln Leu Gln Gln  
20 25 30  
Ser Pro Ala Arg Leu Ser Ala Ala Ser Pro Ala Ala Gln Gln Trp Thr  
35 40 45  
Gly Leu Arg Arg Arg Pro Arg Ser Cys Arg Arg Gly Ser Gly Ser Thr  
50 55 60  
Leu Pro Thr Arg Ser Trp Ser Cys Cys Thr Ser Ala Gly Xaa Xaa Trp  
65 70 75 80  
Leu Ala Arg Cys Arg Pro Pro Ser Ser Pro Ser Ser Thr Ser Arg Gln  
85 90 95  
Ala Arg Ser Val Gly Arg Pro Trp Gly Glu Arg Arg Gly Gly Leu Leu  
100 105 110  
Leu Gln Pro Ala Ala Xaa Arg Xaa Ala Thr Gly Arg Arg Gly Arg  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1600287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2159:

His Lys Ser Ile Ser Leu Ala Leu Gln Ala Pro Ala Arg Leu Ser Cys  
1 5 10 15  
Ser Ala Ser Val Leu Leu Thr Val His Ser Gln Pro Ala Ser Ala Glu  
20 25 30  
Ser Gly Ser Ala Val Gly Cys Glu Ser Cys Ser Ala Thr Met Asp Arg  
35 40 45  
Pro Ala Gln Ala Pro Thr Gln Leu Pro Pro Gly Phe Arg Phe His Pro  
50 55 60  
Thr Asp Glu Glu Leu Val Leu Tyr Leu Arg Lys Xaa Leu Ala  
65 70 75 80  
Arg Pro Leu Pro Ala Val Ile Pro Val Val His Glu Ser Pro Gly  
85 90 95  
Ser Ile Arg Gly Thr Ser Leu Gly Arg Ala Lys Gly Arg Ala Thr Ser  
100 105 110  
Ser Ala Cys Gly Xaa Ala Xaa Gly Asp Arg Pro Gln Arg Glu Gly  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1600288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2160:

Met Asp Arg Pro Ala Gln Ala Pro Thr Gln Leu Pro Pro Gly Phe Arg  
1 5 10 15  
Phe His Pro Thr Asp Glu Glu Leu Val Val Leu Tyr Leu Arg Arg Lys  
20 25 30  
Xaa Leu Ala Arg Pro Leu Pro Ala Ala Val Ile Pro Val Val His Glu  
35 40 45

0369930 10369930

Ser Pro Gly Ser Ile Arg Gly Thr Ser Leu Gly Arg Ala Lys Gly Arg  
50 55 60  
Ala Thr Ser Ser Ala Cys Gly Xaa Ala Xaa Gly Asp Arg Pro Gln Arg  
65 70 75 80  
Glu Gly

(2) INFORMATION FOR SEQ ID NO:2161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..482
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600289

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2161:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| tcaaattcag | gccaaaggaa | ctggaagatt | gcatgctaag  | gcttgaccca | gaattgattg | 60  |
| gtctgaatac | taggctgaaa | gagatgaaga | aacaaaatgc  | cagcatctcg | gaaatggaga | 120 |
| ccatacggag | gagtatgact | attcggatga | agcagttgat  | gcctatttat | actcaggttg | 180 |
| ccacacgatt | tgccgaattg | catgacacct | ctgctagaat  | ggccgccaaa | ggtgtgatcg | 240 |
| gtaaggttgt | tgattggaaa | gagtctcggg | cctttcttcta | caggagattg | cgaaggagag | 300 |
| ttgctgagga | tgccctggcc | aaggaagtta | aagaagctgc  | tggcgagcag | cttttcccac | 360 |
| agatcagcat | tagactgtat | caagaaatgg | tatctagcgt  | ccaaaggaac | tgaaggtgat | 420 |
| ggtgaaatgt | ggaatgatga | tgaatctttc | tttgctggaa  | ggatgatccc | aaaaactatg | 480 |

ag

(2) INFORMATION FOR SEQ ID NO:2162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2162:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Phe | Arg | Pro | Lys | Glu | Leu | Glu | Asp | Cys | Met | Leu | Arg | Leu | Asp | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Leu | Ile | Gly | Leu | Asn | Thr | Arg | Leu | Lys | Glu | Met | Lys | Lys | Gln | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ala | Ser | Ile | Ser | Glu | Met | Glu | Thr | Ile | Arg | Arg | Ser | Met | Thr | Ile | Arg |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Met | Lys | Gln | Leu | Met | Pro | Ile | Tyr | Thr | Gln | Val | Ala | Thr | Arg | Phe | Ala |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Glu | Leu | His | Asp | Thr | Ser | Ala | Arg | Met | Ala | Ala | Lys | Gly | Val | Ile | Gly |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Val | Val | Asp | Trp | Lys | Glu | Ser | Arg | Ala | Phe | Phe | Tyr | Arg | Arg | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Arg | Arg | Val | Ala | Glu | Asp | Ala | Leu | Ala | Lys | Glu | Val | Lys | Glu | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Ala | Gly | Glu | Gln | Leu | Phe | Pro | Gln | Ile | Ser | Ile | Arg | Leu | Tyr | Gln | Glu |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Met | Val | Ser | Ser | Val | Gln | Arg | Asn |     |     |     |     |     |     |     |     |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid

09689980-10300

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..126  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1600291  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2163:

Met Leu Arg Leu Asp Pro Glu Leu Ile Gly Leu Asn Thr Arg Leu Lys  
1                   5                   10                   15  
Glu Met Lys Lys Gln Asn Ala Ser Ile Ser Glu Met Glu Thr Ile Arg  
                  20                   25                   30  
Arg Ser Met Thr Ile Arg Met Lys Gln Leu Met Pro Ile Tyr Thr Gln  
                  35                   40                   45  
Val Ala Thr Arg Phe Ala Glu Leu His Asp Thr Ser Ala Arg Met Ala  
                  50                   55                   60  
Ala Lys Gly Val Ile Gly Lys Val Val Asp Trp Lys Glu Ser Arg Ala  
65                   70                   75                   80  
Phe Phe Tyr Arg Arg Leu Arg Arg Arg Val Ala Glu Asp Ala Leu Ala  
                  85                   90                   95  
Lys Glu Val Lys Glu Ala Ala Gly Glu Gln Leu Phe Pro Gln Ile Ser  
                  100                   105                   110  
Ile Arg Leu Tyr Gln Glu Met Val Ser Ser Val Gln Arg Asn  
                  115                   120                   125

(2) INFORMATION FOR SEQ ID NO:2164:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 109 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..109  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1600292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2164:

Met Lys Lys Gln Asn Ala Ser Ile Ser Glu Met Glu Thr Ile Arg Arg  
1                   5                   10                   15  
Ser Met Thr Ile Arg Met Lys Gln Leu Met Pro Ile Tyr Thr Gln Val  
                  20                   25                   30  
Ala Thr Arg Phe Ala Glu Leu His Asp Thr Ser Ala Arg Met Ala Ala  
                  35                   40                   45  
Lys Gly Val Ile Gly Lys Val Val Asp Trp Lys Glu Ser Arg Ala Phe  
50                   55                   60  
Phe Tyr Arg Arg Leu Arg Arg Arg Val Ala Glu Asp Ala Leu Ala Lys  
65                   70                   75                   80  
Glu Val Lys Glu Ala Ala Gly Glu Gln Leu Phe Pro Gln Ile Ser Ile  
                  85                   90                   95  
Arg Leu Tyr Gln Glu Met Val Ser Ser Val Gln Arg Asn  
                  100                   105

(2) INFORMATION FOR SEQ ID NO:2165:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 448 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
    (B) LOCATION: 1..448  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1600293

09639980-10300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2165:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gtggatttaa | aagtctaaaa | tgctattttc | agaaaatgta | ccttgattct | ttttagat   | 60  |
| gctatgcata | agcagcattt | aatatcatga | taataacatt | ctctgtacta | acagcacatg | 120 |
| tggggttgca | ggaaaagatt | aatgtccatg | gaggagctgt | gtctctaggg | catcctcttg | 180 |
| ggtgcagcgg | tgctcgcatt | ttggtcaccc | ttcttggtgt | ccttagggaa | aagggcggca | 240 |
| agatcggtgt | tgctgggtgc | tgcaacggcg | gaggtggagc | atcagctctt | gtctcgaac  | 300 |
| tcgcataaga | agtattggct | tgaagcactg | gatatgtagc | taattcagtc | gcattcatct | 360 |
| atacatgatg | aagtattgaa | aaaaaaagac | cctacgatat | ccatgccggg | tgccactgtc | 420 |
| tgcttaattc | amcagaatat | gattgtgc   |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2166:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Phe | Lys | Ser | Leu | Lys | Cys | His | Phe | Gln | Lys | Met | Tyr | Leu | Asp | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Val | Val | Cys | Tyr | Ala | Ser | Ala | Ala | Phe | Asn | Ile | Met | Ile | Ile | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Ser | Val | Leu | Thr | Ala | His | Val | Gly | Leu | Gln | Glu | Lys | Ile | Asn | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Gly | Gly | Ala | Val | Ser | Leu | Gly | His | Pro | Leu | Gly | Cys | Ser | Gly | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Ile | Leu | Val | Thr | Leu | Leu | Gly | Val | Leu | Arg | Glu | Lys | Gly | Gly | Lys |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Gly | Val | Ala | Gly | Val | Cys | Asn | Gly | Gly | Gly | Gly | Ala | Ser | Ala | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Val | Leu | Glu | Leu | Ala |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2167:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Leu | Asp | Ser | Phe | Val | Val | Cys | Tyr | Ala | Ser | Ala | Ala | Phe | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Met | Ile | Ile | Thr | Phe | Ser | Val | Leu | Thr | Ala | His | Val | Gly | Leu | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Lys | Ile | Asn | Val | His | Gly | Gly | Ala | Val | Ser | Leu | Gly | His | Pro | Leu |
|     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Gly | Cys | Ser | Gly | Ala | Arg | Ile | Leu | Val | Thr | Leu | Leu | Gly | Val | Leu | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Lys | Gly | Gly | Lys | Ile | Gly | Val | Ala | Gly | Val | Cys | Asn | Gly | Gly | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Ala | Ser | Ala | Leu | Val | Leu | Glu | Leu | Ala |     |     |     |     |     |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..73
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1600296
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2168:

Met Ile Ile Thr Phe Ser Val Leu Thr Ala His Val Gly Leu Gln Glu  
1 5 10 15  
Lys Ile Asn Val His Gly Gly Ala Val Ser Leu Gly His Pro Leu Gly  
20 25 30  
Cys Ser Gly Ala Arg Ile Leu Val Thr Leu Leu Gly Val Leu Arg Glu  
35 40 45  
Lys Gly Gly Lys Ile Gly Val Ala Gly Val Cys Asn Gly Gly Gly Gly  
50 55 60  
Ala Ser Ala Leu Val Leu Glu Leu Ala  
65 70

- (2) INFORMATION FOR SEQ ID NO:2169:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 498 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..498
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1600310

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2169:

atccagatcc ggaccctacc gccgatccat ccaaatcacc ctcccccttc cccttctctt 60  
ccaccaccac caccaccagg ccgcckccks sgtcgctctc aattctcctt tcgaatttag 120  
aatccccgtg ctgagagttg agtgccgcct tggttgctcc gtactggact cgattcctca 180  
tcgcagcaga agcatcccgt cccctccgct tctccttgct ctgctctgac aaaaaaatag 240  
catcatgtcg gaggtgaagg actccaatgt gcctgctgca cttgatggaa atcctcaacc 300  
tatggaccac actgaagaca attctatgcc ctcagcacag caacaggaag aagcaatcaa 360  
gaagaagttt ggaggactaa tgcccaaaaa gcccccactc atctcaaagg atcatgagcg 420  
ggcctatttt gattctgctg actgggctct agggaagcaa ggtgttgcca aacaaaaagg 480  
accgctggag gcacttag

- (2) INFORMATION FOR SEQ ID NO:2170:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 75 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..75
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1600311

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2170:

Ser Arg Ser Gly Pro Tyr Arg Arg Ser Ile Gln Ile Thr Leu Pro Leu  
1 5 10 15  
Pro Leu Leu Phe His His His His His Gln Ala Ala Xaa Xaa Val Val  
20 25 30  
Leu Asn Ser Pro Phe Glu Phe Arg Ile Pro Val Leu Arg Val Glu Cys  
35 40 45  
Arg Leu Gly Cys Ser Val Leu Asp Ser Ile Pro His Arg Ser Arg Ser  
50 55 60

00669900 00669900

Ile Pro Ser Pro Pro Leu Leu Leu Ala Leu Leu  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2171:

Met Ser Glu Val Lys Asp Ser Asn Val Pro Ala Ala Leu Asp Gly Asn  
1 5 10 15  
Pro Gln Pro Met Asp Gln Thr Glu Asp Asn Ser Met Pro Ser Ala Gln  
20 25 30  
Gln Gln Glu Glu Ala Ile Lys Lys Lys Phe Gly Gly Leu Met Pro Lys  
35 40 45  
Lys Pro Pro Leu Ile Ser Lys Asp His Glu Arg Ala Tyr Phe Asp Ser  
50 55 60  
Ala Asp Trp Ala Leu Gly Lys Gln Gly Val Ala Lys Pro Lys Gly Pro  
65 70 75 80  
Leu Glu Ala Leu

(2) INFORMATION FOR SEQ ID NO:2172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2172:

Met Asp Gln Thr Glu Asp Asn Ser Met Pro Ser Ala Gln Gln Gln Glu  
1 5 10 15  
Glu Ala Ile Lys Lys Lys Phe Gly Gly Leu Met Pro Lys Lys Pro Pro  
20 25 30  
Leu Ile Ser Lys Asp His Glu Arg Ala Tyr Phe Asp Ser Ala Asp Trp  
35 40 45  
Ala Leu Gly Lys Gln Gly Val Ala Lys Pro Lys Gly Pro Leu Glu Ala  
50 55 60  
Leu  
65

(2) INFORMATION FOR SEQ ID NO:2173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..501
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2173:

cgaaaatcca acacaagccg ccgtcatgtc gaagcgaggt aggggaggtt cggctgggaa

```

caagttccgc atgtcactgg gtctaccggg ggccggccacg gtgaactgcg cggacaacac 120
gggcgcggaag aacctctaca tcatctccgt caagggaatc aagggccgcc tcaaccgcct 180
cccgtccgcc tgcgtcggcg acatgggtcat ggccaccgctc aagaagggaag agcccgcact 240
caggaagaaa gtgatgcctg ccgtcatcgt ccgccagcgc aagccgtggc gtcgcaagga 300
cgtgtctac atgtacttcg aagataatgc tggagtgtt gtgaatccca aggggtgagat 360
gaaagggttct gcaatcactg gacctatcgg caaggagtgt gctgaccttt ggcctaggat 420
cgctagtgcg gcaaagtcca tcgtttgaga gcttggttga atgtgttttag acttgagtat 480
gatcatctca attgtgtgtt g

```

(2) INFORMATION FOR SEQ ID NO:2174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1600323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2174:

```

Glu Asn Pro Thr Gln Ala Ala Val Met Ser Lys Arg Gly Arg Gly Gly
1 5 10 15
Ser Ala Gly Asn Lys Phe Arg Met Ser Leu Gly Leu Pro Val Ala Ala
20 25 30
Thr Val Asn Cys Ala Asp Asn Thr Gly Ala Lys Asn Leu Tyr Ile Ile
35 40 45
Ser Val Lys Gly Ile Lys Gly Arg Leu Asn Arg Leu Pro Ser Ala Cys
50 55 60
Val Gly Asp Met Val Met Ala Thr Val Lys Lys Gly Lys Pro Asp Leu
65 70 75 80
Arg Lys Lys Val Met Pro Ala Val Ile Val Arg Gln Arg Lys Pro Trp
85 90 95
Arg Arg Lys Asp Gly Val Tyr Met Tyr Phe Glu Asp Asn Ala Gly Val
100 105 110
Ile Val Asn Pro Lys Gly Glu Met Lys Gly Ser Ala Ile Thr Gly Pro
115 120 125
Ile Gly Lys Glu Cys Ala Asp Leu Trp Pro Arg Ile Ala Ser Ala Ala
130 135 140
Asn Ala Ile Val
145

```

(2) INFORMATION FOR SEQ ID NO:2175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1600324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2175:

```

Met Ser Lys Arg Gly Arg Gly Gly Ser Ala Gly Asn Lys Phe Arg Met
1 5 10 15
Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn Thr
20 25 30
Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly Arg
35 40 45
Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala Thr
50 55 60
Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Met Pro Ala Val

```

DOCKET# 00000000

(2) INFORMATION FOR SEQ ID NO:2176:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1600325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2176:

(2) INFORMATION FOR SEO ID NO:2177:

(A) LENGTH: 490 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..490

(D) OTHER INFORMATION: / Ceres Seq. ID 1600326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2177:

(2) INFORMATION FOR SEO ID NO:2178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

[illegible]







| (X1) SEQUENCE DESCRIPTION: SEQ 1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|----------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met                              | Ser | Arg | Ser | Cys | Cys | Leu | Ala | Val | Ser | Val | Leu | Leu | Ala | Val | Ala |
| 1                                |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg                              | Gln | Pro | Ala | Ala | Pro | Ser | Arg | Arg | Arg | Cys | Cys | Thr | Arg | Gly | Ala |
|                                  |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser                              | Arg | Ile | Ser | Thr | Arg | Ala | Pro | Pro | Ser | Ala | Arg | Ser | Thr | Ser | Arg |
|                                  |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

Arg Ser Gly Leu Thr Ser Cys His His Arg Pro Thr Arg Ser Asp Thr  
50 55 60  
Cys Ser Arg Ala Arg Pro Gly Thr Ala Ser Ser Thr Ser Thr Arg Ala  
65 70 75 80  
Trp Ala Ala Arg Ser Ser Ser Arg Arg Ser Cys Arg Gly Trp Ser Ser  
85 90 95  
Pro Ser Pro Ser Leu Ser Arg Gly Thr Ser His Asn Gly Leu Pro Thr  
100 105 110  
Lys Gly Lys Val Arg Leu Leu Thr Leu  
115 120

(2) INFORMATION FOR SEQ ID NO:2185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..503
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2185:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aaaaaaacca gcgactcaca caccgcgcgc ccgcttctgt agggcccca ccaaccgcgc   | 60  |
| agggagaaaa ccaccacagc acatgcagcg cctgcctcc tcccgaggc tcctccaggc    | 120 |
| cgcgctcgcc ccgcccggg ccaactccag cctctccgc gccgcccgc ccgcgccgc      | 180 |
| gccagcgaat ggcgccttcc cgaagatgcc ggcccttcgac tacacgcgc cgcgcgtacga | 240 |
| cgggcccgc gccgaggaga tcttccggaa gcgcgctcag ttctcagcc catccctttt    | 300 |
| tcatttctac gatcgcccat tgaacatagt cgaaggaaag atgcagtacc tatttgatga  | 360 |
| ggatggccgt cgttacctgg atgcttccgg tggcattgca acagtttggt gtgggcactg  | 420 |
| ccatccagat gtgttgaagc catagtaaac caggcaaagc ggatccagca ctccacagtt  | 480 |
| ctatatctca atcatgcaat tgc                                          |     |

(2) INFORMATION FOR SEQ ID NO:2186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2186:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Lys Lys Pro Ala Thr His Thr Pro Ala Arg Phe Cys Arg Ala Pro     |  |
| 1 5 10 15                                                       |  |
| Thr Asn Arg Ala Gly Arg Lys Pro Pro Gln His Met Gln Arg Leu Ala |  |
| 20 25 30                                                        |  |
| Ser Ser Arg Arg Leu Leu Gln Ala Ala Leu Ala Pro Ala Arg Ala Asn |  |
| 35 40 45                                                        |  |
| Ser Ser Leu Ser Ala Ala Val Ala Ala Pro Ala Pro Ala Asn Gly     |  |
| 50 55 60                                                        |  |
| Ala Phe Pro Lys Met Pro Ala Phe Asp Tyr Thr Pro Pro Pro Tyr Asp |  |
| 65 70 75 80                                                     |  |
| Gly Pro Arg Ala Glu Glu Ile Phe Arg Lys Arg Ala Gln Phe Leu Ser |  |
| 85 90 95                                                        |  |
| Pro Ser Leu Phe His Phe Tyr Asp Arg Pro Leu Asn Ile Val Glu Gly |  |
| 100 105 110                                                     |  |
| Lys Met Gln Tyr Leu Phe Asp Glu Asp Gly Arg Arg Tyr Leu Asp Ala |  |
| 115 120 125                                                     |  |
| Phe Gly Ile Ala Thr Val Cys Cys Gly His Cys His Pro Asp Val     |  |
| 130 135 140                                                     |  |

00669900 00669900

Leu Lys Pro  
145

(2) INFORMATION FOR SEQ ID NO:2187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2187:

Lys Asn Gln Arg Leu Thr His Pro Arg Ala Ala Ser Val Gly Pro Gln  
1 5 10 15  
Pro Thr Ala Gln Gly Glu Asn His His Ser Thr Cys Ser Ala Ser Pro  
20 25 30  
Pro Pro Gly Gly Ser Ser Arg Pro Arg Ser Pro Pro Pro Gly Pro Thr  
35 40 45  
Pro Ala Ser Pro Arg Pro Pro Ser Pro Arg Pro Arg Gln Arg Met Ala  
50 55 60  
Pro Ser Arg Arg Cys Arg Pro Ser Thr Thr Arg Arg Arg Arg Thr Thr  
65 70 75 80  
Gly Arg Ala Pro Arg Arg Ser Ser Gly Ser Ala Leu Ser Ser Ser Ala  
85 90 95  
His Pro Phe Phe Ile Ser Thr Ile Ala His  
100 105

(2) INFORMATION FOR SEQ ID NO:2188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2188:

Met Gln Arg Leu Ala Ser Ser Arg Arg Leu Leu Gln Ala Ala Leu Ala  
1 5 10 15  
Pro Ala Arg Ala Asn Ser Ser Leu Ser Ala Ala Ala Val Ala Ala Pro  
20 25 30  
Ala Pro Ala Asn Gly Ala Phe Pro Lys Met Pro Ala Phe Asp Tyr Thr  
35 40 45  
Pro Pro Pro Tyr Asp Gly Pro Arg Ala Glu Glu Ile Phe Arg Lys Arg  
50 55 60  
Ala Gln Phe Leu Ser Pro Ser Leu Phe His Phe Tyr Asp Arg Pro Leu  
65 70 75 80  
Asn Ile Val Glu Gly Lys Met Gln Tyr Leu Phe Asp Glu Asp Gly Arg  
85 90 95  
Arg Tyr Leu Asp Ala Phe Gly Gly Ile Ala Thr Val Cys Cys Gly His  
100 105 110  
Cys His Pro Asp Val Leu Lys Pro  
115 120

(2) INFORMATION FOR SEQ ID NO:2189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

09669980 101300



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2191:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Leu | Ile | Gln | Lys | Ala | Thr | Ser | Pro | Gln | Pro | Asn | Pro | Val | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Leu | Ser | Leu | His | Cys | Leu | Arg | Asn | Thr | Leu | Ala | Met | Glu | Pro | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ser | Ile | Pro | Pro | Pro | Val | Met | Gly | Ala | Ala | Val | Ala | Tyr | Pro | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Ala | Gly | Ala | Ala | Tyr | Ser | Ala | Gly | Pro | Tyr | Ala | His | Ala | His | Ala |
|     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ala | Leu | Gly | Ala | Leu | Tyr | Pro | Pro | Pro | Pro | Ala | Pro | Gly | Pro | Pro | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | His | Gln | Gly | Gly | Thr | Ala | Ala | Ala | Gln | Leu | Gln | Leu | Phe | Trp | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Glu | Gln | Tyr | Arg | Glu | Ile | Glu | Ala | Thr | Thr | Asp | Phe | Lys | Asn | His | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Pro | Leu | Ala | Arg | Ile | Lys | Lys | Ile | Met | Lys | Ala | Asp | Glu | Asp | Val |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Arg | Met | Ile | Ala | Ala | Glu | Ala | Pro | Val | Val | Phe | Ala | Arg | Ala | Cys | Glu |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Met | Phe | Ile | Leu | Glu | Leu | Thr | His | Arg | Gly | Trp | Ala | His | Ala | Glu | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asn |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2192:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1600364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2192:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Pro | Asn | Ser | Ser | Ile | Pro | Pro | Pro | Val | Met | Gly | Ala | Ala | Val |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Tyr | Pro | Pro | Ala | Ala | Gly | Ala | Ala | Tyr | Ser | Ala | Gly | Pro | Tyr | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Ala | His | Ala | Ala | Leu | Gly | Ala | Leu | Tyr | Pro | Pro | Pro | Pro | Ala | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Pro | Pro | Ser | Ser | His | Gln | Gly | Gly | Thr | Ala | Ala | Ala | Gln | Leu | Gln |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Leu | Phe | Trp | Ala | Glu | Gln | Tyr | Arg | Glu | Ile | Glu | Ala | Thr | Thr | Asp | Phe |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Lys | Asn | His | Asn | Leu | Pro | Leu | Ala | Arg | Ile | Lys | Lys | Ile | Met | Lys | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asp | Glu | Asp | Val | Arg | Met | Ile | Ala | Ala | Glu | Ala | Pro | Val | Val | Phe | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Ala | Cys | Glu | Met | Phe | Ile | Leu | Glu | Leu | Thr | His | Arg | Gly | Trp | Ala |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| His | Ala | Glu | Glu | Asn |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 130 |

(2) INFORMATION FOR SEQ ID NO:2193:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 455 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

DOCKET "0866960"





(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..56

(D) OTHER INFORMATION: / Ceres Seq. ID 1600386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2196:

Met Pro Pro Arg Gln Arg Arg Gly Ala Gly Ser Ser Arg Ala Gly Ser  
1 5 10 15  
Gly Pro Thr Ser Asp Thr Thr Arg Ile Ser Arg Cys Ala Thr Arg Leu  
20 25 30  
Gly Ser Phe Trp Ala Thr Ala Ser Ser Ala Thr Pro Leu Pro Pro Ser  
35 40 45  
Ile Ala Pro Pro Pro Ser Ala Ser  
50 55

(2) INFORMATION FOR SEQ ID NO:2197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..502

(D) OTHER INFORMATION: / Ceres Seq. ID 1600395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2197:

ctcccgacaga gcagccgaca actctctacc gtccgagacc ccaagcacca gcgcggcgccg 60  
ggcggcgccg gcgaccatgg ctgtcgggaa gaacaagagg atctccaagg gaaagaaggg 120  
tggaagaaa aagaccgtcg accctttctc taagaaggat tggtatgaca tcaaggcacc 180  
gtcgggtgttc agtgtgcgca acatcgggaa ccgcgcgcca cgccgcagga ggagacgcat 240  
cgagttagc acgcgaagaa gcgaccatga gggccaagtga gaagaagaag cgcgatgagga 300  
ggctcaagag gaagcgcaga aagatgagggc agagatccaa gtaggcagat cgagatggat 360  
tgtggacctg atgacatgcg tgggtacata catttcttcg gatgcgttgg tgtgcctgtg 420  
gagagatgtc aacctgccat ggtgtcacgg tccgcoatca gttgaacgct ttgcctgcac 480  
ttcagtaggc catttttcat gg

(2) INFORMATION FOR SEQ ID NO:2198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1600396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2198:

Ser Arg Arg Ala Ala Asp Asn Ser Leu Pro Ser Glu Thr Pro Ser Thr  
1 5 10 15  
Ser Ala Ala Ala Ala Ala Ala Ala Thr Met Ala Val Gly Lys Asn Lys  
20 25 30  
Arg Ile Ser Lys Gly Lys Lys Gly Gly Lys Lys Lys Thr Val Asp Pro  
35 40 45  
Phe Ser Lys Lys Asp Trp Tyr Asp Ile Lys Ala Pro Ser Val Phe Ser  
50 55 60  
Val Arg Asn Ile Gly Asn Arg Arg Arg Arg Arg Arg Arg Arg Ile  
65 70 75 80  
Glu Phe Ser Thr Arg Arg Ser Asp His Glu Gly Gln Val Glu Glu Glu  
85 90 95  
Ala His Glu Glu Ala Gln Glu Glu Ala Gln Lys Asp Glu Ala Glu Ile  
100 105 110  
Gln Val Gly Arg Ser Arg Trp Ile Val Asp Leu Met Thr Cys Val Gly

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115 120 125  
Thr Tyr Ile Ser Ser Asp Ala Leu Val Cys Leu Trp Arg Asp Val Asn  
130 135 140  
Leu Pro Trp Cys His Gly Pro Pro Ser Val Glu Arg Leu Ala Cys Thr  
145 150 155 160  
Ser Val Gly His Phe Ser Trp  
165

(2) INFORMATION FOR SEQ ID NO:2199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1600397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2199:

Pro Ala Glu Gln Pro Thr Thr Leu Tyr Arg Pro Arg Pro Gln Ala Pro  
1 5 10 15  
Ala Arg Arg Arg Arg Arg Arg Arg Pro Trp Leu Ser Gly Arg Thr Arg  
20 25 30  
Gly Ser Pro Arg Glu Arg Arg Val Ala Arg Lys Arg Pro Ser Thr Leu  
35 40 45  
Ser Leu Arg Arg Ile Gly Met Thr Ser Arg His Arg Arg Cys Ser Val  
50 55 60  
Cys Ala Thr Ser Gly Thr Ala Ala Asp Ala Ala Gly Gly Asp Ala Ser  
65 70 75 80  
Ser Leu Ala Arg Glu Glu Ala Thr Met Arg Ala Lys Trp Lys Lys Lys  
85 90 95  
Arg Met Arg Arg Leu Lys Arg Lys Arg Arg Lys Met Arg Gln Arg Ser  
100 105 110  
Lys

(2) INFORMATION FOR SEQ ID NO:2200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1600398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2200:

Met Ala Val Gly Lys Asn Lys Arg Ile Ser Lys Gly Lys Lys Gly Gly  
1 5 10 15  
Lys Lys Lys Thr Val Asp Pro Phe Ser Lys Lys Asp Trp Tyr Asp Ile  
20 25 30  
Lys Ala Pro Ser Val Phe Ser Val Arg Asn Ile Gly Asn Arg Arg Arg  
35 40 45  
Arg Arg Arg Arg Arg Arg Ile Glu Phe Ser Thr Arg Arg Ser Asp His  
50 55 60  
Glu Gly Gln Val Glu Glu Ala His Glu Glu Ala Gln Glu Glu Ala  
65 70 75 80  
Gln Lys Asp Glu Ala Glu Ile Gln Val Gly Arg Ser Arg Trp Ile Val  
85 90 95  
Asp Leu Met Thr Cys Val Gly Thr Tyr Ile Ser Ser Asp Ala Leu Val  
100 105 110

09689980 101300

(D) OTHER INFORMATION: / Ceres Seq. ID 1600401

[illegible]

(A) LENGTH: 157 amino acids

[illegible]

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..157
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1600435
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2206:

Met Thr Glu Arg Gln Val Ala Glu Leu Gly Pro Gly Thr Ala Cys Cys  
1 5 10 15  
Gly Trp Asn His Cys Gly Arg Arg Leu Ala Ala Gly Ala Val Asp Gly  
20 25 30  
Ser Val Ser Val Tyr Asp Ser Gln Pro Pro Pro Ser Phe Lys Trp Gln  
35 40 45  
Ala His Glu Gln Ala Ile Val Asn Val Val Trp Leu Pro Pro Glu Tyr  
50 55 60  
Gly Asp Ala Ile Ala Cys Val Cys Ala Asp Gly Thr Leu Ser Leu Trp  
65 70 75 80  
Glu Glu Val Ala Ala Asp Asp Gln Leu Pro Thr Trp Arg Asn Cys Lys  
85 90 95  
Ile Phe Glu Asp Gly Asn Ser His Ile Leu Asn Val His Phe Gly Leu  
100 105 110  
His Leu Gly Ile Leu Lys Met Val Thr Ala Tyr Ser Asp Gly Gln Val  
115 120 125  
Lys Val Tyr Glu Leu Leu Asp Ser Leu Glu Leu Asp Lys Trp Gln Leu  
130 135 140  
Gln Ala Glu Phe Gln Asn Ile Thr Asp Pro Ile Ser Arg  
145 150 155

- (2) INFORMATION FOR SEQ ID NO:2207:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 452 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..452
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1600436
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2207:

gcggtgccac acatccgtkt gcctctkctc cctcttgccg gtcccgaata aagagcagca 60  
gcgcaagagg tcggtagasc gagaagaagg caatggcggc cgagaccttc cttttcacct 120  
cggagtcctg gaacgagggg caccocgaca agctgtgcca ccaggtgtcg gacgccgtgc 180  
ttgacgcatt cctgcgcag gaccccgaca gcaaggtggc ctgcgagacc tgcaccaaga 240  
ccaacatggt gayggtgtyc ggcgagatca cgaccaaggc gaccgtggac tacgagaaga 300  
tcgtgcgcga cacctgccgc ragatcgggt tcacctcga cgacgtgggc ctgcagcgccg 360  
accgctgcaa ggtgctggtg aacatcgagc agcagtcgcc cgacatcgcg cagggcgtgc 420  
acgggcactt cacgaagcgg ccgaggaga tc

- (2) INFORMATION FOR SEQ ID NO:2208:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 120 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..120
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1600437
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2208:

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Met Ala Ala Glu Thr Phe Leu Phe Thr Ser Glu Ser Val Asn Glu Gly  
1 5 10 15  
His Pro Asp Lys Leu Cys Asp Gln Val Ser Asp Ala Val Leu Asp Ala  
20 25 30  
Cys Leu Ala Gln Asp Pro Asp Ser Lys Val Ala Cys Glu Thr Cys Thr  
35 40 45  
Lys Thr Asn Met Val Xaa Val Xaa Gly Glu Ile Thr Thr Lys Ala Thr  
50 55 60  
Val Asp Tyr Glu Lys Ile Val Arg Asp Thr Cys Arg Xaa Ile Gly Phe  
65 70 75 80  
Thr Ser Asp Asp Val Gly Leu Asp Ala Asp Arg Cys Lys Val Leu Val  
85 90 95  
Asn Ile Glu Gln Gln Ser Pro Asp Ile Ala Gln Gly Val His Gly His  
100 105 110  
Phe Thr Lys Arg Pro Glu Glu Ile  
115 120

(2) INFORMATION FOR SEQ ID NO:2209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2209:

Met Pro Arg Ala Gly Pro Arg Gln Gln Gly Leu Arg Asp Leu His  
1 5 10 15  
Gln Asp Gln His Gly Xaa Gly Xaa Arg Arg Asp His Asp Gln Gly Asp  
20 25 30  
Arg Gly Leu Arg Glu Asp Arg Ala Arg His Leu Pro Xaa Asp Arg Val  
35 40 45  
His Leu Arg Arg Arg Gly Pro Arg Arg Arg Pro Leu Gln Gly Ala Gly  
50 55 60  
Glu His Arg Ala Ala Val Pro Arg His Arg Ala Gly Arg Ala Arg Ala  
65 70 75 80  
Leu His Glu Ala Ala Arg Gly Asp  
85

(2) INFORMATION FOR SEQ ID NO:2210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2210:

Met Val Xaa Val Xaa Gly Glu Ile Thr Thr Lys Ala Thr Val Asp Tyr  
1 5 10 15  
Glu Lys Ile Val Arg Asp Thr Cys Arg Xaa Ile Gly Phe Thr Ser Asp  
20 25 30  
Asp Val Gly Leu Asp Ala Asp Arg Cys Lys Val Leu Val Asn Ile Glu  
35 40 45  
Gln Gln Ser Pro Asp Ile Ala Gln Gly Val His Gly His Phe Thr Lys  
50 55 60  
Arg Pro Glu Glu Ile

00000000 101300

65

(2) INFORMATION FOR SEQ ID NO:2211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..456
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2211:

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| ctctcggcga  | gtctttctct | ttccccacct | tcacttggcc | gtcctcccgga | gctgcggcgg  | 60  |
| cgcacgcgatt | gctaggatga | aaatccgttc | tcccggcgat | ttttggctct  | cgggaaacaga | 120 |
| caggaggatc  | cgcggaagg  | attcggtgc  | gtcctagtgt | agtgtcgaca  | tggctgggcg  | 180 |
| caaggagacc  | gcactcgacc | tggcgaagtt | cgtcgacaag | ggcgtccagg  | tgaagctcac  | 240 |
| cggcggcgcc  | caagtgcag  | gaactttaaa | gggatatgac | cagctactca  | acctagtgt   | 300 |
| agatgaagca  | gttgaatatg | aaagagagca | agatgaccca | ttgaagctat  | cagggaaaac  | 360 |
| cagacagctt  | ggcctcattg | tgtgcagagg | cacggcagtc | atgctgtgtct | caccgactga  | 420 |
| tggaacctga  | tgasatcgcc | aaccttttc  | ttgcgg     |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2212:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Arg | Arg | Val | Phe | Leu | Phe | Pro | His | Leu | His | Leu | Ala | Val | Leu | Pro |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Cys | Gly | Gly | Ala | Ser | Ile | Ala | Arg | Met | Lys | Ile | Arg | Ser | Pro | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Phe | Trp | Leu | Ser | Gly | Thr | Asp | Arg | Arg | Ile | Arg | Gly | Lys | Asp | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Ala | Ala | Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 50  |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2213:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Arg | Lys | Glu | Thr | Ala | Leu | Asp | Leu | Ala | Lys | Phe | Val | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Gly | Val | Gln | Val | Lys | Leu | Thr | Gly | Gly | Arg | Gln | Val | Thr | Gly | Thr |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Lys | Gly | Tyr | Asp | Gln | Leu | Leu | Asn | Leu | Val | Leu | Asp | Glu | Ala | Val |
|     |     |     | 35  |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Glu | Tyr | Glu | Arg | Glu | Gln | Asp | Asp | Pro | Leu | Lys | Leu | Ser | Gly | Lys | Thr |
|     |     |     | 50  |     |     | 55  |     |     |     |     |     | 60  |     |     |     |

00669900 101300

Arg Gln Leu Gly Leu Ile Val Cys Arg Gly Thr Ala Val Met Leu Val  
65 70 75 80  
Ser Pro Thr Asp Gly Thr  
85

(2) INFORMATION FOR SEQ ID NO:2214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..477
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2214:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| acaaaaacct tccggcgccg ccgcctgacg gctccagcgc cctcgccgtc ggcagctcgg  | 60  |
| ccgccgtact cccgctaccg agctaggagg catcaccttc gccgggtccaa catgggtaag | 120 |
| acacgtggta tgggagctgg gcgcaagctc aagaccaca gaaggaacca gaggtgggct   | 180 |
| gacaaagcct acaagaagag ccattctcggc aacgagtgga agaaaccctt tgctgggtca | 240 |
| tctcacgcaa agggaatcgt ccttgagaag atcggcattg aggctaagca gcctaactct  | 300 |
| gctatccgta agtgcgctcg tgtccagctg gtgaagaacg ggaagaagat tgctgccttt  | 360 |
| gtgcaaaacg atggttgctt gaactacatc gaggagaacg atgaggtgct gattgctgga  | 420 |
| ttcggtcgta agggccatgc tgtgggagat attccggcgc tccgtttcaa ggctcgtg    |     |

(2) INFORMATION FOR SEQ ID NO:2215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2215:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Thr Lys Thr Phe Arg Arg Arg Arg Leu Ile Ala Pro Ala Pro Ser Pro |  |
| 1 5 10 15                                                       |  |
| Ser Ala Ala Arg Pro Pro Tyr Ser Arg Tyr Arg Ala Arg Arg His His |  |
| 20 25 30                                                        |  |
| Leu Arg Arg Ser Asn Met Gly Lys Thr Arg Gly Met Gly Ala Gly Arg |  |
| 35 40 45                                                        |  |
| Lys Leu Lys Thr His Arg Arg Asn Gln Arg Trp Ala Asp Lys Ala Tyr |  |
| 50 55 60                                                        |  |
| Lys Lys Ser His Leu Gly Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser |  |
| 65 70 75 80                                                     |  |
| Ser His Ala Lys Gly Ile Val Leu Glu Lys Ile Gly Ile Glu Ala Lys |  |
| 85 90 95                                                        |  |
| Gln Pro Asn Ser Ala Ile Arg Lys Cys Ala Arg Val Gln Leu Val Lys |  |
| 100 105 110                                                     |  |
| Asn Gly Lys Lys Ile Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn |  |
| 115 120 125                                                     |  |
| Tyr Ile Glu Glu Asn Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys |  |
| 130 135 140                                                     |  |
| Gly His Ala Val Gly Asp Ile Pro Gly Val Arg Phe Lys Val Val     |  |
| 145 150 155                                                     |  |

(2) INFORMATION FOR SEQ ID NO:2216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

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(A) NAME/KEY: peptide
(B) LOCATION: 1..122
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2216:

(2) INFORMATION FOR SEQ ID NO:2217:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1600454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2217:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2218:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 501 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..501

| Descriptive statistics |      | Correlation |      |
|------------------------|------|-------------|------|
| Mean                   | SD   | 1           | 2    |
| 1.00                   | 0.00 | 1.00        | 0.00 |
| 2.00                   | 0.00 | 0.00        | 1.00 |
| 3.00                   | 0.00 | 0.00        | 0.00 |
| 4.00                   | 0.00 | 0.00        | 0.00 |
| 5.00                   | 0.00 | 0.00        | 0.00 |
| 6.00                   | 0.00 | 0.00        | 0.00 |
| 7.00                   | 0.00 | 0.00        | 0.00 |
| 8.00                   | 0.00 | 0.00        | 0.00 |
| 9.00                   | 0.00 | 0.00        | 0.00 |
| 10.00                  | 0.00 | 0.00        | 0.00 |
| 11.00                  | 0.00 | 0.00        | 0.00 |
| 12.00                  | 0.00 | 0.00        | 0.00 |
| 13.00                  | 0.00 | 0.00        | 0.00 |
| 14.00                  | 0.00 | 0.00        | 0.00 |
| 15.00                  | 0.00 | 0.00        | 0.00 |
| 16.00                  | 0.00 | 0.00        | 0.00 |
| 17.00                  | 0.00 | 0.00        | 0.00 |
| 18.00                  | 0.00 | 0.00        | 0.00 |
| 19.00                  | 0.00 | 0.00        | 0.00 |
| 20.00                  | 0.00 | 0.00        | 0.00 |
| 21.00                  | 0.00 | 0.00        | 0.00 |
| 22.00                  | 0.00 | 0.00        | 0.00 |
| 23.00                  | 0.00 | 0.00        | 0.00 |
| 24.00                  | 0.00 | 0.00        | 0.00 |
| 25.00                  | 0.00 | 0.00        | 0.00 |
| 26.00                  | 0.00 | 0.00        | 0.00 |
| 27.00                  | 0.00 | 0.00        | 0.00 |
| 28.00                  | 0.00 | 0.00        | 0.00 |
| 29.00                  | 0.00 | 0.00        | 0.00 |
| 30.00                  | 0.00 | 0.00        | 0.00 |
| 31.00                  | 0.00 | 0.00        | 0.00 |
| 32.00                  | 0.00 | 0.00        | 0.00 |
| 33.00                  | 0.00 | 0.00        | 0.00 |
| 34.00                  | 0.00 | 0.00        | 0.00 |
| 35.00                  | 0.00 | 0.00        | 0.00 |
| 36.00                  | 0.00 | 0.00        | 0.00 |
| 37.00                  | 0.00 | 0.00        | 0.00 |
| 38.00                  | 0.00 | 0.00        | 0.00 |
| 39.00                  | 0.00 | 0.00        | 0.00 |
| 40.00                  | 0.00 | 0.00        | 0.00 |
| 41.00                  | 0.00 | 0.00        | 0.00 |
| 42.00                  | 0.00 | 0.00        | 0.00 |
| 43.00                  | 0.00 | 0.00        | 0.00 |
| 44.00                  | 0.00 | 0.00        | 0.00 |
| 45.00                  | 0.00 | 0.00        | 0.00 |
| 46.00                  | 0.00 | 0.00        | 0.00 |
| 47.00                  | 0.00 | 0.00        | 0.00 |
| 48.00                  | 0.00 | 0.00        | 0.00 |
| 49.00                  | 0.00 | 0.00        | 0.00 |
| 50.00                  | 0.00 | 0.00        | 0.00 |
| 51.00                  | 0.00 | 0.00        | 0.00 |
| 52.00                  | 0.00 | 0.00        | 0.00 |
| 53.00                  | 0.00 | 0.00        | 0.00 |
| 54.00                  | 0.00 | 0.00        | 0.00 |
| 55.00                  | 0.00 | 0.00        | 0.00 |
| 56.00                  | 0.00 | 0.00        | 0.00 |
| 57.00                  | 0.00 | 0.00        | 0.00 |
| 58.00                  | 0.00 | 0.00        | 0.00 |
| 59.00                  | 0.00 | 0.00        | 0.00 |
| 60.00                  | 0.00 | 0.00        | 0.00 |
| 61.00                  | 0.00 | 0.00        | 0.00 |
| 62.00                  | 0.00 | 0.00        | 0.00 |
| 63.00                  | 0.00 | 0.00        | 0.00 |
| 64.00                  | 0.00 | 0.00        | 0.00 |
| 65.00                  | 0.00 | 0.00        | 0.00 |
| 66.00                  | 0.00 | 0.00        | 0.00 |
| 67.00                  | 0.00 | 0.00        | 0.00 |
| 68.00                  | 0.00 | 0.00        | 0.00 |
| 69.00                  | 0.00 | 0.00        | 0.00 |
| 70.00                  | 0.00 | 0.00        | 0.00 |
| 71.00                  | 0.00 | 0.00        | 0.00 |
| 72.00                  | 0.00 | 0.00        | 0.00 |
| 73.00                  | 0.00 | 0.00        | 0.00 |
| 74.00                  | 0.00 | 0.00        | 0.00 |
| 75.00                  | 0.00 | 0.00        | 0.00 |
| 76.00                  | 0.00 | 0.00        | 0.00 |
| 77.00                  | 0.00 | 0.00        | 0.00 |
| 78.00                  | 0.00 | 0.00        | 0.00 |
| 79.00                  | 0.00 | 0.00        | 0.00 |
| 80.00                  | 0.00 | 0.00        | 0.00 |
| 81.00                  | 0.00 | 0.00        | 0.00 |
| 82.00                  | 0.00 | 0.00        | 0.00 |
| 83.00                  | 0.00 | 0.00        | 0.00 |
| 84.00                  | 0.00 | 0.00        | 0.00 |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2218:

(2) INFORMATION FOR SEQ ID NO:2219:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1600460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2219:

(2) INFORMATION FOR SEQ ID NO:2220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1600461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2220:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Leu | Ala | Pro | Glu | Gly | Ser | Gln | Phe | Asp | Asp | Lys | Gln | Tyr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asp | Lys | Lys | Met | Gln | Glu | Ile | Leu | Thr | Glu | Asp | Phe | Phe | Thr | Ser | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

(A) LENGTH: 103 amino acids

| General Information |                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|---------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Author(s)           | W. J. G. Meijer, J. H. M. M. van't Hof, J. H. M. M. van't Hof, J. H. M. M. van't Hof                                                                                                                                                                                                                                                                                                                                                                                   |
| Title               | Effect of the type of substrate on the growth of <i>Escherichia coli</i> O157:H7                                                                                                                                                                                                                                                                                                                                                                                       |
| Journal             | Journal of Food Protection                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| Volume              | 65                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| Issue               | 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| Year                | 2002                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| Pages               | 100-105                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Abstract            | <p>The growth of <i>Escherichia coli</i> O157:H7 on different types of substrate was studied. The growth of the bacterium was determined by the number of bacteria per gram of substrate. The results showed that the growth of <i>E. coli</i> O157:H7 was highest on meat and lowest on vegetables. The growth of the bacterium was also influenced by the pH of the substrate. The growth of the bacterium was highest at a pH of 7.0 and lowest at a pH of 5.0.</p> |
| Keywords            | <i>Escherichia coli</i> O157:H7, growth, substrate, pH                                                                                                                                                                                                                                                                                                                                                                                                                 |
| Subject             | Food Microbiology                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| Classification      | Q631.3                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| Indexing            | MeSH: <i>Escherichia coli</i> , <i>Growth</i> , <i>Substrate</i> , <i>pH</i>                                                                                                                                                                                                                                                                                                                                                                                           |
| Summary             | <p>The growth of <i>Escherichia coli</i> O157:H7 on different types of substrate was studied. The growth of the bacterium was determined by the number of bacteria per gram of substrate. The results showed that the growth of <i>E. coli</i> O157:H7 was highest on meat and lowest on vegetables. The growth of the bacterium was also influenced by the pH of the substrate. The growth of the bacterium was highest at a pH of 7.0 and lowest at a pH of 5.0.</p> |
| Conclusions         | <p>The growth of <i>Escherichia coli</i> O157:H7 was highest on meat and lowest on vegetables. The growth of the bacterium was also influenced by the pH of the substrate. The growth of the bacterium was highest at a pH of 7.0 and lowest at a pH of 5.0.</p>                                                                                                                                                                                                       |
| References          | <p>1. Meijer WJG, van't Hof JHM, van't Hof JHM, van't Hof JHM. Effect of the type of substrate on the growth of <i>Escherichia coli</i> O157:H7. <i>J Food Prot</i> 2002;65:100-105.</p>                                                                                                                                                                                                                                                                               |

(B) LOCATION: 1..146

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2225:

(2) INFORMATION FOR SEQ ID NO:2226:

(A) LENGTH: 468 base pairs

(B) TYPE: nucleic acid

```
(C) STRANDEDNESS: single
```

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..468

(D) OTHER INFORMATION: / Ceres Seq. ID 1600471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2226:

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:2220: |             |             |             |             |            |     |
|--------------------------------------------|-------------|-------------|-------------|-------------|------------|-----|
| ttttagcaaaag                               | gatatgacgg  | caagggatgtg | gtggtccaga  | acttgcgcca  | agtttgtgtc | 60  |
| tttaaggttg                                 | ctaaggagca  | caagaagcct  | tggttatggt  | gggactacgt  | tactgatttt | 120 |
| gcgattcggg                                 | gcccgatgaa  | ggaaaaaag   | tacacaaagg  | agtggtgccga | tgagattatc | 180 |
| aagtcacttg                                 | gctctgatca  | taaaagcaata | gataagtgtg  | ttggtgatcc  | agatgcagat | 240 |
| gaggaaaaacc                                | atgtttctgaa | agctgaacag  | gatgcacaga  | ttggcaagggt | ttctcgtggt | 300 |
| gatgttaccg                                 | tcttaccac   | tcttggaatc  | aacaatagac  | aatacagagg  | gaagcttgac | 360 |
| aaaggagcag                                 | ttcttaaagc  | actttgysst  | ggncttttagg | gaaaccaccg  | agccagccgt | 420 |
| ttgcttgagt                                 | gatgatatac  | aaacaaacga  | gtgcctagag  | aacaatgg    |            |     |

(2) INFORMATION FOR SEQ ID NO:2227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1600472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2227:

| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe                                     | Ser | Lys | Gly | Tyr | Asp | Gly | Lys | Asp | Val | Val | Val | Gln | Asn | Leu | Arg |
| 1                                       |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln                                     | Val | Cys | Val | Phe | Lys | Val | Ala | Lys | Glu | His | Lys | Lys | Pro | Trp | Leu |
|                                         |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Trp                                     | Trp | Asp | Tyr | Val | Thr | Asp | Phe | Ala | Ile | Arg | Cys | Pro | Met | Lys | Glu |
|                                         |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys                                     | Lys | Tyr | Thr | Lys | Glu | Cys | Ala | Asp | Gly | Val | Ile | Lys | Ser | Leu | Gly |

50 55 60  
Leu Asp His Lys Ala Ile Asp Lys Cys Ile Gly Asp Pro Asp Ala Asp  
65 70 75 80  
Glu Glu Asn His Val Leu Lys Ala Glu Gln Asp Ala Gln Ile Gly Lys  
85 90 95  
Gly Ser Arg Gly Asp Val Thr Ile Leu Pro Thr Leu Val Ile Asn Asn  
100 105 110  
Arg Gln Tyr Arg Gly Lys Leu Asp Lys Gly Ala Val Leu Lys Ala Leu  
115 120 125  
Xaa Xaa Xaa Leu  
130

(2) INFORMATION FOR SEQ ID NO:2228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2228:

Met Lys Glu Lys Lys Tyr Thr Lys Glu Cys Ala Asp Gly Val Ile Lys  
1 5 10 15  
Ser Leu Gly Leu Asp His Lys Ala Ile Asp Lys Cys Ile Gly Asp Pro  
20 25 30  
Asp Ala Asp Glu Glu Asn His Val Leu Lys Ala Glu Gln Asp Ala Gln  
35 40 45  
Ile Gly Lys Gly Ser Arg Gly Asp Val Thr Ile Leu Pro Thr Leu Val  
50 55 60  
Ile Asn Asn Arg Gln Tyr Arg Gly Lys Leu Asp Lys Gly Ala Val Leu  
65 70 75 80  
Lys Ala Leu Xaa Xaa Xaa Leu  
85

(2) INFORMATION FOR SEQ ID NO:2229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..491
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2229:

atcttcaacc tctagctgat tgatctctgc agcatggaca cgacgagtga caagcgtgcg 60  
tcatccatgc tggcccctaa ccctggcaag gccacgatcc tcgcccttgg ccacgccttc 120  
ccgcagcagc ttgtcatgca ggactacgtc gtcgacggct tcatgaagaa caccaactgt 180  
gacgacccgg agctcaagga gaagtcacc agactctgca agacgacgac cgtgaggact 240  
cggtagctgg tgatgtcgga tgagatcctc aagaactacc cggagctggc ccaggagggg 300  
ctgccgacga tgaaccagcg tctggacatc tcgaacgcgg cggtagcgca gatggcgacg 360  
gaggcgcccc tgctcgtcgt ccgctcgtgg ggcggcgcgc tctcgtccat taccacctg 420  
gtgtacgtct cgtcgagcga ggcgcgcttc ccgggcggcg acctgcacct ggcgcgcgcg 480  
ctggggctga g

(2) INFORMATION FOR SEQ ID NO:2230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

DOCKET# 08669960

```
(A) NAME/KEY: peptide
(B) LOCATION: 1..152
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2230:

(2) INFORMATION FOR SEQ ID NO:2231:

(A) LENGTH: 141 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..141

(D) OTHER INFORMATION: / Ceres Seq. ID 1600480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2231:

(2) INFORMATION FOR SEQ ID NO:2232:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

[illegible]

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..118  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1600481  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2232:

Met Gln Asp Tyr Val Val Asp Gly Phe Met Lys Asn Thr Asn Cys Asp  
1                   5                   10                   15  
Asp Pro Glu Leu Lys Glu Lys Leu Thr Arg Leu Cys Lys Thr Thr  
                  20                   25                   30  
Val Arg Thr Arg Tyr Val Val Met Ser Asp Glu Ile Leu Lys Asn Tyr  
                  35                   40                   45  
Pro Glu Leu Ala Gln Glu Gly Leu Pro Thr Met Asn Gln Arg Leu Asp  
                  50                   55                   60  
Ile Ser Asn Ala Ala Val Thr Gln Met Ala Thr Glu Ala Ser Leu Ser  
65                   70                   75                   80  
Cys Val Arg Ser Trp Gly Gly Ala Leu Ser Ser Ile Thr His Leu Val  
                  85                   90                   95  
Tyr Val Ser Ser Ser Glu Ala Arg Phe Pro Gly Gly Asp Leu His Leu  
                  100                   105                   110  
Ala Arg Ala Leu Gly Leu  
                  115

(2) INFORMATION FOR SEQ ID NO:2233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..511  
(D) OTHER INFORMATION: / Ceres Seq. ID 1600496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2233:

gcgcacacgg cagacggcac acacaccaca ccacacctcc tcgcttccac tccgctcgtc                   60  
tgacatctcg tcccgtcctt tcgtttcgaa gcctcgcgag ccccgacgat ggccaccgcg                   120  
gcggtgtcgg tcgacgagaa gctcgacaag ctctcgcgccg aggtcgccaa gctcgaccag                   180  
atcagcgaga acgagaagtc cgggttcacg agcctcgtgt cacgctacct cagtggggaa                   240  
gcggagcaga tcgagtgagg caagatccag acccctacgg atgaggtggt ggtgccctac                   300  
gataaccgtc cgtcgcctcc cgaagatctc gaggagacga agaagctgct ggataagctc                   360  
gttgtgtcga agcttaacgg agggctcggg acgaccatgg gctgcactgg gcccaagtct                   420  
gtcattgaag tccgcaatgg gtccacattc cttgacctta ttgtgattca aattgagtc                   480  
ctgaacaaga agtatggatg caatgtccct t

(2) INFORMATION FOR SEQ ID NO:2234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..154  
(D) OTHER INFORMATION: / Ceres Seq. ID 1600497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2234:

Arg Thr Arg Gln Thr Ala His Thr Pro His His Thr Ser Ser Leu Pro  
1                   5                   10                   15  
Leu Arg Ser Ser Asp Ile Ser Ser Arg Pro Phe Val Ser Lys Pro Arg  
                  20                   25                   30

DOCKET# 08668950



Glu Pro Arg Arg Trp Pro Pro Arg Arg Cys Arg Ser Thr Arg Ser Ser  
35 40 45  
Thr Ser Phe Ala Pro Arg Ser Pro Ser Ser Thr Arg Ser Ala Arg Thr  
50 55 60  
Arg Ser Pro Gly Ser Ser Ala Ser Cys His Ala Thr Ser Val Gly Lys  
65 70 75 80  
Arg Ser Arg Ser Ser Gly Ala Arg Ser Arg Pro Leu Arg Met Arg Trp  
85 90 95  
Trp Cys Pro Thr Ile Pro Ser Arg Arg Leu Pro Lys Ile Ser Arg Arg  
100 105 110  
Arg Arg Ser Cys Trp Ile Ser Ser Leu Cys Ser Ser Leu Thr Glu Gly  
115 120 125  
Ser Gly Arg Pro Trp Ala Ala Leu Gly Pro Ser Leu Ser Leu Lys Ser  
130 135 140  
Ala Met Gly Ser His Ser Leu Thr Leu Leu  
145 150

(2) INFORMATION FOR SEQ ID NO:2235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1600498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2235:

Ala His Gly Arg Arg His Thr His His Thr Pro Pro Arg Phe His  
1 5 10 15  
Ser Ala Arg Leu Thr Ser Arg Pro Val Leu Ser Phe Arg Ser Leu Ala  
20 25 30  
Ser Pro Asp Asp Gly His Arg Gly Gly Val Gly Arg Arg Glu Ala Arg  
35 40 45  
Gln Ala Ser Arg Arg Gly Arg Gln Ala Arg Pro Asp Gln Arg Glu Arg  
50 55 60  
Glu Val Arg Val His Gln Pro Arg Val Thr Leu Pro Gln Trp Gly Ser  
65 70 75 80  
Gly Ala Asp Arg Val Glu Gln Asp Pro Asp Pro Tyr Gly  
85 90

(2) INFORMATION FOR SEQ ID NO:2236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1600499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2236:

Met Ala Thr Ala Ala Val Ser Val Asp Glu Lys Leu Asp Lys Leu Arg  
1 5 10 15  
Ala Glu Val Ala Lys Leu Asp Gln Ile Ser Glu Asn Glu Lys Ser Gly  
20 25 30  
Phe Ile Ser Leu Val Ser Arg Tyr Leu Ser Gly Glu Ala Glu Gln Ile  
35 40 45  
Glu Trp Ser Lys Ile Gln Thr Pro Thr Asp Glu Val Val Val Pro Tyr  
50 55 60  
Asp Thr Val Ala Ser Pro Pro Glu Asp Leu Glu Glu Thr Lys Lys Leu

00669990-101300

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2239:

(2) INFORMATION FOR SEQ ID NO:2240:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1600503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2240:

(2) INFORMATION FOR SEQ ID NO:2241:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 513 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..513

(D) OTHER INFORMATION: / Ceres Seq. ID 1600504

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2241:  
aaaaccaaatt tcccaattcc caaaccccta gtagaccac gtctccggtc cccctctcct 60  
cgcgcccgc atggcagcct gcgccggcgc cggcgccggc tgcgggccc agtgctcgtc 120  
ctcctcctcc gcgccggcgc aggaggatgc tctggcggag agcatgggac gcctttcgac 180  
cgcctccgcc gccgcgcgt gccgcaagtgc cgacggcggc ggcgcggccg tcgcggtggc 240  
cggcggcgtc ggcattgtgc cgggtgctt cggggtcac ctcttcggca agttcaagct 300  
ctccgtcacg agcaacgcc tgggtgcgcc cacagacgcc gtcctcctcg ccttctccgg 360  
cgggtcccgc tccagggtgg ctctgcagtt catacacgag atgcagtcca aggcgatcca 420  
gagctgggag gcgagcaact cccaggccct gccggtcttc agccttcggc gtcgtgttcg 480  
tcgacgagag gagcgctctc tcagcgagtc ttc

(2) INFORMATION FOR SEQ ID NO:2242:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1600505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2242:

Lys Thr Lys Phe Pro Ile Pro Lys Pro Leu Val Asp Pro Arg Leu Arg  
1 5 10 15  
Ser Pro Ser Pro Arg Ala Arg His Gly Ser Leu Arg Arg Arg Arg Arg  
20 25 30  
Arg Leu Arg Ala Ala Val Leu Val Leu Leu Leu Arg Gly Arg Pro Gly  
35 40 45  
Gly Cys Ser Gly Gly Glu His Gly Thr Pro Phe Asp Arg Leu Arg Arg  
50 55 60  
Arg Arg Val Arg Gln Val Arg Arg Arg Arg Arg Gly Arg Arg Gly Gly  
65 70 75 80  
Arg Arg Arg Arg His Val Arg Arg Leu Leu Pro Gly Ser Pro Leu Arg  
85 90 95  
Gln Val Gln Ala Leu Arg His Glu Gln Arg His Gly Ala Pro His Arg  
100 105 110  
Arg Arg Pro Pro Arg Leu Leu Arg Arg Ser Arg Leu Gln Gly Gly Ser  
115 120 125  
Ala Val His Thr Arg Asp Ala Val Gln Gly Asp Pro Glu Leu Gly Gly  
130 135 140  
Glu Gln Leu Pro Gly Pro Ala Gly Leu Gln Pro Ser Ala Ser Cys Ser  
145 150 155 160  
Ser Thr Arg Gly Ala Ser Ser Gln Arg Val Phe  
165 170

(2) INFORMATION FOR SEQ ID NO:2243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1600506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2243:

Asn Gln Ile Pro Asn Ser Gln Thr Pro Ser Arg Pro Thr Ser Pro Val  
1 5 10 15  
Pro Leu Ser Ser Arg Pro Pro Trp Gln Pro Ala Ala Ala Pro Ala Pro  
20 25 30  
Ala Ala Gly Arg Ser Ala Arg Pro Pro Pro Arg Ala Ala Arg Arg

00000000 00000000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2245:

| Table 1. Demographic characteristics of the study population |                |
|--------------------------------------------------------------|----------------|
| Age (years)                                                  | Mean (SD)      |
| 18-24                                                        | 20.5 (2.5)     |
| 25-34                                                        | 29.5 (4.5)     |
| 35-44                                                        | 39.5 (5.5)     |
| 45-54                                                        | 49.5 (6.5)     |
| 55-64                                                        | 59.5 (7.5)     |
| 65-74                                                        | 69.5 (8.5)     |
| 75-84                                                        | 79.5 (9.5)     |
| 85-94                                                        | 89.5 (10.5)    |
| 95-104                                                       | 99.5 (11.5)    |
| 105-114                                                      | 109.5 (12.5)   |
| 115-124                                                      | 119.5 (13.5)   |
| 125-134                                                      | 129.5 (14.5)   |
| 135-144                                                      | 139.5 (15.5)   |
| 145-154                                                      | 149.5 (16.5)   |
| 155-164                                                      | 159.5 (17.5)   |
| 165-174                                                      | 169.5 (18.5)   |
| 175-184                                                      | 179.5 (19.5)   |
| 185-194                                                      | 189.5 (20.5)   |
| 195-204                                                      | 199.5 (21.5)   |
| 205-214                                                      | 209.5 (22.5)   |
| 215-224                                                      | 219.5 (23.5)   |
| 225-234                                                      | 229.5 (24.5)   |
| 235-244                                                      | 239.5 (25.5)   |
| 245-254                                                      | 249.5 (26.5)   |
| 255-264                                                      | 259.5 (27.5)   |
| 265-274                                                      | 269.5 (28.5)   |
| 275-284                                                      | 279.5 (29.5)   |
| 285-294                                                      | 289.5 (30.5)   |
| 295-304                                                      | 299.5 (31.5)   |
| 305-314                                                      | 309.5 (32.5)   |
| 315-324                                                      | 319.5 (33.5)   |
| 325-334                                                      | 329.5 (34.5)   |
| 335-344                                                      | 339.5 (35.5)   |
| 345-354                                                      | 349.5 (36.5)   |
| 355-364                                                      | 359.5 (37.5)   |
| 365-374                                                      | 369.5 (38.5)   |
| 375-384                                                      | 379.5 (39.5)   |
| 385-394                                                      | 389.5 (40.5)   |
| 395-404                                                      | 399.5 (41.5)   |
| 405-414                                                      | 409.5 (42.5)   |
| 415-424                                                      | 419.5 (43.5)   |
| 425-434                                                      | 429.5 (44.5)   |
| 435-444                                                      | 439.5 (45.5)   |
| 445-454                                                      | 449.5 (46.5)   |
| 455-464                                                      | 459.5 (47.5)   |
| 465-474                                                      | 469.5 (48.5)   |
| 475-484                                                      | 479.5 (49.5)   |
| 485-494                                                      | 489.5 (50.5)   |
| 495-504                                                      | 499.5 (51.5)   |
| 505-514                                                      | 509.5 (52.5)   |
| 515-524                                                      | 519.5 (53.5)   |
| 525-534                                                      | 529.5 (54.5)   |
| 535-544                                                      | 539.5 (55.5)   |
| 545-554                                                      | 549.5 (56.5)   |
| 555-564                                                      | 559.5 (57.5)   |
| 565-574                                                      | 569.5 (58.5)   |
| 575-584                                                      | 579.5 (59.5)   |
| 585-594                                                      | 589.5 (60.5)   |
| 595-604                                                      | 599.5 (61.5)   |
| 605-614                                                      | 609.5 (62.5)   |
| 615-624                                                      | 619.5 (63.5)   |
| 625-634                                                      | 629.5 (64.5)   |
| 635-644                                                      | 639.5 (65.5)   |
| 645-654                                                      | 649.5 (66.5)   |
| 655-664                                                      | 659.5 (67.5)   |
| 665-674                                                      | 669.5 (68.5)   |
| 675-684                                                      | 679.5 (69.5)   |
| 685-694                                                      | 689.5 (70.5)   |
| 695-704                                                      | 699.5 (71.5)   |
| 705-714                                                      | 709.5 (72.5)   |
| 715-724                                                      | 719.5 (73.5)   |
| 725-734                                                      | 729.5 (74.5)   |
| 735-744                                                      | 739.5 (75.5)   |
| 745-754                                                      | 749.5 (76.5)   |
| 755-764                                                      | 759.5 (77.5)   |
| 765-774                                                      | 769.5 (78.5)   |
| 775-784                                                      | 779.5 (79.5)   |
| 785-794                                                      | 789.5 (80.5)   |
| 795-804                                                      | 799.5 (81.5)   |
| 805-814                                                      | 809.5 (82.5)   |
| 815-824                                                      | 819.5 (83.5)   |
| 825-834                                                      | 829.5 (84.5)   |
| 835-844                                                      | 839.5 (85.5)   |
| 845-854                                                      | 849.5 (86.5)   |
| 855-864                                                      | 859.5 (87.5)   |
| 865-874                                                      | 869.5 (88.5)   |
| 875-884                                                      | 879.5 (89.5)   |
| 885-894                                                      | 889.5 (90.5)   |
| 895-904                                                      | 899.5 (91.5)   |
| 905-914                                                      | 909.5 (92.5)   |
| 915-924                                                      | 919.5 (93.5)   |
| 925-934                                                      | 929.5 (94.5)   |
| 935-944                                                      | 939.5 (95.5)   |
| 945-954                                                      | 949.5 (96.5)   |
| 955-964                                                      | 959.5 (97.5)   |
| 965-974                                                      | 969.5 (98.5)   |
| 975-984                                                      | 979.5 (99.5)   |
| 985-994                                                      | 989.5 (100.5)  |
| 995-1004                                                     | 999.5 (101.5)  |
| 1005-1014                                                    | 1009.5 (102.5) |
| 1015-1024                                                    | 1019.5 (103.5) |
| 1025-1034                                                    | 1029.5 (104.5) |
| 1035-1044                                                    | 1039.5 (105.5) |
| 1045-1054                                                    | 1049.5 (106.5) |
| 1055-1064                                                    | 1059.5 (107.5) |
| 1065-1074                                                    | 1069.5 (108.5) |
| 1075-1084                                                    | 1079.5 (109.5) |
| 1085-1094                                                    | 1089.5 (110.5) |
| 1095-1104                                                    | 1099.5 (111.5) |
| 1105-1114                                                    | 1109.5 (112.5) |
| 1115-1124                                                    | 1119.5 (113.5) |
| 1125-1134                                                    |                |

atcgatccgc agcagtgtccc aaagaggaag agagcaagca aggtgtcttt ggcaacgctc 60  
atcagatcac acacccccgc gcggtgctagc tagctagctg ctgtgttagga tcctctcgcc 120  
agccggtgca ccgcccggccg ggcgccctcc tcccggcgtc tgtcatcatc cgccggccgg 180  
cgccggcgcg tggatcatc agtacgtact tctgctgctt cgtttaagta gtagctcatc 240  
gcttcaccgc cgcgccgaag agagatagag agagagagag agacagatcg gtatcatcat 300  
cgatcatggcg ccggtggggc tcccggcggtt cttccggttc caccgacgg acgaggagct 360  
ggtgaactac tacctgaagc gcaagatcca cgggctgaag atcgagctgg acatcatccc 420  
tgaggctcac ctctacaagt gcgagccatg gg

(2) INFORMATION FOR SEQ ID NO:2246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2246:

Ile Asp Pro Gln Gln Cys Pro Lys Arg Lys Arg Ala Ser Lys Val Ser  
1 5 10 15  
Leu Ala Thr Leu Ile Arg Ser His Thr Pro Ala Arg Ala Ser  
20 25 30

(2) INFORMATION FOR SEQ ID NO:2247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2247:

Ser Ile Arg Ser Ser Ala Gln Arg Gly Arg Glu Gln Ala Arg Cys Leu  
1 5 10 15  
Trp Gln Arg Ser Ser Asp His Thr Pro Pro Arg Val Leu Ala Ser  
20 25 30

(2) INFORMATION FOR SEQ ID NO:2248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2248:

Met Ala Pro Val Gly Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp  
1 5 10 15  
Glu Glu Leu Val Asn Tyr Tyr Leu Lys Arg Lys Ile His Gly Leu Lys  
20 25 30  
Ile Glu Leu Asp Ile Ile Pro Glu Val Asp Leu Tyr Lys Cys Glu Pro  
35 40 45  
Trp

(2) INFORMATION FOR SEQ ID NO:2249:

00000000 00000000

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:2249: |             |            |             |            |            |     |
|--------------------------------------------|-------------|------------|-------------|------------|------------|-----|
| aaggcgctca                                 | tcgactccag  | ccagccgccc | aaaaattccag | gcgcaaatca | caacctcgca | 60  |
| tctcttctg                                  | tcccgctctc  | agctcttctg | tcttccctcc  | ctcgccgccc | gtctcccccg | 120 |
| cggtcgagga                                 | gccgccaaata | gcaaggagag | ggtttctctc  | tccctccacg | gctccaccga | 180 |
| gtccccgat                                  | ccctccgccc  | caaatcccac | acacccggtt  | ggccaccgcn | tgcctatgga | 240 |
| tttgatctg                                  | tggatctcca  | aggtaagga  | gggtcagcac  | ctcgcttagc | acgagcttca | 300 |
| gtccctctgc                                 | gaatatgtga  | aggagatcct | catcgaagag  | tccaactgtc | aaccagtga  | 360 |
| cagccccgtg                                 | acgggtttgc  | gtgatatcca | tgggcagttc  | catgacctaa | tgaagctctt | 420 |
| cgcgacgggt                                 | ggccacgtcc  | cagagacgaa | ctatatcttc  | atgggtgatt | ttgtggaccg | 480 |
| tggcttcaat                                 | agtctagagg  |            |             |            |            |     |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2250:

(2) INFORMATION FOR SEQ ID NO:2251:

(D) OTHER INFORMATION: / Ceres Seq. ID 1600530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2251:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ala | His | Arg | Leu | Gln | Pro | Ala | Ala | Gln | Lys | Ser | Arg | Arg | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Pro | Arg | Ile | Leu | Phe | Cys | Pro | Val | Ser | Ser | Ser | Ser | Phe | Val | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ser | Pro | Pro | Val | Ser | Pro | Ala | Val | Glu | Glu | Pro | Pro | Ile | Ala | Arg |

35 40 45  
Arg Gly Phe Pro Pro Pro Ser Thr Ala Pro Pro Ser Ser Pro Ile Pro  
50 55 60  
Pro Pro Gln Ile Pro His Thr Arg Leu Ala Thr Xaa Ser Pro Trp Ile  
65 70 75 80  
Trp Ile Cys Gly Ser Pro Arg Ser Arg Arg Val Ser Thr Ser Pro Ser  
85 90 95  
Thr Ser Phe Ser Pro Ser Ala Asn Met  
100 105

(2) INFORMATION FOR SEQ ID NO:2252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..503
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2252:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gtctcgacct | ggcttcctcc | tctctgagga | ccgccgtgca | ggagcggagc | tccccgcgcg | 60  |
| ttctctctcc | gccttccgag | aggcccgacc | cctgatacca | cgtgagggc  | ggtggtatta | 120 |
| ggagattagc | gatggcgagg | tggcgcccg  | cggcgtgct  | ggtagtggct | ctggcggcgg | 180 |
| ttctatcggc | ggcgtggcgg | gcggatgcgc | tatcggttac | ggtgaccgac | accgagtgc  | 240 |
| tccacgagtt | cgtgccctat | gagggcgaca | ccgtgtccgg | gaacttcgtc | gtcgtcgacc | 300 |
| acgacatctt | ctggagctcc | gaccaccag  | gaatcgacct | cacggtaacg | tcaccaggtg | 360 |
| gcaacactgt | gtacacattg | aagggaaaat | ctggtgagaa | atttgagttt | aaagctccaa | 420 |
| gaggtggcat | gtataagttc | tgcttcata  | acccatatgg | agcacctgaa | actgtttctt | 480 |
| tctacatcca | tgttggggca | cat        |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600536

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2253:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Arg | Trp | Arg | Pro | Ala | Ala | Leu | Leu | Val | Val | Ala | Leu | Ala | Ala |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Val | Leu | Ser | Ala | Ala | Trp | Arg | Ala | Asp | Ala | Leu | Ser | Val | Thr | Val | Thr |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asp | Thr | Glu | Cys | Ile | His | Glu | Phe | Val | Pro | Tyr | Glu | Gly | Asp | Thr | Val |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Gly | Asn | Phe | Val | Val | Val | Asp | His | Asp | Ile | Phe | Trp | Ser | Ser | Asp |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| His | Pro | Gly | Ile | Asp | Leu | Thr | Val | Thr | Ser | Pro | Gly | Gly | Asn | Thr | Val |  |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |  |
| Tyr | Thr | Leu | Lys | Gly | Lys | Ser | Gly | Glu | Lys | Phe | Glu | Phe | Lys | Ala | Pro |  |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |  |
| Arg | Gly | Gly | Met | Tyr | Lys | Phe | Cys | Phe | His | Asn | Pro | Tyr | Gly | Ala | Pro |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Glu | Thr | Val | Ser | Phe | Tyr | Ile | His | Val | Gly | Ala | His |     |     |     |     |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs

DOCKET "08662860"



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2230:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Trp | Gln | Ala | Ala | Ser | Ser | Leu | Thr | Ala | Thr | His | Thr | Gly | Arg | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Ser | Ala | Gly | Glu | Arg | Cys | Gly | Arg | Leu | Asn | Pro | Leu | Gln | Leu | Arg |

20 25 30  
His Arg Ile Arg Thr Pro Ala Lys Pro Arg Ile Gly Glu Asp Arg Gly  
35 40 45  
Val Met Asp Ala Ala Ala Ala Ala Ala Ala Ala Ser Pro Thr Ser  
50 55 60  
Lys Arg Ile Ala Leu Val Thr Gly Gly Asn Lys Gly Ile Gly Leu Glu  
65 70 75 80  
Thr Cys Arg Gln Leu Ala Ser Arg Gly Val Arg Val Val Leu Thr Ala  
85 90 95  
Arg Asn Glu Ala Arg Gly Leu Glu Ala Val Glu Arg Val Arg Cys Ala  
100 105 110  
Arg Gly Asp Ala Glu Val Tyr Phe His Gln Leu Asp Val Thr Asp Pro  
115 120 125  
Cys Ser  
130

(2) INFORMATION FOR SEQ ID NO:2257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..81

(D) OTHER INFORMATION: / Ceres Seq. ID 1600540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2257:

Met Asp Ala Ala Ala Ala Ala Ala Ala Ala Ser Pro Thr Ser Lys  
1 5 10 15  
Arg Ile Ala Leu Val Thr Gly Gly Asn Lys Gly Ile Gly Leu Glu Thr  
20 25 30  
Cys Arg Gln Leu Ala Ser Arg Gly Val Arg Val Val Leu Thr Ala Arg  
35 40 45  
Asn Glu Ala Arg Gly Leu Glu Ala Val Glu Arg Val Arg Cys Ala Arg  
50 55 60  
Gly Asp Ala Glu Val Tyr Phe His Gln Leu Asp Val Thr Asp Pro Cys  
65 70 75 80  
Ser

(2) INFORMATION FOR SEQ ID NO:2258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..462

(D) OTHER INFORMATION: / Ceres Seq. ID 1600552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2258:

atcgctctcgt ttcagttcct cgtegcacctc gccacttcgc cgccgccgct ttggctccac 60  
ccagtcgcgt tccggcatcc gcccatggct gcggcccccgc ccgcccacct cgcgcgggcc 120  
ttcacggccg ccgctgcgca ccagcgcgtc gcgttcaggc gcgtccaggc cggggccccg 180  
tgtgtccgcc tctctctcct tcccgccgcg ccatcccgcg acatttcgcg gcagggccag 240  
cctcgctcgc ccgcccgcgc cctctctatc cgtccctcgc ggccgcgcgc ctccgggctc 300  
cgtgccattc aacctcctgc cgcgcgactc cgaccctttc atcgagtggg acccgcccc 360  
ggcgactcc gcccccctgc cgtcgcgtgg cggcggtgct gccgggggtg ccacgctggt 420  
cgtgctgctc ggctggctcg gcgcgcgcga gaagcacctg cg

(2) INFORMATION FOR SEQ ID NO:2259:

(i) SEQUENCE CHARACTERISTICS:

DOCTOP "03558960

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..154
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1600553
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2259:

Ile Val Ser Phe Gln Phe Leu Val Ala Leu Ala Thr Ser Pro Pro Pro  
1 5 10 15  
Leu Trp Leu His Pro Val Arg Phe Arg His Pro Pro Met Ala Ala Ala  
20 25 30  
Pro Ala Arg His Leu Ala Ala Ala Phe Thr Ala Ala Ala Ala His Gln  
35 40 45  
Arg Val Ala Phe Arg Arg Val Gln Val Arg Ala Pro Cys Val Arg Leu  
50 55 60  
Ser Leu Leu Pro Ala Ala Pro Ser Arg Asp Ile Ser Arg Gln Gly Gln  
65 70 75 80  
Pro Arg Leu Pro Arg Arg Arg Leu Ser Ile Arg Pro Leu Arg Arg Arg  
85 90 95  
Ala Ser Gly Leu Arg Ala Ile Gln Pro Pro Ala Ala Arg Leu Arg Pro  
100 105 110  
Phe His Arg Val Gly Pro Ala Pro Gly Arg Leu Arg Pro Leu Ala Ala  
115 120 125  
Arg Trp Arg Arg Cys Cys Arg Gly Cys His Ala Gly Arg Ala Ala Arg  
130 135 140  
Leu Ala Arg Arg Ala Pro Glu Ala Pro Ala  
145 150

(2) INFORMATION FOR SEQ ID NO:2260:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 153 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..153
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1600554
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2260:

Ser Ser Arg Phe Ser Ser Ser Ser Pro Ser Pro Leu Arg Arg Arg Arg  
1 5 10 15  
Phe Gly Ser Thr Gln Ser Ala Ser Gly Ile Arg Pro Trp Leu Arg Pro  
20 25 30  
Pro Pro Ala Thr Ser Pro Arg Pro Ser Arg Pro Pro Leu Arg Thr Ser  
35 40 45  
Ala Ser Arg Ser Gly Ala Ser Arg Ser Gly Pro Arg Val Ser Ala Ser  
50 55 60  
Leu Ser Phe Pro Pro Arg His Pro Ala Thr Phe Arg Gly Arg Ala Ser  
65 70 75 80  
Leu Ala Cys Pro Ala Ala Ala Ser Leu Ser Val Pro Ser Gly Ala Ala  
85 90 95  
Pro Pro Gly Ser Val Pro Phe Asn Leu Leu Pro Pro Asp Ser Asp Pro  
100 105 110  
Phe Ile Glu Trp Asp Pro Pro Pro Gly Asp Ser Ala Pro Ser Pro Leu  
115 120 125  
Ala Gly Gly Gly Ala Ala Gly Gly Ala Thr Leu Val Val Leu Leu Gly  
130 135 140  
Trp Leu Gly Ala Arg Gln Lys His Leu

00609930 101300

145

150

(2) INFORMATION FOR SEQ ID NO:2261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2261:

Arg Leu Val Ser Val Pro Arg Arg Pro Arg His Phe Ala Ala Ala Ala  
1 5 10 15  
Leu Ala Pro Pro Ser Pro Leu Pro Ala Ser Ala His Gly Cys Gly Pro  
20 25 30  
Arg Pro Pro Pro Arg Arg Gly Leu His Gly Arg Arg Cys Ala Pro Ala  
35 40 45  
Arg Arg Val Gln Ala Arg Pro Gly Pro Gly Pro Val Cys Pro Pro Leu  
50 55 60  
Ser Pro Ser Arg Arg Ala Ile Pro Arg His Phe Ala Ala Gly Pro Ala  
65 70 75 80  
Ser Pro Ala Pro Pro Pro Pro Leu Tyr Pro Ser Pro Pro Ala Pro Arg  
85 90 95  
Leu Arg Ala Pro Cys His Ser Thr Ser Cys Arg Pro Thr Pro Thr Leu  
100 105 110  
Ser Ser Ser Gly Thr Arg Pro Arg Ala Thr Pro Pro Pro Arg Arg Ser  
115 120 125  
Leu Ala Ala Val Leu Pro Gly Val Pro Arg Trp Ser Cys Cys Ser Ala  
130 135 140  
Gly Ser Ala Arg Ala Arg Ser Thr Cys  
145 150

(2) INFORMATION FOR SEQ ID NO:2262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..409
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2262:

ataacagata caggcacccc ctctctctct ctctctctct stctctccct ctcatnbccr 60  
aagaactgca actaggaacg gktcgccaca aaaaaagaac gtacggctat gaagacgagg 120  
cgcggtgcct gccacgcggc ggcggcgccc acggcgccgg gcgagkggcc kgatggcgca 180  
acgccggaag cggcgccagga cggcggcggc cgaggggtcg ccagcgggcg ccggcactcc 240  
aggtgtccgc ccggtgggca gagacatgtt cgagagagct gcctgacgat ctctctctct 300  
ccatactacg ggacgtcgcc gcgtccgcca gtctcgccggc cgatctcgcc ggcgccatgc 360  
tcacgtgcaa gaggttcagg gagctcgggc agagcaaggt ggtgctggc

(2) INFORMATION FOR SEQ ID NO:2263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

DOCKET# 00669960

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1600560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2263:

Asn Arg Tyr Arg His Pro Leu Leu Ser Ser Pro Leu Xaa Ser Leu Pro  
1 5 10 15  
Leu Xaa Xaa Xaa Glu Leu Gln Leu Gly Thr Xaa Arg His Lys Lys Arg  
20 25 30  
Thr Tyr Gly Tyr Glu Asp Glu Ala Arg Cys Leu Pro Arg Gly Gly Gly  
35 40 45  
Gly His Gly Ala Gly Arg Xaa Ala Xaa Trp Arg Asn Ala Gly Ser Gly  
50 55 60  
Ala Gly Arg Arg Arg Pro Arg Gly Arg Gln Arg Arg Pro Ala Leu Gln  
65 70 75 80  
Val Ser Ala Arg Trp Ala Glu Thr Cys Ser Arg Glu Leu Pro Asp Asp  
85 90 95  
Leu Val Val Ser Ile Leu Arg Asp Val Ala Ala Ser Ala Ser Ser Pro  
100 105 110  
Ala Asp Leu Ala Gly Ala Met Leu Thr Cys Lys Arg Phe Arg Glu Leu  
115 120 125  
Gly Gln Ser Lys Val Val Leu  
130 135

(2) INFORMATION FOR SEQ ID NO:2264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1600561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2264:

Met Lys Thr Arg Arg Gly Ala Cys His Ala Ala Ala Ala Ala Thr Ala  
1 5 10 15  
Pro Gly Glu Xaa Xaa Asp Gly Ala Thr Pro Glu Ala Ala Gln Asp Gly  
20 25 30  
Gly Gly Arg Gly Val Ala Ser Gly Gly Arg His Ser Arg Cys Pro Pro  
35 40 45  
Gly Gly Gln Arg His Val Arg Glu Ser Cys Leu Thr Ile Ser Ser Ser  
50 55 60  
Pro Tyr Tyr Gly Thr Ser Pro Arg Pro Pro Val Arg Arg Pro Ile Ser  
65 70 75 80  
Pro Ala Pro Cys Ser Arg Ala Arg Gly Ser Gly Ser Ser Gly Arg Ala  
85 90 95  
Arg Trp Cys Trp  
100

(2) INFORMATION FOR SEQ ID NO:2265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 501 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..501

(D) OTHER INFORMATION: / Ceres Seq. ID 1600562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2265:

acatttttggga aggagagaga gagaggcaga gggagagatt ggagggaggc cctgcccaag 60  
gcaagagaaa ccgcggcgcg cggagaggga ggaagggcag cacgcagacg cagacggrac 120

00669900 101400

gaacaagatg agggagatca tcagcatcca catcggccag gccgggatcc aggtcggcaa 180  
cgctgtctgg gagctctact gcctcgagca cggcatcgag cacgatggca ccatgcccag 240  
tgattcctcg gttggcgctcg cacatgatgc cttcaacaag ttcttcagcg agactgggtc 300  
cggcaagcat gtgccccagg gccatcttcg tcgaccttga gcccactgtc atcgacgagg 360  
ttcgactgg ctgctaccgc cagctcttcc acccagagca gctcatctcg gggaaggagg 420  
atgcagctaa caactttgcc cgtggccact acacggttgg gaaggagatt gtcgatctat 480  
gcctggaccg tgtgcgcrag c

(2) INFORMATION FOR SEQ ID NO:2266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1600563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2266:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Trp | Lys | Glu | Arg | Glu | Arg | Gly | Arg | Gly | Arg | Asp | Trp | Arg | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Leu | Pro | Lys | Ala | Arg | Glu | Thr | Ala | Ala | Arg | Gly | Glu | Gly | Gly | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ala | Arg | Arg | Arg | Arg | Arg | Xaa | Glu | Gln | Asp | Glu | Gly | Asp | His | Gln |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| His | Pro | His | Arg | Pro | Gly | Arg | Asp | Pro | Gly | Arg | Gln | Arg | Leu | Leu | Gly |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ala | Leu | Leu | Pro | Arg | Ala | Arg | His | Arg | Ala | Arg | Trp | His | His | Ala | Gln |
| 65  |     |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |

(2) INFORMATION FOR SEQ ID NO:2267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1600564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2267:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Phe | Gly | Arg | Arg | Glu | Arg | Glu | Ala | Glu | Gly | Glu | Ile | Gly | Gly | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Pro | Cys | Pro | Arg | Gln | Glu | Lys | Pro | Arg | Arg | Ala | Glu | Arg | Glu | Gly | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | His | Ala | Asp | Ala | Asp | Xaa | Thr | Asn | Lys | Met | Arg | Glu | Ile | Ile | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Ile | His | Ile | Gly | Gln | Ala | Gly | Ile | Gln | Val | Gly | Asn | Ala | Cys | Trp | Glu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Leu | Tyr | Cys | Leu | Glu | His | Gly | Ile | Glu | His | Asp | Gly | Thr | Met | Pro | Ser |
|     |     |     |     |     |     |     | 70  |     |     | 75  |     |     |     | 80  |     |
| Asp | Ser | Ser | Val | Gly | Val | Ala | His | Asp | Ala | Phe | Asn | Thr | Phe | Phe | Ser |
|     |     |     |     |     |     |     |     |     |     | 90  |     |     |     | 95  |     |
| Glu | Thr | Gly | Ser | Gly | Lys | His | Val | Pro | Gln | Gly | His | Leu | Arg | Arg | Pro |
|     |     |     |     |     |     |     | 100 |     |     | 105 |     |     |     | 110 |     |

(2) INFORMATION FOR SEQ ID NO:2268:

(i) SEQUENCE CHARACTERISTICS:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Phe | Leu | Phe | Ser | Lys | Pro | His | Ser | Pro | Gln | Arg | Ala | Ala | Gly | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Ala | Gly | Lys | Asp | Gly | Ser | Val | Pro | Ser | Pro | Pro | Pro | Xaa | Arg | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ser | Tyr | Pro | Glu | Met | Ile | Val | Glu | Ala | Ile | Arg | Ala |     | Leu | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

Glu Asn Gly Cys Asn Lys Thr Ala Ile Ser Asp Tyr Ile Lys Gly Ser  
50 55 60  
Tyr Gly Ser Asn Leu Pro Ala Gln His Asn Ala Val Leu Thr Gly His  
65 70 75 80  
Leu Ala Arg Met Lys Ala Thr Gly Glu Leu Ala Phe Leu Arg Asn Asn  
85 90 95  
Tyr Leu Leu Pro Asn Glu Asp Glu Ala Ser Pro Leu Ser Thr Gly Gly  
100 105 110  
His Lys Gly Pro Ala Ala Ala Glu Glu Ser Thr Gly Val Leu Asp Val  
115 120 125  
Gly Asp Asp Val Leu Leu Ala Ser Pro Leu Val Ile Asp Ala Asp Ala  
130 135 140  
Val Asp Ile Asp Val Pro Ala Pro Ala Pro Val Val Xaa Ala Asp Val  
145 150 155 160  
Asp Asp Phe Asp Val Leu Ala Ser Ser  
165

(2) INFORMATION FOR SEQ ID NO:2271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2271:

Met Ala Gly Lys Asp Gly Ser Val Pro Ser Pro Pro Xaa Arg Leu  
1 5 10 15  
Pro Ser Tyr Pro Glu Met Ile Val Glu Ala Ile Arg Ala Leu Gly Leu  
20 25 30  
Glu Asn Gly Cys Asn Lys Thr Ala Ile Ser Asp Tyr Ile Lys Gly Ser  
35 40 45  
Tyr Gly Ser Asn Leu Pro Ala Gln His Asn Ala Val Leu Thr Gly His  
50 55 60  
Leu Ala Arg Met Lys Ala Thr Gly Glu Leu Ala Phe Leu Arg Asn Asn  
65 70 75 80  
Tyr Leu Leu Pro Asn Glu Asp Glu Ala Ser Pro Leu Ser Thr Gly Gly  
85 90 95  
His Lys Gly Pro Ala Ala Ala Glu Glu Ser Thr Gly Val Leu Asp Val  
100 105 110  
Gly Asp Asp Val Leu Leu Ala Ser Pro Leu Val Ile Asp Ala Asp Ala  
115 120 125  
Val Asp Ile Asp Val Pro Ala Pro Ala Pro Val Val Xaa Ala Asp Val  
130 135 140  
Asp Asp Phe Asp Val Leu Ala Ser Ser  
145 150

(2) INFORMATION FOR SEQ ID NO:2272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2272:

Met Ile Val Glu Ala Ile Arg Ala Leu Gly Leu Glu Asn Gly Cys Asn

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| Met Gly Asp Ser Gln Tyr Ser Phe Ser Leu Thr Thr Phe Ser Pro Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1 5 10 15                                                       |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Gly                                                             | Lys | Leu | Val | Gln | Ile | Glu | His | Ala | Leu | Thr | Ala | Val | Gly | Ser | Gly |
| 20 25 30                                                        |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Gln                                                             | Thr | Ser | Leu | Gly | Ile | Lys | Ala | Ala | Asn | Gly | Val | Val | Ile | Ala | Thr |
| 35 40 45                                                        |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Glu                                                             | Lys | Lys | Leu | Pro | Ser | Ile | Leu | Val | Asp | Glu | Thr | Ser | Val | Gln | Lys |
| 50 55 60                                                        |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ile                                                             | Gln | Ala | Leu | Thr | Pro | Asn | Ile | Gly | Val | Val | Tyr | Ser | Gly | Met | Gly |
| 65 70 75 80                                                     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

Pro Asp Phe Arg Val Leu Val Arg Lys Ser Arg Lys Gln Ala Gln Gln  
85 90 95  
Tyr Tyr Arg Leu Tyr Lys Gly Thr Tyr Thr Cys Asn Thr Ala Cys Thr  
100 105 110  
Arg Asp Cys Cys Cys His Ala Gly Val His Thr Val Arg Trp Cys Glu  
115 120 125  
Thr Phe Gly Val Ser Leu Leu Ile Ala Gly Tyr Asp Asp  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..360

(D) OTHER INFORMATION: / Ceres Seq. ID 1600603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2275:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gagccatccg gtcccaaaag tagaaaaggg caagcgacga gcacagcaca gcacgccttc  | 60  |
| cgttttggga aggcgaggag aggggaaccc gnggagagtt gggggatcgg cggcgaggga  | 120 |
| gatggaggag cgggagaagc tcgtgtgcct ggccaagctt gccgagcagg cggassggta  | 180 |
| cgacgatatg gtggaattca tgaagaatct tgctaggatg gacgtggata tgagtgtcta  | 240 |
| agaraggcat ttgtttctcag ttggtttcaa gaacactatt ggagcaaaga gagcatcatg | 300 |
| gagaatcatt tgttcacatg agcaaaaggt cgcagctgat cgtcnactg gtgtgatgat   | 360 |

(2) INFORMATION FOR SEQ ID NO:2276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1600604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2276:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Glu Pro Ser Gly Pro Lys Ser Arg Lys Gly Gln Ala Thr Ser Thr Ala |  |
| 1 5 10 15                                                       |  |
| Gln His Ala Phe Arg Phe Gly Lys Ala Arg Arg Gly Glu Pro Xaa Glu |  |
| 20 25 30                                                        |  |
| Ser Trp Gly Ile Gly Gly Gly Gly Asp Gly Gly Ala Gly Glu Ala Arg |  |
| 35 40 45                                                        |  |
| Val Pro Gly Gln Ala Cys Arg Ala Gly Gly Xaa Val Arg Arg Tyr Gly |  |
| 50 55 60                                                        |  |
| Gly Ile His Glu Glu Ser Cys                                     |  |
| 65 70                                                           |  |

(2) INFORMATION FOR SEQ ID NO:2277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1600605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2277:

09669900 10300

Ser His Pro Val Pro Lys Val Glu Lys Gly Lys Arg Arg Ala Gln His  
1 5 10 15  
Ser Thr Pro Ser Val Leu Gly Arg Arg Gly Glu Gly Asn Pro Xaa Arg  
20 25 30  
Val Gly Gly Ser Ala Ala Glu Glu Met Glu Glu Arg Glu Lys Leu Val  
35 40 45  
Cys Leu Ala Lys Leu Ala Glu Gln Ala Xaa Xaa Tyr Asp Asp Met Val  
50 55 60  
Glu Phe Met Lys Asn Leu Ala Arg Met Asp Val Asp Met Ser Ala Glu  
65 70 75 80  
Xaa Arg His Leu Phe Ser Val Gly Phe Lys Asn Thr Ile Gly Ala Lys  
85 90 95  
Arg Ala Ser Trp Arg Ile Ile Cys Ser His Glu Gln Lys Val Ala Ala  
100 105 110  
Asp Arg Xaa Thr Gly Val Met  
115

(2) INFORMATION FOR SEQ ID NO:2278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1600606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2278:

Met Glu Glu Arg Glu Lys Leu Val Cys Leu Ala Lys Leu Ala Glu Gln  
1 5 10 15  
Ala Xaa Xaa Tyr Asp Asp Met Val Glu Phe Met Lys Asn Leu Ala Arg  
20 25 30  
Met Asp Val Asp Met Ser Ala Glu Xaa Arg His Leu Phe Ser Val Gly  
35 40 45  
Phe Lys Asn Thr Ile Gly Ala Lys Arg Ala Ser Trp Arg Ile Ile Cys  
50 55 60  
Ser His Glu Gln Lys Val Ala Ala Asp Arg Xaa Thr Gly Val Met  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..430

(D) OTHER INFORMATION: / Ceres Seq. ID 1600624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2279:

agcagtcagc agtgaccaac tcgaagcttg cgttcttgta gtagaggtag gcagcaagcg 60  
gtagagcgag acgtcgagaa gatgaagagc agcactctgt tggcgatcct agttctccag 120  
gcccttcttg tctctacggc cgtggcaaag gacctgcagg gccgaagaag cagtgtctggt 180  
gcggcgagtg caccasstgg tcgggctgtt ggacctgcga cgacctctc accaagtgcg 240  
ccgccacctg cragaactgc gtcccgtct ccacggacaa gggcgccacc aagtacagat 300  
gccgcgactt cctccccgaa aactgcggct gcaagatcca ctagactcat ccacagcggc 360  
acagccgatg gatccttcca tgctctccg tccgtccgcc ttntacaag caggcagcca 420  
ccaatrrgct

(2) INFORMATION FOR SEQ ID NO:2280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids

DOCTOP 08553360

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Leu | Ser | Arg | Trp | Arg | Arg | Gly | Gln | Leu | His | His | Leu | Leu | Arg |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Arg | Val | Gly | Arg | Pro | Leu | Ala | Asp | Ala | Arg | Xaa | Val | Pro | His |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ile | His | Arg | Leu | Ile | His | His | Met | Ala | Glu | Phe | Glu | Leu | Leu | Thr | Asp |

| (xi) SEQUENCE DESCRIPTION: Say 15 No |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|--------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met                                  | Ala | Glu | Phe |     | Glu | Leu | Leu | Thr | Asp | Leu | Phe | Ala | Ala | Thr | Glu | Glu |
| 1                                    |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu                                  | Leu | Thr | Ser | Thr | Leu | Phe | Pro | Ser | Pro | Thr | Pro | Pro | Pro | Pro | Phe | Thr |
|                                      |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ser                                  | Phe | Thr | Ala | Leu | Val | Leu | Asp | Leu | Ser | Pro | Thr | Pro | Ile | Leu | Pro |     |
|                                      |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |

Asp Ser Ser Ser Thr Ile Ala Ser Arg Arg Leu Asp Leu Ser Ala Ser  
50 55 60  
Pro Leu Ala Asp Pro Glu Ala Ala Thr Phe Ala Ser Pro Arg Gly Gly  
65 70 75 80  
Gly Xaa Arg His Gly Arg Val Arg Asp Leu Leu  
85 90

(2) INFORMATION FOR SEQ ID NO:2285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..220
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2285:

acacacaaca gaaacaccac ctccaggctt cccaaatccc aacaagggtt accgcccacc 60  
ggccaccacc ccacgcgcgt ctacgccat ggcagcgcg tcgtccccgc catctcacag 120  
gcggtggagc tggggctcgg cgctggcggg cgcggcgacg acggccgccg ccacggccct 180  
agtgtgtgc cggcgcggg acccssgttc gagtcacat

(2) INFORMATION FOR SEQ ID NO:2286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2286:

Thr His Asn Arg Asn Thr Thr Ser Arg Leu Pro Lys Ser Gln Gln Gly  
1 5 10 15  
Leu Pro Pro Thr Gly His His Pro Thr Arg Val Ser Arg His Gly Gln  
20 25 30  
Arg Val Val Pro Ala Ile Ser Gln Ala Val Glu Leu Gly Leu Gly Ala  
35 40 45  
Gly Gly Arg Gly Asp Asp Gly Arg Arg His Gly Pro Ser Ala Val Pro  
50 55 60  
Ala Ala Gly Pro Xaa Phe Glu Leu Ile  
65 70

(2) INFORMATION FOR SEQ ID NO:2287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2287:

His Thr Thr Glu Thr Pro Pro Pro Gly Phe Pro Asn Pro Asn Lys Gly  
1 5 10 15  
Tyr Arg Pro Pro Ala Thr Thr Pro Arg Ala Ser His Ala Met Gly Ser  
20 25 30  
Ala Ser Ser Pro Pro Ser His Arg Arg Trp Ser Trp Gly Ser Ala Leu

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35 40 45  
Ala Gly Ala Ala Thr Thr Ala Ala Thr Ala Leu Val Leu Cys Arg  
50 55 60  
Pro Arg Asp Xaa Xaa Ser Ser Ser Ser  
65 70

(2) INFORMATION FOR SEQ ID NO:2288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..59
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2288:

Thr Gln Gln Lys His His Leu Gln Ala Ser Gln Ile Pro Thr Arg Ala  
1 5 10 15  
Thr Ala His Arg Pro Pro Pro His Ala Arg Leu Thr Pro Trp Ala Ala  
20 25 30  
Arg Arg Pro Arg His Leu Thr Gly Gly Ala Gly Ala Arg Arg Trp  
35 40 45  
Arg Ala Arg Arg Arg Arg Pro Pro Pro Arg Pro  
50 55

(2) INFORMATION FOR SEQ ID NO:2289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..448
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2289:

agrettggtgc gccatcacac acaagacaca accccactca cccggcagga ggccctcttc 60  
gtcggcggag gccatggttt cctcaagcc gcagaagagg ctgcgcgcgg gagtcctaaa 120  
atgtggcaag gggaagggtgt ggcttgaccc caacgagggtc tacgagatct cgatggctaa 180  
ctgcgcgtcag aacattcgta agctgggtgaa ggatggattc ataattaaga agccacagaa 240  
aatccactca aggtcccggg caaggagggc ccatgaggcc aagcagaagg ggaggcactc 300  
tggttacggg aagcgcaggg gtaccaggga ggctaggctc cccaccaaga tcctttggat 360  
gcgcaggatg sktntcctca ggcgtctgct gcgcaagtrt cgtnaancaa agaaaatcga 420  
caaacacatg taccacnata tctatatc

(2) INFORMATION FOR SEQ ID NO:2290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2290:

Xaa Leu Cys Ala Ile Thr His Lys Thr Gln Pro His Ser Pro Gly Arg  
1 5 10 15  
Arg Pro Ser Ser Ser Ala Glu Ala Met Val Ser Leu Lys Pro Gln Lys  
20 25 30

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Arg Leu Ala Ala Gly Val Leu Lys Cys Gly Lys Gly Lys Val Trp Leu  
35 40 45  
Asp Pro Asn Glu Val Tyr Glu Ile Ser Met Ala Asn Ser Arg Gln Asn  
50 55 60  
Ile Arg Lys Leu Val Lys Asp Gly Phe Ile Ile Lys Lys Pro Gln Lys  
65 70 75 80  
Ile His Ser Arg Ser Arg Ala Arg Arg Ala His Glu Ala Lys Gln Lys  
85 90 95  
Gly Arg His Ser Gly Tyr Gly Lys Arg Arg Gly Thr Arg Glu Ala Arg  
100 105 110  
Leu Pro Thr Lys Ile Leu Trp Met Arg Arg Met Xaa Xaa Leu Arg Arg  
115 120 125  
Leu Leu Arg Lys Xaa Arg Xaa Xaa Lys Lys Ile Asp Lys His Met Tyr  
130 135 140  
His Xaa Ile Tyr Ile  
145

(2) INFORMATION FOR SEQ ID NO:2291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2291:

Met Val Ser Leu Lys Pro Gln Lys Arg Leu Ala Ala Gly Val Leu Lys  
1 5 10 15  
Cys Gly Lys Gly Lys Val Trp Leu Asp Pro Asn Glu Val Tyr Glu Ile  
20 25 30  
Ser Met Ala Asn Ser Arg Gln Asn Ile Arg Lys Leu Val Lys Asp Gly  
35 40 45  
Phe Ile Ile Lys Lys Pro Gln Lys Ile His Ser Arg Ser Arg Ala Arg  
50 55 60  
Arg Ala His Glu Ala Lys Gln Lys Gly Arg His Ser Gly Tyr Gly Lys  
65 70 75 80  
Arg Arg Gly Thr Arg Glu Ala Arg Leu Pro Thr Lys Ile Leu Trp Met  
85 90 95  
Arg Arg Met Xaa Xaa Leu Arg Arg Leu Leu Arg Lys Xaa Arg Xaa Xaa  
100 105 110  
Lys Lys Ile Asp Lys His Met Tyr His Xaa Ile Tyr Ile  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2292:

Met Ala Asn Ser Arg Gln Asn Ile Arg Lys Leu Val Lys Asp Gly Phe  
1 5 10 15  
Ile Ile Lys Lys Pro Gln Lys Ile His Ser Arg Ser Arg Ala Arg Arg  
20 25 30  
Ala His Glu Ala Lys Gln Lys Gly Arg His Ser Gly Tyr Gly Lys Arg

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Ser Arg Ser Arg Pro Leu Pro Phe Arg Gln Glu Lys Thr Met Ser Arg  
20 25 30  
Arg Asn Ser Arg Thr Ile Tyr Val Gly Asn Leu Pro Gly Asp Ile Arg  
35 40 45  
Glu Arg Glu Val Glu Asp Leu Phe Tyr Lys Tyr Gly Arg Ile Leu Asp  
50 55 60  
Ile Asp Leu Lys Ile Pro Pro Arg Pro Pro Gly Tyr Ala Phe Xaa  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1600655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2296:

Met Ser Arg Arg Ser Arg Thr Ile Tyr Val Gly Asn Leu Pro Gly  
1 5 10 15  
Asp Ile Arg Glu Arg Glu Val Glu Asp Leu Phe Tyr Lys Tyr Gly Arg  
20 25 30  
Ile Leu Asp Ile Asp Leu Lys Ile Pro Pro Arg Pro Pro Gly Tyr Ala  
35 40 45  
Phe Xaa  
50

(2) INFORMATION FOR SEQ ID NO:2297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..422

(D) OTHER INFORMATION: / Ceres Seq. ID 1600660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2297:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gcgtttgttc tctgttcat caccgtgcg tgctctctct ctctctctctg              | 60  |
| tgcggaact gcgaggccgc cgacgccga cggcaggggt gccagggcct tcttcgggtcc   | 120 |
| catcgcgagg ccatagtgtgc atcattcgcc tgagacgact gccagcacc aggactgatc  | 180 |
| tctcactag gggcgtagag gtgaagagaa gaacttgaca atgagcagca taggcacagg   | 240 |
| ttacgatctg tctgtcacca ctttctcccc agatggctgc gtcttccagg tcgaatatgc  | 300 |
| taccaaggcc gtcgacaaca gcgggactgt tnttgggatc aagtgcaaag atggcattgt  | 360 |
| ssctgggtgt tgagaagctg gtaacctcag agatgatgct ggarggggtca raccggagat | 420 |
| cc                                                                 |     |

(2) INFORMATION FOR SEQ ID NO:2298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1600661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2298:

Ala Phe Val Leu Leu Phe Ile Thr Arg Ala Cys Ser Leu Ser Leu Ser

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(2) INFORMATION FOR SEQ ID NO:2299:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1600662

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1600663

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..209

(D) OTHER INFORMATION: / Ceres Seq. ID 1600688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2301:

| Overall sample                 |          | Non-Black |          | Black |          |     |
|--------------------------------|----------|-----------|----------|-------|----------|-----|
|                                | Mean     | SD        | Mean     | SD    | Mean     | SD  |
| <b>Demographic variables</b>   |          |           |          |       |          |     |
| Age                            | 21.5     | 1.5       | 21.5     | 1.5   | 21.5     | 1.5 |
| Gender                         | 50%      |           | 50%      |       | 50%      |     |
| Marital status                 | 10%      |           | 10%      |       | 10%      |     |
| Employment                     | 20%      |           | 20%      |       | 20%      |     |
| Income                         | \$10,000 |           | \$10,000 |       | \$10,000 |     |
| <b>Psychological variables</b> |          |           |          |       |          |     |
| Depression                     | 15%      |           | 15%      |       | 15%      |     |
| Anxiety                        | 10%      |           | 10%      |       | 10%      |     |
| Stress                         | 25%      |           | 25%      |       | 25%      |     |
| Self-esteem                    | 30%      |           | 30%      |       | 30%      |     |
| Life satisfaction              | 40%      |           | 40%      |       | 40%      |     |
| Resilience                     | 50%      |           | 50%      |       | 50%      |     |
| Optimism                       | 60%      |           | 60%      |       | 60%      |     |
| Hope                           | 70%      |           | 70%      |       | 70%      |     |
| Gratitude                      | 80%      |           | 80%      |       | 80%      |     |
| Forgiveness                    | 90%      |           | 90%      |       | 90%      |     |
| Compassion                     | 100%     |           | 100%     |       | 100%     |     |

agtttgccgc tctgtgacct gctgccgtct tcttccgccg ccgccgccgt cgtcgtcttc 60  
gtccgtagat cagagagcgg ggaggaagaa aaagcgatcg atggcgcca actacgtgga 120  
cacgccgggc gaggaggac ggttccacgg ccctcacagc cacagcacca gcacgacccc 180  
gacggcggcg cggcggcggc ggcggcatc

(2) INFORMATION FOR SEQ ID NO:2302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1600689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2302:

Ser Leu Pro Leu Cys Asp Leu Leu Pro Ser Ser Ser Ala Ala Ala Ala  
1 5 10 15  
Val Val Val Phe Val Arg Arg Ser Glu Ser Gly Glu Glu Glu Lys Ala  
20 25 30  
Ile Asp Gly Val Gln Leu Arg Gly His Ala Gly Arg Gly Gly Thr Val  
35 40 45  
Pro Arg Pro Ser Gln Pro Gln His Gln His Asp Pro Asp Gly Gly Ala  
50 55 60  
Ala Ala Ala Ala Ala  
65

(2) INFORMATION FOR SEQ ID NO:2303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1600690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2303:

Val Cys Arg Ser Val Thr Cys Cys Arg Leu Leu Pro Pro Pro Pro Pro  
1 5 10 15  
Ser Ser Ser Ser Ser Val Asp Gln Arg Ala Gly Arg Lys Lys Lys Arg  
20 25 30  
Ser Met Ala Ser Asn Tyr Val Asp Thr Pro Gly Glu Glu Gly Arg Phe  
35 40 45  
His Gly Pro His Ser His Ser Thr Ser Thr Thr Pro Thr Ala Ala Arg  
50 55 60  
Arg Arg Arg Arg His  
65

(2) INFORMATION FOR SEQ ID NO:2304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..36

(D) OTHER INFORMATION: / Ceres Seq. ID 1600691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2304:

Met Ala Ser Asn Tyr Val Asp Thr Pro Gly Glu Glu Gly Arg Phe His

DO NOT WRITE IN THESE SPACES

(D) OTHER INFORMATION: / Ceres Seq. ID 1600709

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2307:  
Met Ala Gly Thr Val Thr Ala Thr Ala Thr Thr Xaa Thr Thr Glu Xaa  
1 5 10 15  
Gly Thr Thr Val Thr Ala Ala Thr Ser Glu Xaa Glu Ala Thr Ala Thr  
20 25 30  
Ala Ala Thr Ser Glu Leu Glu Ala Thr Ala Thr Ala Ala Ala Ile Gly  
35 40 45  
Pro Pro Ser Ala Ile Pro Asp Lys Tyr Met His Xaa Asn Arg Leu Gln  
50 55 60  
Ser Phe Ala Glu Arg Thr Tyr Lys Lys Asn Ala Asn Leu Gln Gly  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2308:

atccacagct cgcacccgat ttccaatttc aaatccttcg atcgcgcnvc gcccgccctc 60  
tcgcrctct ctccgatggc ccgcacgaag cagacggcga ggaantcaac tggcggaag 120  
gcgcccggga as

(2) INFORMATION FOR SEQ ID NO:2309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2309:

Ile His Ser Ser His Pro Ile Ser Asn Phe Lys Ser Phe Asp Arg Xaa  
1 5 10 15  
Xaa Pro Ala Leu Ser Xaa Leu Ser Pro Met Ala Arg Thr Lys Gln Thr  
20 25 30  
Ala Arg Xaa Ser Thr Gly Gly Lys Ala Pro Arg  
35 40

(2) INFORMATION FOR SEQ ID NO:2310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2310:

Ser Thr Ala Arg Ile Arg Phe Pro Ile Ser Asn Pro Ser Ile Ala Xaa  
1 5 10 15  
Arg Pro Pro Ser Arg Xaa Ser Leu Arg Trp Pro Ala Arg Ser Arg Arg  
20 25 30  
Arg Gly Xaa Gln Leu Ala Ala Arg Arg Arg Gly

DOCKET# 08669560







(D) OTHER INFORMATION: / Ceres Seq. ID 1600747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2317:

Met Gly Gly Cys Asp Lys Gln Gly Phe Pro Met Lys Gln Gly Val Leu  
1 5 10 15  
Thr Ser Gly Arg Val Arg Leu Leu Leu His Arg Gly Thr Pro Cys Phe  
20 25 30  
Arg Gly Tyr Xaa Arg Arg Asn Arg Arg Ala Gln Glu Glu Xaa Ser Pro  
35 40 45  
Trp Phe  
50

(2) INFORMATION FOR SEQ ID NO:2318:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 516 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..516

(D) OTHER INFORMATION: / Ceres Seq. ID 1600768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2318:

cacatctcct tccttttctc ggcacgtctg acacctcacc ggcctccgat ctctccacga 60  
gcctccgctc caatccgagg atccgcggcg gcgggcagtg gtcggccggc gatggcgac 120  
cgagtggaca acgagtacga ctacctcttc aagatcgtgc tcatcggcga ctccggcgctc 180  
ggcaagtcca acatcctttc ccggttcacc cgcaacgagt tctgcctcga gtccaagtcc 240  
accatcggcg tccgagttcg caccgcgacc ctccagatcg aagggaacac catcaaagct 300  
caaatatggg atactgcggg gcaagagagg taccgtgcaa tcacaagtgc ttactacaga 360  
ggagccgtgg gtgcacttct agtctatgac atcacgaaga agcagacatt tgaaaacata 420  
cagaggtggc tcccgcgagc tcgtgaccac gcggactcca acatcgatgat catgatggtc 480  
ggcmacaagt ccgacctgaa accacctgag gtcggt

(2) INFORMATION FOR SEQ ID NO:2319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..172

(D) OTHER INFORMATION: / Ceres Seq. ID 1600769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2319:

His Ile Ser Phe Leu Phe Ser Ala Ser Ser Thr Pro His Arg Pro Pro  
1 5 10 15  
Ile Ser Pro Arg Ala Ser Ala Pro Ile Arg Gly Ser Ala Ala Gly  
20 25 30  
Ser Gly Arg Pro Ala Met Ala His Arg Val Asp Asn Glu Tyr Asp Tyr  
35 40 45  
Leu Phe Lys Ile Val Leu Ile Gly Asp Ser Gly Val Gly Lys Ser Asn  
50 55 60  
Ile Leu Ser Arg Phe Thr Arg Asn Glu Phe Cys Leu Glu Ser Lys Ser  
65 70 75 80  
Thr Ile Gly Val Glu Phe Ala Thr Arg Thr Leu Gln Ile Glu Gly Lys  
85 90 95  
Thr Ile Lys Ala Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Tyr Arg  
100 105 110  
Ala Ile Thr Ser Ala Tyr Tyr Arg Gly Ala Val Gly Ala Leu Leu Val  
115 120 125  
Tyr Asp Ile Thr Lys Lys Gln Thr Phe Glu Asn Ile Gln Arg Trp Leu  
130 135 140

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(2) INFORMATION FOR SEQ ID NO:2320:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1600770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2320:

(2) INFORMATION FOR SEQ ID NO:2321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1600771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2321:

| (X1) SEQUENCE DESCRIPTION SHEET |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met                             | Ala | His | Arg | Val | Asp | Asn | Glu | Tyr | Asp | Tyr | Leu | Phe | Lys | Ile | Val |
| 1                               |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu                             | Ile | Gly | Asp | Ser | Gly | Val | Gly | Lys | Ser | Asn | Ile | Leu | Ser | Arg | Phe |
|                                 |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr                             | Arg | Asn | Glu | Phe | Cys | Leu | Glu | Ser | Lys | Ser | Thr | Ile | Gly | Val | Glu |
|                                 |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe                             | Ala | Thr | Arg | Thr | Leu | Gln | Ile | Glu | Gly | Lys | Thr | Ile | Lys | Ala | Gln |
|                                 |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile                             | Trp | Asp | Thr | Ala | Gly | Gln | Glu | Arg | Tyr | Arg | Ala | Ile | Thr | Ser | Ala |
| 65                              |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Tyr                             | Tyr | Arg | Gly | Ala | Val | Gly | Ala | Leu | Leu | Val | Tyr | Asp | Ile | Thr | Lys |
|                                 |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Lys                             | Gln | Thr | Phe | Glu | Asn | Ile | Gln | Arg | Trp | Leu | Pro | Arg | Ala | Arg | Asp |
|                                 |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| His                             | Ala | Asp | Ser | Asn | Ile | Val | Ile | Met | Met | Val | Gly | Xaa | Lys | Ser | Asp |

| Hauptstadt: Berlin    |                                                 |
|-----------------------|-------------------------------------------------|
| Land                  | Deutschland                                     |
| Gründungsdatum        | 1871                                            |
| Fläche                | 3.706 km²                                       |
| Einwohner             | 3.500.000                                       |
| Wirtschaftliche Daten |                                                 |
| BIP (2019)            | 1.350 Mrd. €                                    |
| BIP pro Kopf          | 38.000 €                                        |
| Währung               | Euro (€)                                        |
| Politische Daten      |                                                 |
| Regierung             | Parlamentarische Demokratie                     |
| Präsident             | Frank-Walter Steinmeier                         |
| Chancellor            | Angela Merkel                                   |
| Soziale Daten         |                                                 |
| Lebenserwartung       | 81 Jahre                                        |
| Arbeitslosenquote     | 5,2 %                                           |
| Kulturelle Daten      |                                                 |
| Religion              | Christen (50 %), Muslime (5 %), Sonstige (45 %) |
| Sprache               | Deutsch                                         |
| Geographische Daten   |                                                 |
| Gründungsdatum        | 1871                                            |
| Fläche                | 3.706 km²                                       |
| Einwohner             | 3.500.000                                       |
| Wirtschaftliche Daten |                                                 |
| BIP (2019)            | 1.350 Mrd. €                                    |
| BIP pro Kopf          | 38.000 €                                        |
| Währung               | Euro (€)                                        |
| Politische Daten      |                                                 |
| Regierung             | Parlamentarische Demokratie                     |
| Präsident             | Frank-Walter Steinmeier                         |
| Chancellor            | Angela Merkel                                   |
| Soziale Daten         |                                                 |
| Lebenserwartung       | 81 Jahre                                        |
| Arbeitslosenquote     | 5,2 %                                           |
| Kulturelle Daten      |                                                 |
| Religion              | Christen (50 %), Muslime (5 %), Sonstige (45 %) |
| Sprache               | Deutsch                                         |
| Geographische Daten   |                                                 |
| Gründungsdatum        | 1871                                            |
| Fläche                | 3.706 km²                                       |
| Einwohner             | 3.500.000                                       |

115 120 125  
Leu Lys Pro Pro Glu Val Gly  
130 135  
(2) INFORMATION FOR SEQ ID NO:2322:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 484 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..484  
(D) OTHER INFORMATION: / Ceres Seq. ID 1600772  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2322:  
atcctgaacc cgaaagctga actaccacac acaacaaata actgacgcag gcgatccatc 60  
actccacagt gtccacacac cggctgggaac cgaggccaac cgccgcccgc gccgccaatg 120  
tcgtccccctg cagcgccggg gcagccgcgc gcgcgcgcgc cgggtgcgctt cggcgtcctg 180  
ggatgcgctg acatcgcgcg taagatctcg cgcgcaatgc tgatgctccc tccgggcgcc 240  
gccaccatcg ccgccgtagg cagtcgctcc gatgacaagg cccgcccgtt catctccgaa 300  
atcggcttcc ccgcggcgcg cgtccacggg tcctacgagt ctctcctaga ggaccgcggac 360  
gtggaggccg tgtacctccc gctccccact agtctccacg tgccctgggc cacagccgtc 420  
gctgcgcgtg gcaagcacct gctcctcgag aagcccaccg cgctctgcac tgcsgaactc 480  
gacg  
(2) INFORMATION FOR SEQ ID NO:2323:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 122 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..122  
(D) OTHER INFORMATION: / Ceres Seq. ID 1600773  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2323:  
Met Ser Ser Pro Ala Ala Pro Val Gln Pro Pro Ala Pro Arg Ala Val  
1 5 10 15  
Arg Phe Gly Val Leu Gly Cys Ala Asp Ile Ala Arg Lys Ile Ser Arg  
20 25 30  
Ala Met Leu Met Leu Pro Pro Gly Ala Ala Thr Ile Ala Ala Val Gly  
35 40 45  
Ser Arg Ser Asp Asp Lys Ala Arg Arg Phe Ile Ser Glu Ile Gly Phe  
50 55 60  
Pro Ala Ala Arg Val His Gly Ser Tyr Glu Ser Leu Leu Glu Asp Pro  
65 70 75 80  
Asp Val Glu Ala Val Tyr Leu Pro Leu Pro Thr Ser Leu His Val Pro  
85 90 95  
Trp Ala Thr Ala Val Ala Ala Arg Gly Lys His Leu Leu Leu Glu Lys  
100 105 110  
Pro Thr Ala Leu Cys Thr Xaa Glu Leu Asp  
115 120  
(2) INFORMATION FOR SEQ ID NO:2324:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 89 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide

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(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1600774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2324:

Met Leu Met Leu Pro Gly Ala Ala Thr Ile Ala Ala Val Gly Ser  
1 5 10 15  
Arg Ser Asp Asp Lys Ala Arg Arg Phe Ile Ser Glu Ile Gly Phe Pro  
20 25 30  
Ala Ala Arg Val His Gly Ser Tyr Glu Ser Leu Leu Glu Asp Pro Asp  
35 40 45  
Val Glu Ala Val Tyr Leu Pro Leu Pro Thr Ser Leu His Val Pro Trp  
50 55 60  
Ala Thr Ala Val Ala Ala Arg Gly Lys His Leu Leu Leu Glu Lys Pro  
65 70 75 80  
Thr Ala Leu Cys Thr Xaa Glu Leu Asp  
85

(2) INFORMATION FOR SEQ ID NO:2325:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1600775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2325:

Met Leu Pro Pro Gly Ala Ala Thr Ile Ala Ala Val Gly Ser Arg Ser  
1 5 10 15  
Asp Asp Lys Ala Arg Arg Phe Ile Ser Glu Ile Gly Phe Pro Ala Ala  
20 25 30  
Arg Val His Gly Ser Tyr Glu Ser Leu Leu Glu Asp Pro Asp Val Glu  
35 40 45  
Ala Val Tyr Leu Pro Leu Pro Thr Ser Leu His Val Pro Trp Ala Thr  
50 55 60  
Ala Val Ala Ala Arg Gly Lys His Leu Leu Leu Glu Lys Pro Thr Ala  
65 70 75 80  
Leu Cys Thr Xaa Glu Leu Asp  
85

(2) INFORMATION FOR SEQ ID NO:2326:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..382

(D) OTHER INFORMATION: / Ceres Seq. ID 1600776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2326:

|             |            |             |             |            |            |     |
|-------------|------------|-------------|-------------|------------|------------|-----|
| ccattaggggt | tcacttccaa | actoggcacc  | tataaacact  | tctctcacgc | cccacggtcg | 60  |
| cccgccgctc  | cgctcgccac | catcggtgtag | gttaggctag  | gttcgaccag | ctagcggaaa | 120 |
| tggtggcctt  | caggttccat | cagtaccagg  | tggtggggcg  | cgcgctgccg | acgccggcg  | 180 |
| atgagcacc   | caagatctac | cgcatgaagc  | tctggggccac | caacgaggtc | cgcgccaaga | 240 |
| gcaagttctg  | gtacttcttg | aggaagttga  | agaaggctaa  | gaagagcaac | ggccaggtcc | 300 |
| tggccatcaa  | cgagatcttt | gagcgtaacc  | cgacgcacaat | caagaactac | ggcatctggc | 360 |
| tgcgctacca  | gagcagaacc | gg          |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

DOCKET# 00666666



tgg

(2) INFORMATION FOR SEQ ID NO:2330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1600783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2330:

Ser Phe Ser Ala Phe Leu Ser Leu Ala Pro Arg Arg Arg Arg His Ser  
1 5 10 15  
Ile Arg Pro Leu Arg Arg Arg Gln His Ile Pro Gly Arg Leu Val Leu  
20 25 30  
Ala Leu Arg Thr Gly Gly His Gly Phe Arg Arg His Arg Pro Gln Arg  
35 40 45  
Cys Met Cys Cys Trp Gly Cys Thr His Pro Asn Gly Arg Phe Pro Trp  
50 55 60  
Cys Leu Val Ser Leu Ala Cys Tyr Glu Thr Trp Leu Tyr Ser Asn Ser  
65 70 75 80  
Ser Cys Ser Gly Lys Ser Lys Arg Gly Ser Ser Pro Arg Ala Gly Gly  
85 90 95  
Leu Leu Trp Lys Arg Leu Glu Cys  
100

(2) INFORMATION FOR SEQ ID NO:2331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1600784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2331:

Met Ala Ser Asp Gly Ile Gly Pro Arg Asp Val Cys Val Val Gly Val  
1 5 10 15  
Ala Arg Thr Pro Met Gly Gly Phe Leu Gly Ala Leu Ser Pro Leu Pro  
20 25 30  
Ala Thr Lys Leu Gly Ser Ile Val Ile Gln Ala Ala Leu Glu Arg Ala  
35 40 45  
Asn Val Asp Pro Ala Leu Val Gln Glu Val Tyr Phe Gly Asn Val Leu  
50 55 60  
Ser Ala Asn Leu Gly Gln Ala Pro Ala Arg Gln Ala Ala Leu Gly Ala  
65 70 75 80  
Gly Ile Pro Asn Ser Val Val Cys Thr Thr Val Asn Lys Val Cys Ala  
85 90 95  
Ser Gly Met Lys Ala Thr Met Phe Ala Ala Gln Ser Ile Gln Leu Gly  
100 105 110  
Ile Asn Asp Ile Val Val Ala Gly Gly Met  
115 120

(2) INFORMATION FOR SEQ ID NO:2332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

00000000 101300

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..102  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1600785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2332:  
Met Gly Gly Phe Leu Gly Ala Leu Ser Pro Leu Pro Ala Thr Lys Leu  
1                    5                    10                    15  
Gly Ser Ile Val Ile Gln Ala Ala Leu Glu Arg Ala Asn Val Asp Pro  
                    20                    25                    30  
Ala Leu Val Gln Glu Val Tyr Phe Gly Asn Val Leu Ser Ala Asn Leu  
                    35                    40                    45  
Gly Gln Ala Pro Ala Arg Gln Ala Ala Leu Gly Ala Gly Ile Pro Asn  
                    50                    55                    60  
Ser Val Val Cys Thr Thr Val Asn Lys Val Cys Ala Ser Gly Met Lys  
65                    70                    75                    80  
Ala Thr Met Phe Ala Ala Gln Ser Ile Gln Leu Gly Ile Asn Asp Ile  
                    85                    90                    95  
Val Val Ala Gly Gly Met  
                    100

(2) INFORMATION FOR SEQ ID NO:2333:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 520 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..520  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1600786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2333:  
cagaaggaga gcaccctcca cctggtgctc cgcctcaggg gtggcatgca gatttttgtg 60  
aagacattga ctggcaagac catcaccttg gaggtggaga gctctgacac cattgacaat 120  
gtgaaggcca agatccagga caaggagggc attccccag accagcagcg tctgatcttt 180  
gctggcaagc agctggagga tggctgcacc ctgcgcgact acaacatcca gaaggagagt 240  
acccttcacc ttgtttctccg cctcaggggt ggtatgcaga tctttgtgaa gacctgact 300  
ggaaaaacca taaccctgga ggttgagagc tcggacacca tcgacaatgt gaaggcgaag 360  
atccaggaca aggagggcat cccccggac cagcagcgtc tgatcttcgc cggcaaacag 420  
ctggaggatg gccgcacctt agcagactac aacatccaaa aggagagcac cctccacttg 480  
tgctcrgtgt cgtggtggt cagtaagtca tgggtcgttt

(2) INFORMATION FOR SEQ ID NO:2334:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 173 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..173  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1600787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2334:  
Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met  
1                    5                    10                    15  
Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val  
                    20                    25                    30  
Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys  
                    35                    40                    45  
Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln  
50                    55                    60

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Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser  
65 70 75 80  
Thr Leu His Leu Val Leu Arg Leu Arg Gly Met Gln Ile Phe Val  
85 90 95  
Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser Asp  
100 105 110  
Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro  
115 120 125  
Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly  
130 135 140  
Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu  
145 150 155 160  
Cys Xaa Val Ser Val Val Val Ser Lys Ser Trp Val Val  
165 170

(2) INFORMATION FOR SEQ ID NO:2335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2335:

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu  
1 5 10 15  
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp  
20 25 30  
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys  
35 40 45  
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu  
50 55 60  
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe  
65 70 75 80  
Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser  
85 90 95  
Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile  
100 105 110  
Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp  
115 120 125  
Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His  
130 135 140  
Leu Cys Xaa Val Ser Val Val Val Ser Lys Ser Trp Val Val  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..500
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2336:

ccccgaagt ctgaacatac tagaagcgta accctaagtc tcggacccca accctcgagg 60  
aaggcgaccg gagatggcgg cgtcgtcggc agtggagaag ctcaagggtcc tctggggactc 120  
gcagggtcaac gacgaggagc agtgggagct caattataag ctgctgaagg cgcgtggtct 180

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gtttgcggga tccatcttcc tgatgcggaa cttcgggtgat ctgatggcca tttagtaggc 240  
ttatcagcag cattacccat cgctcgccaa cgtgcagact aaggaagcac tgaccggccg 300  
gtcatggcga ggatccaact ctacgtcgtc gccgcggcct gcgcgcgtgc cctcgcgctc 360  
gccggcgacc cggacatgct ccaggacgtc tgcgtggctg actacgcttc cccggtcaag 420  
ctgaacgggt tcccgtgcaa ggcaacatc tcggcggacg acttcttctt cgacgggctg 480  
aggagccggg caacaccaac

(2) INFORMATION FOR SEQ ID NO:2337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52

(D) OTHER INFORMATION: / Ceres Seq. ID 1600791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2337:

Pro Pro Lys Ser Glu His Thr Arg Ser Val Thr Leu Ser Leu Gly Pro  
1 5 10 15  
Gln Pro Ser Arg Lys Ala Thr Gly Asp Gly Gly Val Val Gly Ser Gly  
20 25 30  
Glu Ala Gln Gly Pro Leu Gly Leu Ala Gly Gln Arg Arg Gly Ala Val  
35 40 45  
Gly Ala Gln Leu  
50

(2) INFORMATION FOR SEQ ID NO:2338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1600792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2338:

Met Ala Ala Ser Ser Ala Val Glu Lys Leu Lys Val Leu Trp Asp Ser  
1 5 10 15  
Gln Val Asn Asp Glu Glu Gln Trp Ala Leu Asn Tyr Lys Leu Leu Lys  
20 25 30  
Ala Ala Gly Leu Phe Ala Gly Ser Ile Phe Leu Met Arg Asn Phe Gly  
35 40 45  
Asp Leu Met Ala Ile  
50

(2) INFORMATION FOR SEQ ID NO:2339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1600793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2339:

Met Ala Arg Ile His Leu Tyr Val Val Ala Ala Ala Cys Ala Val Ala  
1 5 10 15  
Leu Ala Leu Ala Gly Asp Pro Asp Met Leu Gln Asp Val Cys Val Ala

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- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..156
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1600796
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2342:

Ile Leu Thr Pro Pro Leu Pro Asn Asn Ser Leu Pro Ile Asp Leu Ala  
1 5 10 15  
Ala Pro Phe Leu Pro Ile Ser Ala Pro Arg Pro Val Ala His Ala Ala  
20 25 30  
Gly Pro Ser Pro Lys Thr Phe Leu His Pro Leu Leu Ser Ser Pro Arg  
35 40 45  
Trp Pro Pro Pro Pro Pro Arg Arg Thr Pro Ser Ser Ser Ala Pro  
50 55 60  
Arg Ser Arg Pro Arg Leu Arg Gly Arg Arg Arg Pro Trp Leu Arg Arg  
65 70 75 80  
Arg Arg Pro Trp Leu Arg Trp Arg Trp Arg Pro Arg Leu Arg Arg Arg  
85 90 95  
Pro Trp Leu Arg Gly Arg Arg Arg Leu Trp Arg Trp Val Arg Trp Arg  
100 105 110  
Arg Arg Trp Arg Arg Pro Arg Leu Leu Gln Val Arg Arg Gly Gly Pro  
115 120 125  
His Gly Lys Gly Leu Leu Pro Gly Arg Arg Leu Arg Gly Arg Ala  
130 135 140  
Ala Ala Ala Arg Gln Arg Val Leu Gln Leu Arg Pro  
145 150 155

- (2) INFORMATION FOR SEQ ID NO:2343:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 109 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..109
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1600797
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2343:

Met Ala Ala Ala Ala Thr Thr Pro His Ser Leu Leu Leu Gln Arg Ala  
1 5 10 15  
Ala Ile Pro Ala Ala Ala Thr Gly Glu Ala Thr Val Ala Thr Ala  
20 25 30  
Ala Ala Thr Val Val Thr Val Glu Val Ala Thr Ala Ala Thr Ala Ala  
35 40 45  
Thr Val Ala Thr Gly Glu Ala Ala Ala Met Ala Val Gly Thr Val Glu  
50 55 60  
Ala Ala Val Glu Ala Ala Ala Ala Ala Ser Ser Ala Ala Arg Arg Ala  
65 70 75 80  
Thr Trp Gln Gly Thr Ala Pro Arg Ala Ala Thr Glu Gly Glu Gly  
85 90 95  
Gly Gly Gly Ala Ala Ser Ala Thr Thr Ala Ala Arg  
100 105

- (2) INFORMATION FOR SEQ ID NO:2344:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 326 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single

DOCKET "08663950"





(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1600822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2349:

Xaa Ile Val Lys Xaa Ala Met Ser Met Asp Tyr Leu Ala Ala Ala Val  
1 5 10 15  
Pro Val Thr Leu Ala Leu Gly Val Gly Ser Ile Leu Leu Val Leu Arg  
20 25 30  
Trp Thr Tyr Cys Arg Arg Arg Thr Ser Ala Glu Glu Val Arg Leu Pro  
35 40 45  
Pro Gly Ser Arg Gly Leu Leu Phe Leu Gly Glu Thr Leu His Tyr Leu  
50 55 60  
Ala Ala Ser Ser Thr Pro Gly Val Leu Pro Pro Phe Phe Gln Arg Arg  
65 70 75 80  
Leu Glu Arg Tyr Gly Pro Ile Phe Arg Thr Asn Leu Val Gly Glu Asp  
85 90 95  
Leu Val Val Ser Leu Asp Ala Asp  
100

(2) INFORMATION FOR SEQ ID NO:2350:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1600823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2350:

Met Asp Val Leu Pro Pro Pro Asn Lys Arg Arg Arg Ser Glu Thr Ala  
1 5 10 15  
Ala Gly Val Lys Gly Pro Pro Val Pro Gly Gly Asp Ala Pro Leu Pro  
20 25 30  
Gly Ser Val Leu His Pro Gly Gly Ile Ala Thr Ile Leu Pro Ala Thr  
35 40 45  
Val Gly Glu Val Trp Pro His Leu Pro Asp Glu Pro Gly Arg Gly Gly  
50 55 60  
Pro Arg Arg Val Ala Gly Arg Gly Leu Asn Ala His Val Leu Lys Gln  
65 70 75 80  
Glu Glu Arg Gly Phe Gln Ile Trp Tyr Pro Pro Ser Phe Met Arg Val  
85 90 95  
Phe Gly Ala Asp Asn Ile Thr Ala Lys Leu Gly Val Leu His His Tyr  
100 105 110  
Met Arg

(2) INFORMATION FOR SEQ ID NO:2351:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..314

(D) OTHER INFORMATION: / Ceres Seq. ID 1600835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2351:

agcacgtaca gagcaagcga agggagaact caagcgaggg aggcagaggg cgamgtaagc 60  
aagcagctag ctgctcactg cttgctctgt gctgggtcgtt tgctctgtgc tggtcgcggt 120

DOCKET NO. 08663950

```
ccttttgcag gaactcctcg cctgggtgatg gacaggcaca catgcaggct ctgcttccgg 180
cggttccaca acggccgcgc gctggggcggc cacatgcgct cccatgtcat yggccgcgtc 240
gtcgggtgca gcgcactcgc cgctgcgcgcg sagcaattgn gcttcgctct ccctggcgtc 300
cacctcgtcg acgg
```

(2) INFORMATION FOR SEQ ID NO:2352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2352:

```
Ser Thr Tyr Arg Ala Ser Glu Gly Arg Thr Gln Ala Arg Glu Ala Glu
1 5 10 15
Gly Xaa Val Ser Lys Gln Leu Ala Ala His Cys Leu Leu Cys Ala Gly
20 25 30
Arg Leu Leu Cys Ala Gly Arg Val Pro Phe Ala Gly Thr Pro Arg Leu
35 40 45
Val Met Asp Arg His Thr Cys Arg Leu Cys Phe Arg Arg Phe His Asn
50 55 60
Gly Arg Ala Leu Gly Gly His Met Arg Ser His Val Xaa Gly Arg Val
65 70 75 80
Val Gly Cys Ser Ala Leu Ala Ala Ala Ala Xaa Gln Leu Xaa Phe Ala
85 90 95
Leu Pro Gly Val His Leu Val Asp
100
```

(2) INFORMATION FOR SEQ ID NO:2353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2353:

```
His Val Gln Ser Lys Arg Arg Glu Asn Ser Ser Glu Gly Gly Arg Gly
1 5 10 15
Arg Xaa Lys Gln Ala Ala Ser Cys Ser Leu Leu Ala Leu Cys Trp Ser
20 25 30
Phe Ala Leu Cys Trp Ser Arg Ser Phe Cys Arg Asn Ser Ser Pro Gly
35 40 45
Asp Gly Gln Ala His Met Gln Ala Leu Leu Pro Ala Val Pro Gln Arg
50 55 60
Pro Arg Ala Gly Arg Pro His Ala Leu Pro Cys His Xaa Pro Arg Arg
65 70 75 80
Arg Leu Gln Arg Thr Arg Arg Cys Arg Xaa Ala Ile Xaa Leu Arg Ser
85 90 95
Pro Trp Arg Pro Pro Arg Arg Arg
100
```

(2) INFORMATION FOR SEQ ID NO:2354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

0965980 101300











50 55 60  
Ala Val Gln Glu Ala Trp Ala Ser Thr Cys Gly Gly Thr Gly Lys Gln  
65 70 75 80  
Thr Ile Leu Ile Pro Lys Gly Asp Phe Leu Val Gly Gln Leu Asn Phe  
85 90 95  
Thr Gly Pro Cys Lys Gly Asp Val Thr Ile  
100 105

(2) INFORMATION FOR SEQ ID NO:2364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1600857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2364:

Met Ala Tyr Thr Asp Asn Ala Met Arg Ala Leu Leu Arg Ser Ser Thr  
1 5 10 15  
Ser Cys Met Val Arg Arg Lys Ser Pro Arg Ala Ser Met Arg Lys Arg  
20 25 30  
Pro Gly Pro Val Gly Pro Ser Thr Ser Pro Ser Trp Ala Pro Pro Ala  
35 40 45  
Thr Ala Arg Gln Thr Ala Gln Arg Gln Cys Arg Arg His Gly His Gln  
50 55 60  
Arg Val Ala Ala Leu Gly Ser Arg Gln Ser Leu Tyr Pro Arg Ala Thr  
65 70 75 80  
Ser Leu Ser Asp Asn Ser Thr Ser Gln Ala Arg Ala Arg Ala Thr  
85 90 95

(2) INFORMATION FOR SEQ ID NO:2365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1600858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2365:

Met Arg Ala Leu Leu Arg Ser Ser Thr Ser Cys Met Val Arg Arg Lys  
1 5 10 15  
Ser Pro Arg Ala Ser Met Arg Lys Arg Pro Gly Pro Val Gly Pro Ser  
20 25 30  
Thr Ser Pro Ser Trp Ala Pro Pro Ala Thr Ala Arg Gln Thr Ala Gln  
35 40 45  
Arg Gln Cys Arg Arg His Gly His Gln Arg Val Ala Ala Leu Gly Ser  
50 55 60  
Arg Gln Ser Leu Tyr Pro Arg Ala Thr Ser Leu Ser Asp Asn Ser Thr  
65 70 75 80  
Ser Gln Ala Arg Ala Arg Ala Thr  
85

(2) INFORMATION FOR SEQ ID NO:2366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

0968980 101300

(ix) FEATURE:

(B) LOCATION: 1..458

(D) OTHER INFORMATION: / Ceres Seq. ID 1600859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2366:

| (X1) SEQUENCE DESCRIPTION: SEQ 1 NOV 1988                           |     |
|---------------------------------------------------------------------|-----|
| atggttggtat ggcggcattc gtgcaggacc gacccccacc tccacctcgt atgtctctctc | 60  |
| tctctctctc tccttcccat ggctgatgcc tgacacgggtg acacccccaa cattctccct  | 120 |
| cactagctag ctgtgtcctg cctacctagc ggtatcaata cccggctgca gctcaccacc   | 180 |
| accaccaacc aaccaacca cagttcccat ataggcagcc atcggctaca cagcctcgcc    | 240 |
| tccgtaagca gagtgtgtcg ttggaagaga gacgacggcg gccatggcga cctccttcca   | 300 |
| ggggacgacc accaagtgca ccgcctgcga caagacgggtg taccttgtgg acaagctcac  | 360 |
| cgccgacaac cgcattctacc acaaggcctg cttccgctgc caccactgca agggcaccct  | 420 |
| caagctcgcs aactacaact ccttcgaggg agtgcctc                           |     |

(2) INFORMATION FOR SEQ ID NO:2367:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..30

(D) OTHER INFORMATION: / Ceres Seq. ID 1600860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2367:

| (X1) SEQUENCE DESCRIPTION: SEQ ID: 1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|--------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met                                  | Val | Val | Trp | Arg | His | Ser | Cys | Arg | Thr | Asp | Pro | His | Leu | His | Leu |
| 1                                    |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val                                  | Cys | Ser | Leu | Ser | Leu | Ser | Leu | Leu | Pro | Met | Ala | Asp | Ala |     |     |
|                                      |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

(2) INFORMATION FOR SEQ ID NO:2368:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..42

(D) OTHER INFORMATION: / Ceres Seq. ID 1600861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2368:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Trp | Tyr | Gly | Gly | Ile | Arg | Ala | Gly | Pro | Thr | Pro | Thr | Ser | Thr | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Ala | Leu | Ser | Leu | Ser | Leu | Ser | Phe | Pro | Trp | Leu | Met | Pro | Asp | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Thr | Pro | Pro | Thr | Phe | Ser | Leu | Thr | Ser |     |     |     |     |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2369:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1600862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2369:

Met Ala Thr Ser Phe Gln Gly Thr Thr Thr Lys Cys Thr Ala Cys Asp

| 1990-1991 |  | 1991-1992 |  | 1992-1993 |  | 1993-1994 |  | 1994-1995 |  | 1995-1996 |  | 1996-1997 |  | 1997-1998 |  | 1998-1999 |  | 1999-2000 |  | 2000-2001 |  | 2001-2002 |  | 2002-2003 |  | 2003-2004 |  | 2004-2005 |  | 2005-2006 |  | 2006-2007 |  | 2007-2008 |  | 2008-2009 |  | 2009-2010 |  | 2010-2011 |  | 2011-2012 |  | 2012-2013 |  | 2013-2014 |  | 2014-2015 |  | 2015-2016 |  | 2016-2017 |  | 2017-2018 |  | 2018-2019 |  | 2019-2020 |  | 2020-2021 |  | 2021-2022 |  | 2022-2023 |  | 2023-2024 |  | 2024-2025 |  | 2025-2026 |  | 2026-2027 |  | 2027-2028 |  | 2028-2029 |  | 2029-2030 |  | 2030-2031 |  | 2031-2032 |  | 2032-2033 |  | 2033-2034 |  | 2034-2035 |  | 2035-2036 |  | 2036-2037 |  | 2037-2038 |  | 2038-2039 |  | 2039-2040 |  | 2040-2041 |  | 2041-2042 |  | 2042-2043 |  | 2043-2044 |  | 2044-2045 |  | 2045-2046 |  | 2046-2047 |  | 2047-2048 |  | 2048-2049 |  | 2049-2050 |  | 2050-2051 |  | 2051-2052 |  | 2052-2053 |  | 2053-2054 |  | 2054-2055 |  | 2055-2056 |  | 2056-2057 |  | 2057-2058 |  | 2058-2059 |  | 2059-2060 |  | 2060-2061 |  | 2061-2062 |  | 2062-2063 |  | 2063-2064 |  | 2064-2065 |  | 2065-2066 |  | 2066-2067 |  | 2067-2068 |  | 2068-2069 |  | 2069-2070 |  | 2070-2071 |  | 2071-2072 |  | 2072-2073 |  | 2073-2074 |  | 2074-2075 |  | 2075-2076 |  | 2076-2077 |  | 2077-2078 |  | 2078-2079 |  | 2079-2080 |  | 2080-2081 |  | 2081-2082 |  | 2082-2083 |  | 2083-2084 |  | 2084-2085 |  | 2085-2086 |  | 2086-2087 |  | 2087-2088 |  | 2088-2089 |  | 2089-2090 |  | 2090-2091 |  | 2091-2092 |  | 2092-2093 |  | 2093-2094 |  | 2094-2095 |  | 2095-2096 |  | 2096-2097 |  | 2097-2098 |  | 2098-2099 |  | 2099-2100 |  | 2100-2101 |  | 2101-2102 |  | 2102-2103 |  | 2103-2104 |  | 2104-2105 |  | 2105-2106 |  | 2106-2107 |  | 2107-2108 |  | 2108-2109 |  | 2109-2110 |  | 2110-2111 |  | 2111-2112 |  | 2112-2113 |  | 2113-2114 |  | 2114-2115 |  | 2115-2116 |  | 2116-2117 |  | 2117-2118 |  | 2118-2119 |  | 2119-2120 |  | 2120-2121 |  | 2121-2122 |  | 2122-2123 |  | 2123-2124 |  | 2124-2125 |  | 2125-2126 |  | 2126-2127 |  | 2127-2128 |  | 2128-2129 |  | 2129-2130 |  | 2130-2131 |  | 2131-2132 |  | 2132-2133 |  | 2133-2134 |  | 2134-2135 |  | 2135-2136 |  | 2136-2137 |  | 2137-2138 |  | 2138-2139 |  | 2139-2140 |  | 2140-2141 |  | 2141-2142 |  | 2142-2143 |  | 2143-2144 |  | 2144-2145 |  | 2145-2146 |  | 2146-2147 |  | 2147-2148 |  | 2148-2149 |  | 2149-2150 |  | 2150-2151 |  | 2151-2152 |  | 2152-2153 |  | 2153-2154 |  | 2154-2155 |  | 2155-2156 |  | 2156-2157 |  | 2157-2158 |  | 2158-2159 |  | 2159-2160 |  | 2160-2161 |  | 2161-2162 |  | 2162-2163 |  | 2163-2164 |  | 2164-2165 |  | 2165-2166 |  | 2166-2167 |  | 2167-2168 |  | 2168-2169 |  | 2169-2170 |  | 2170-2171 |  | 2171-2172 |  | 2172-2173 |  | 2173-2174 |  | 2174-2175 |  | 2175-2176 |  | 2176-2177 |  | 2177-2178 |  | 2178-2179 |  | 2179-2180 |  | 2180-2181 |  | 2181-2182 |  | 2182-2183 |  | 2183-2184 |  | 2184-2185 |  | 2185-2186 |  | 2186-2187 |  | 2187-2188 |  | 2188-2189 |  | 2189-2190 |  | 2190-2191 |  | 2191-2192 |  | 2192-2193 |  | 2193-2194 |  | 2194-2195 |  | 2195-2196 |  | 2196-2197 |  | 2197-2198 |  | 2198-2199 |  | 2199-2200 |  | 2200-2201 |  | 2201-2202 |  | 2202-2203 |  | 2203-2204 |  | 2204-2205 |  | 2205-2206 |  | 2206-2207 |  | 2207-2208 |  | 2208-2209 |  | 2209-2210 |  | 2210-2211 |  | 2211-2212 |  | 2212-2213 |  | 2213-2214 |  | 2214-2215 |  | 2215-2216 |  | 2216-2217 |  |
|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|
|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|

| Met | Ser | Thr | Pro | Ala | Ser | Pro | Pro | Pro | Ala | Thr | Ser | Ser | Thr | Ser |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |







Ser Ile Pro Asp Gln Ala Asp Arg His Arg Ala Ser Asp Pro Cys  
50 55 60

(2) INFORMATION FOR SEQ ID NO:2379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..526
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2379:

|            |             |            |             |            |             |     |
|------------|-------------|------------|-------------|------------|-------------|-----|
| actctctcct | ctcggcgtcc  | ccgttcccca | acctctcgtc  | tgctgcctgc | ctgcctgcaa  | 60  |
| aaaggagttt | gtcatggcgt  | ctaagcgc   | cctcaaggag  | ctgaaggacc | tgacagaaaga | 120 |
| ccccccaca  | tcatgcagtg  | caggtcctgc | tggtgaggac  | atgtttcatt | ggcaagcaac  | 180 |
| aattatggga | ccacctgaca  | gtccctatgc | tggcgggtgtt | ttcttagtga | acattcattt  | 240 |
| cccgccagat | taccoccttca | aacctccaaa | ggtttctttc  | aagacaaagg | tcttccatcc  | 300 |
| taatatcaac | agcaatggaa  | gtatatgcct | tgacattctc  | aaagagcagt | ggagccctgc  | 360 |
| tctgacaatt | tctaaggtcc  | tgctctccat | ctgctccctg  | ctgaccgact | ccaacccgga  | 420 |
| cgaccctctt | gtcccgagga  | ttgccacat  | gtacaagacg  | gaccggccga | agtacgagtc  | 480 |
| gacggccccg | agctggacgc  | agaagtagcg | gatgggctga  | cgaacg     |             |     |

(2) INFORMATION FOR SEQ ID NO:2380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..172
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2380:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Pro | Leu | Gly | Val | Pro | Val | Pro | Gln | Pro | Leu | Val | Cys | Cys | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Pro | Ala | Cys | Lys | Glu | Phe | Val | Met | Ala | Ser | Lys | Arg | Ile | Leu | Lys |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Glu | Leu | Lys | Asp | Leu | Gln | Lys | Asp | Pro | Pro | Thr | Ser | Cys | Ser | Ala | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Ala | Gly | Glu | Asp | Met | Phe | His | Trp | Gln | Ala | Thr | Ile | Met | Gly | Pro |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Pro | Asp | Ser | Pro | Tyr | Ala | Gly | Gly | Val | Phe | Leu | Val | Asn | Ile | His | Phe |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Pro | Asp | Tyr | Pro | Phe | Lys | Pro | Pro | Lys | Val | Ser | Phe | Lys | Thr | Lys |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Phe | His | Pro | Asn | Ile | Asn | Ser | Asn | Gly | Ser | Ile | Cys | Leu | Asp | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Lys | Glu | Gln | Trp | Ser | Pro | Ala | Leu | Thr | Ile | Ser | Lys | Val | Leu | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Ile | Cys | Ser | Leu | Leu | Thr | Asp | Ser | Asn | Pro | Asp | Asp | Pro | Leu | Val |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Pro | Glu | Ile | Ala | His | Met | Tyr | Lys | Thr | Asp | Arg | Pro | Lys | Tyr | Glu | Ser |
|     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Thr | Ala | Arg | Ser | Trp | Thr | Gln | Lys | Tyr | Ala | Met | Gly |     |     |     |     |
|     |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid

00559301 00559301

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..148  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1600901  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2381:

Met Ala Ser Lys Arg Ile Leu Lys Glu Leu Lys Asp Leu Gln Lys Asp  
1                  5                  10                  15  
Pro Pro Thr Ser Cys Ser Ala Gly Pro Ala Gly Glu Asp Met Phe His  
                  20                  25                  30  
Trp Gln Ala Thr Ile Met Gly Pro Pro Asp Ser Pro Tyr Ala Gly Gly  
                  35                  40                  45  
Val Phe Leu Val Asn Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro  
50                  55                  60  
Pro Lys Val Ser Phe Lys Thr Lys Val Phe His Pro Asn Ile Asn Ser  
65                  70                  75                  80  
Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala  
                  85                  90                  95  
Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp  
                  100                 105                 110  
Ser Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Met Tyr Lys  
                 115                 120                 125  
Thr Asp Arg Pro Lys Tyr Glu Ser Thr Ala Arg Ser Trp Thr Gln Lys  
130                 135                 140  
Tyr Ala Met Gly  
145

- (2) INFORMATION FOR SEQ ID NO:2382:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 119 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..119  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1600902  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2382:

Met Phe His Trp Gln Ala Thr Ile Met Gly Pro Pro Asp Ser Pro Tyr  
1                  5                  10                  15  
Ala Gly Gly Val Phe Leu Val Asn Ile His Phe Pro Pro Asp Tyr Pro  
                  20                  25                  30  
Phe Lys Pro Pro Lys Val Ser Phe Lys Thr Lys Val Phe His Pro Asn  
35                  40                  45  
Ile Asn Ser Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp  
50                  55                  60  
Ser Pro Ala Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu  
65                  70                  75                  80  
Leu Thr Asp Ser Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His  
                  85                  90                  95  
Met Tyr Lys Thr Asp Arg Pro Lys Tyr Glu Ser Thr Ala Arg Ser Trp  
100                 105                 110  
Thr Gln Lys Tyr Ala Met Gly  
115

- (2) INFORMATION FOR SEQ ID NO:2383:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 452 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single

09669300-10300

```
(A) NAME/KEY: -
(B) LOCATION: 1
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2383:

(2) INFORMATION FOR SEQ ID NO:2384:

(A) LENGTH: 150 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

```
(A) NAME/KEY: peptide
(B) LOCATION: 1..150
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1600904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2384:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2385:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

```
(A) NAME/KEY: peptide
(B) LOCATION: 1..93
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1600905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2385:

| Met | Ala | Met | Asp | Pro | Asp | Ala | Val | Ala | Lys | Ala | Phe | Val | Glu | His | Tyr |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Tyr Arg Thr Phe Asp Thr Asn Arg Ala Ala Leu Val Gly Leu Tyr Gln  
20 25 30  
Glu Thr Ser Met Leu Thr Phe Glu Gly Gln Lys Phe Gln Gly Pro Ser  
35 40 45  
Ala Ile Ala Gly Lys Leu Gly Ser Leu Pro Phe Gln Ala Cys Glu His  
50 55 60  
Gln Ile Val Thr Val Asp Cys Gln Pro Ser Gly Pro Gln Gly Gly Met  
65 70 75 80  
Leu Val Phe Val Ser Gly Ser Ile Arg Thr Gly Pro Arg  
85 90

(2) INFORMATION FOR SEQ ID NO:2386:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1600906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2386:

Met Asp Pro Asp Ala Val Ala Lys Ala Phe Val Glu His Tyr Tyr Arg  
1 5 10 15  
Thr Phe Asp Thr Asn Arg Ala Ala Leu Val Gly Leu Tyr Gln Glu Thr  
20 25 30  
Ser Met Leu Thr Phe Glu Gly Gln Lys Phe Gln Gly Pro Ser Ala Ile  
35 40 45  
Ala Gly Lys Leu Gly Ser Leu Pro Phe Gln Ala Cys Glu His Gln Ile  
50 55 60  
Val Thr Val Asp Cys Gln Pro Ser Gly Pro Gln Gly Gly Met Leu Val  
65 70 75 80  
Phe Val Ser Gly Ser Ile Arg Thr Gly Pro Arg  
85 90

(2) INFORMATION FOR SEQ ID NO:2387:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..377

(D) OTHER INFORMATION: / Ceres Seq. ID 1600932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2387:

ttctactggt caccgcgct gcgctcgctc actcgctctc tcccctctgg ctctgagtgg 60  
cgctagtggg cgaccgcgc gcgtccctcc gtcagtgcc aggtgtagcc tcgtcagccc 120  
ctccgtcagt cttegtcggc cccctcgccg acgagcacc accaggcatg agagcgcgct 180  
tctagaataa tgtctgtgct tacctgcgtg attgaaagca tgggctcatc ctgtagcaga 240  
tcccattctt tcgacgaggc tgaagcagct gaaaatgcaa agtctgcaga cattgaccgg 300  
agattttgca agadacaaaa gccgaacaac acatccacaa gctcttactt ctcggtgctg 360  
gagaatcggg gaagtct

(2) INFORMATION FOR SEQ ID NO:2388:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

DOCKET "08659360"

(A) NAME/KEY: peptide  
(B) LOCATION: 1..62  
(D) OTHER INFORMATION: / Ceres Seq. ID 1600933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2388:

Ser Thr Val His Pro Ala Cys Ala Arg Ser Leu Ala Leu Ser Pro Leu  
1 5 10 15  
Ala Leu Ser Gly Ala Ser Gly Arg Pro Arg Arg Val Pro Pro Ser Val  
20 25 30  
Pro Arg Cys Ser Leu Val Ser Pro Ser Val Ser Leu Arg Arg Pro Pro  
35 40 45  
Arg Arg Arg Ala Pro Thr Arg His Glu Ser Ala Leu Leu Glu  
50 55 60

(2) INFORMATION FOR SEQ ID NO:2389:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..62  
(D) OTHER INFORMATION: / Ceres Seq. ID 1600934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2389:

Met Ser Val Leu Thr Cys Val Ile Glu Ser Met Gly Ser Ser Cys Ser  
1 5 10 15  
Arg Ser His Ser Phe Asp Glu Ala Glu Ala Ala Glu Asn Ala Lys Ser  
20 25 30  
Ala Asp Ile Asp Arg Arg Phe Cys Lys Xaa Gln Lys Pro Asn Asn Thr  
35 40 45  
Ser Thr Ser Ser Tyr Phe Ser Val Leu Glu Asn Arg Gly Ser  
50 55 60

(2) INFORMATION FOR SEQ ID NO:2390:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..52  
(D) OTHER INFORMATION: / Ceres Seq. ID 1600935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2390:

Met Gly Ser Ser Cys Ser Arg Ser His Ser Phe Asp Glu Ala Glu Ala  
1 5 10 15  
Ala Glu Asn Ala Lys Ser Ala Asp Ile Asp Arg Arg Phe Cys Lys Xaa  
20 25 30  
Gln Lys Pro Asn Asn Thr Ser Thr Ser Ser Tyr Phe Ser Val Leu Glu  
35 40 45  
Asn Arg Gly Ser  
50

(2) INFORMATION FOR SEQ ID NO:2391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 388 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

03539900 101300

(B) LOCATION: 1..388

(D) OTHER INFORMATION: / Ceres Seq. ID 1600949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2391:

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| ccattaaccc | cggccccggc  | aactcccca  | gtcgagcaac | aggccaaacc  | cccagcggcc | 60  |
| ggaagcgcgt | accgctagca  | cctccgacg  | agtcggcgcc | atggaagacg  | tcatcaccga | 120 |
| cgtgcgcgcg | ccttcccgcg  | tttcccctga | cgacctcgac | aacttcggcg  | ctccgccagc | 180 |
| gcagcccacc | cccattcttcg | tcgtttcccc | gaaccctagc | ccaccggccc  | cgcgcctcct | 240 |
| cgctgtattc | atctccccc   | cctccctcgc | gtcctcggc  | tccccggcgc  | cgctcctcgc | 300 |
| ctccctgctc | ctcccgacc   | tgcccctact | cccgacgcg  | cccattgcgcg | tgtactccac | 360 |
| ccctccggcg | cgtcctcgc   | cgcggcgc   |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1600950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2392:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Asn | Pro | Gly | Pro | Gly | Asn | Ser | Pro | Ser | Arg | Ala | Thr | Gly | Gln | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Ser | Arg | Arg | Lys | Pro | Leu | Pro | Leu | Ala | Pro | Pro | Xaa | Glu | Ser | Ala |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Pro | Trp | Lys | Thr | Ser | Ser | Pro | Thr | Cys | Arg | Arg | Leu | Pro | Ala | Phe | Pro |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Leu | Thr | Thr | Ser | Thr | Thr | Ser | Pro | Leu | Arg | Gln | Arg | Ser | Pro | Pro | Pro |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Ser | Ser | Ser | Phe | Pro | Arg | Thr | Leu | Ala | His | Arg | Pro | Arg | Ala | Ser | Ser |
|     |     |     |     |     |     |     |     | 70  |     |     |     |     |     | 80  |     |
| Ser | Tyr | Ser | Ser | Pro | Pro | Pro | Pro | Ser | Arg | Ser | Ser | Pro | Pro | Arg | Arg |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 95  |     |
| Arg | Ser | Ser | Pro | Pro | Cys | Ser | Ser | Arg | Thr | Cys | Pro | Tyr | Ser | Arg | Thr |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 110 |     |
| Arg | Pro | Cys | Ala | Cys | Thr | Pro | Pro | Leu | Arg | Arg | Ala | Pro | Arg | Arg | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 125 |     |

(2) INFORMATION FOR SEQ ID NO:2393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1600951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2393:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asp | Val | Ile | Thr | Asp | Val | Pro | Pro | Pro | Ser | Arg | Phe | Ser | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asp | Asp | Leu | Asp | Asn | Phe | Ala | Ala | Pro | Pro | Ala | Gln | Pro | Thr | Pro | Ile |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Phe | Val | Val | Ser | Pro | Asn | Pro | Ser | Pro | Pro | Ala | Pro | Arg | Leu | Leu | Val |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 45  |     |
| Val | Phe | Ile | Ser | Pro | Thr | Ser | Leu | Ala | Leu | Leu | Ala | Ser | Pro | Pro | Pro |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 60  |     |
| Leu | Leu | Ala | Ser | Leu | Leu | Leu | Pro | Asp | Leu | Pro | Leu | Leu | Pro | His | Ala |

| 65                                                              | 70 | 75 | 80 |
|-----------------------------------------------------------------|----|----|----|
| Pro Met Arg Val Tyr Ser Thr Pro Pro Ala Arg Ser Ser Pro Arg Arg |    |    |    |
|                                                                 | 85 | 90 | 95 |

(2) INFORMATION FOR SEQ ID NO:2394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..511
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2394:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| acacgaataa agcatcgatc acaataagat ggcggtgtata gacaatgcaa tgagagcctt  | 60  |
| gttcctttta ggcgtcttct gtgtcggtgca tgggtgagaag gcaaagtcaa aggacaacga | 120 |
| tgcaaaagcg tccgggcccc gtgggtcctt cgacatcacc aagttgggcg cctccggcaa   | 180 |
| tggcaagacg gatagcacga aggcgtgtgca ggaggcggtg gcacagcgt gcggcggcac   | 240 |
| cgggaagcag acgatacctca tccccaaagg cgacttcctc gtcggaccac tcaacttcac  | 300 |
| aggcccatgc aagggcgacg tgaccatcca ggtgaatggc aatctgctgg cgaccacgga   | 360 |
| cctaagccag tacaaggatc atggttaattg gatcgagatt ctacgcgtgg acttcgtgaa  | 420 |
| caacggggag gtgtccggga tcacgctgct caactccaag ttcttcacac tgaacatgta   | 480 |
| caagtgaag gacatgctga tcaaggacgt c                                   |     |

(2) INFORMATION FOR SEQ ID NO:2395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1600953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2395:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ala Cys Ile Asp Asn Ala Met Arg Ala Leu Phe Leu Leu Ala Leu |  |
| 1 5 10 15                                                       |  |
| Phe Cys Val Val His Gly Glu Lys Ala Lys Ser Lys Asp Asn Asp Ala |  |
| 20 25 30                                                        |  |
| Lys Ala Ser Gly Pro Gly Gly Ser Phe Asp Ile Thr Lys Leu Gly Ala |  |
| 35 40 45                                                        |  |
| Ser Gly Asn Gly Lys Thr Asp Ser Thr Lys Ala Val Gln Glu Ala Trp |  |
| 50 55 60                                                        |  |
| Ala Ser Ala Cys Gly Gly Thr Gly Lys Gln Thr Ile Leu Ile Pro Lys |  |
| 65 70 75 80                                                     |  |
| Gly Asp Phe Leu Val Gly Pro Leu Asn Phe Thr Gly Pro Cys Lys Gly |  |
| 85 90 95                                                        |  |
| Asp Val Thr Ile Gln Val Asn Gly Asn Leu Leu Ala Thr Thr Asp Leu |  |
| 100 105 110                                                     |  |
| Ser Gln Tyr Lys Asp His Gly Asn Trp Ile Glu Ile Leu Arg Val Asp |  |
| 115 120 125                                                     |  |
| Phe Val Asn Asn Gly Glu Val Ser Gly Ile Thr Leu Leu Asn Ser Lys |  |
| 130 135 140                                                     |  |
| Phe Phe His Met Asn Met Tyr Lys Cys Lys Asp Met Leu Ile Lys Asp |  |
| 145 150 155 160                                                 |  |
| Val                                                             |  |

(2) INFORMATION FOR SEQ ID NO:2396:





(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2398:

(2) INFORMATION FOR SEQ ID NO:2399:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1600957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2399:

(2) INFORMATION FOR SEQ ID NO:2400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

| Met | Phe | Ser | Ala | Pro | Gly | Asn | Asn | Ser | Met | Ala | Leu | Val | Ala | Pro | Arg |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Gly | Met | Glu | Leu | Ala | Asn | Ile | Gln | His | His | Pro | Asn | Gln | Ala | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Pro | Gly | Gly | Lys | Gln | Arg | Thr | Ser | Ser | Leu | Glu | Ala | Pro | Ile | Met |

| Table 1. Demographic characteristics of the study population |              |
|--------------------------------------------------------------|--------------|
| <b>Age (years)</b>                                           |              |
| 18-24                                                        | 100 (10.0)   |
| 25-34                                                        | 150 (15.0)   |
| 35-44                                                        | 200 (20.0)   |
| 45-54                                                        | 250 (25.0)   |
| 55-64                                                        | 300 (30.0)   |
| 65-74                                                        | 350 (35.0)   |
| 75-84                                                        | 400 (40.0)   |
| 85-94                                                        | 450 (45.0)   |
| 95-104                                                       | 500 (50.0)   |
| 105-114                                                      | 550 (55.0)   |
| 115-124                                                      | 600 (60.0)   |
| 125-134                                                      | 650 (65.0)   |
| 135-144                                                      | 700 (70.0)   |
| 145-154                                                      | 750 (75.0)   |
| 155-164                                                      | 800 (80.0)   |
| 165-174                                                      | 850 (85.0)   |
| 175-184                                                      | 900 (90.0)   |
| 185-194                                                      | 950 (95.0)   |
| 195-204                                                      | 1000 (100.0) |
| 205-214                                                      | 1050 (105.0) |
| 215-224                                                      | 1100 (110.0) |
| 225-234                                                      | 1150 (115.0) |
| 235-244                                                      | 1200 (120.0) |
| 245-254                                                      | 1250 (125.0) |
| 255-264                                                      | 1300 (130.0) |
| 265-274                                                      | 1350 (135.0) |
| 275-284                                                      | 1400 (140.0) |
| 285-294                                                      | 1450 (145.0) |
| 295-304                                                      | 1500 (150.0) |
| 305-314                                                      | 1550 (155.0) |
| 315-324                                                      | 1600 (160.0) |
| 325-334                                                      | 1650 (165.0) |
| 335-344                                                      | 1700 (170.0) |
| 345-354                                                      | 1750 (175.0) |
| 355-364                                                      | 1800 (180.0) |
| 365-374                                                      | 1850 (185.0) |
| 375-384                                                      | 1900 (190.0) |
| 385-394                                                      | 1950 (195.0) |
| 395-404                                                      | 2000 (200.0) |
| 405-414                                                      | 2050 (205.0) |
| 415-424                                                      | 2100 (210.0) |
| 425-434                                                      | 2150 (215.0) |
| 435-444                                                      | 2200 (220.0) |
| 445-454                                                      | 2250 (225.0) |
| 455-464                                                      | 2300 (230.0) |
| 465-474                                                      | 2350 (235.0) |
| 475-484                                                      | 2400 (240.0) |
| 485-494                                                      | 2450 (245.0) |
| 495-504                                                      | 2500 (250.0) |
| 505-514                                                      | 2550 (255.0) |
| 515-524                                                      | 2600 (260.0) |
| 525-534                                                      | 2650 (265.0) |
| 535-544                                                      | 2700 (270.0) |
| 545-554                                                      | 2750 (275.0) |
| 555-564                                                      | 2800 (280.0) |
| 565-574                                                      | 2850 (285.0) |
| 575-584                                                      | 2900 (290.0) |
| 585-594                                                      | 2950 (295.0) |
| 595-604                                                      | 3000 (300.0) |
| 605-614                                                      | 3050 (305.0) |
| 615-624                                                      | 3100 (310.0) |
| 625-634                                                      | 3150 (315.0) |
| 635-644                                                      | 3200 (320.0) |
| 645-654                                                      | 3250 (325.0) |
| 655-664                                                      | 3300 (330.0) |
| 665-674                                                      | 3350 (335.0) |
| 675-684                                                      | 3400 (340.0) |
| 685-694                                                      | 3450 (345.0) |
| 695-704                                                      | 3500 (350.0) |
| 705-714                                                      | 3550 (355.0) |
| 715-724                                                      | 3600 (360.0) |
| 725-734                                                      | 3650 (365.0) |
| 735-744                                                      | 3700 (370.0) |
| 745-754                                                      | 3750 (375.0) |
| 755-764                                                      | 3800 (380.0) |
| 765-774                                                      | 3850 (385.0) |
| 775-784                                                      | 3900 (390.0) |
| 785-794                                                      | 3950 (395.0) |
| 795-804                                                      | 4000 (400.0) |
| 805-814                                                      | 4050 (405.0) |
| 815-824                                                      | 4100 (410.0) |
| 825-834                                                      | 4150 (415.0) |
| 835-844                                                      | 4200 (420.0) |
| 845-854                                                      | 4250 (425.0) |
| 855-864                                                      | 4300 (430.0) |
| 865-874                                                      | 4350 (435.0) |
| 875-884                                                      | 4400 (440.0) |
| 885-894                                                      | 4450 (445.0) |
| 895-904                                                      | 4500 (450.0) |
| 905-914                                                      | 4550 (455.0) |
| 915-924                                                      | 4600 (460.0) |
| 925-934                                                      | 4650 (465.0) |
| 935-944                                                      | 4700 (470.0) |
| 945-954                                                      | 4750 (475.0) |
| 955-964                                                      | 4800 (480.0) |
| 965-974                                                      | 4850 (485.0) |
| 975-984                                                      | 4900 (490.0) |
| 985-994                                                      | 4950 (495.0) |
| 995-1004                                                     | 5000 (500.0) |
| 1005-1014                                                    | 5050 (505.0) |
| 1015-1024                                                    | 5100 (510.0) |
| 1025-1034                                                    | 5150 (515.0) |
| 1035-1044                                                    | 5200 (520.0) |
| 1045-1054                                                    | 5250 (525.0) |
| 1055-1064                                                    | 5300 (530.0) |
| 1065-1074                                                    | 5350 (535.0) |
| 1075-1084                                                    | 5400 (540.0) |
| 1085-1094                                                    | 5450 (545.0) |
| 1095-1104                                                    | 5500 (550.0) |
| 1105-1114                                                    | 5550 (555.0) |
| 1115-1124                                                    | 5600 (560.0) |
| 1125-1134                                                    | 5650 (565.0) |
| 1135-1144                                                    | 57           |

(2) INFORMATION FOR SEQ ID NO:2403:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..83

(D) OTHER INFORMATION: / Ceres Seq. ID 1600965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2403:

(2) INFORMATION FOR SEQ ID NO:2404:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1600966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2404:

(2) INFORMATION FOR SEQ ID NO:2405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 513 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..513  
(D) OTHER INFORMATION: / Ceres Seq. ID 1600975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2405:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| ctgtggtttg  | gacagctagc | tacatggact | cctgctttca | cgttctcata | caggcactcc | 60  |
| tgcaactgtgc | tccttcgtct | cctcctcccc | tgcttgccac | caactgccaa | ggtttatggt | 120 |
| caggtggcac  | tgccagcaga | agtgatccgt | tgacttcagc | tatgggcaac | ctgtgctgct | 180 |
| gtgttcaagt  | cgaccagtcg | actgtggcca | tcagggagca | gtttggcaag | tttgacagcg | 240 |
| tgcttgagcc  | aggatgccac | tgcatgcctt | ggttcgccgg | caagcgtgta | gctgggcaac | 300 |
| tcacactcag  | gctgcagcaa | ctggatgtgc | gctgtgagac | aaaaacaaag | gacaatgttt | 360 |
| tcgtgaatgt  | ggtggcatct | attcagtacc | gcgctctggc | tgacaaagca | agtgacgctt | 420 |
| tctacaaact  | gagcaacaca | aggtcccaga | tcccaagcct | acgtctttga | cgtgatcaga | 480 |
| gcaagcggttc | ccaagctcca | tttggacgat | gct        |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..155  
(D) OTHER INFORMATION: / Ceres Seq. ID 1600976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2406:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Trp | Thr | Ala | Ser | Tyr | Met | Asp | Ser | Cys | Phe | His | Val | Leu | Ile |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gln | Ala | Leu | Leu | His | Cys | Ala | Pro | Ser | Ser | Pro | Pro | Pro | Leu | Pro | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Asn | Cys | Gln | Gly | Leu | Cys | Ser | Gly | Gly | Thr | Ala | Ser | Arg | Ser | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Leu | Thr | Ser | Ala | Met | Gly | Asn | Leu | Cys | Cys | Cys | Val | Gln | Val | Asp |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Ser | Thr | Val | Ala | Ile | Arg | Glu | Gln | Phe | Gly | Lys | Phe | Asp | Ser | Val |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Glu | Pro | Gly | Cys | His | Cys | Met | Pro | Trp | Phe | Ala | Gly | Lys | Arg | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Gly | Gln | Leu | Thr | Leu | Arg | Leu | Gln | Gln | Leu | Asp | Val | Arg | Cys | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Lys | Thr | Lys | Asp | Asn | Val | Phe | Val | Asn | Val | Val | Ala | Ser | Ile | Gln |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Tyr | Arg | Ala | Leu | Ala | Asp | Lys | Ala | Ser | Asp | Ala | Phe | Tyr | Lys | Leu | Ser |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Thr | Arg | Ser | Gln | Ile | Pro | Ser | Leu | Arg | Leu |     |     |     |     |     |
|     |     |     | 145 |     | 150 |     |     |     | 155 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..148  
(D) OTHER INFORMATION: / Ceres Seq. ID 1600977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2407:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Ser | Cys | Phe | His | Val | Leu | Ile | Gln | Ala | Leu | Leu | His | Cys | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Pro | Ser | Ser | Pro | Pro | Pro | Leu | Pro | Ala | Thr | Asn | Cys | Gln | Gly | Leu | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

Ser Gly Gly Thr Ala Ser Arg Ser Asp Pro Leu Thr Ser Ala Met Gly  
35 40 45  
Asn Leu Cys Cys Cys Val Gln Val Asp Gln Ser Thr Val Ala Ile Arg  
50 55 60  
Glu Gln Phe Gly Lys Phe Asp Ser Val Leu Glu Pro Gly Cys His Cys  
65 70 75 80  
Met Pro Trp Phe Ala Gly Lys Arg Val Ala Gly Gln Leu Thr Leu Arg  
85 90 95  
Leu Gln Gln Leu Asp Val Arg Cys Glu Thr Lys Thr Lys Asp Asn Val  
100 105 110  
Phe Val Asn Val Val Ala Ser Ile Gln Tyr Arg Ala Leu Ala Asp Lys  
115 120 125  
Ala Ser Asp Ala Phe Tyr Lys Leu Ser Asn Thr Arg Ser Gln Ile Pro  
130 135 140  
Ser Leu Arg Leu  
145

(2) INFORMATION FOR SEQ ID NO:2408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1600978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2408:

Met Gly Asn Leu Cys Cys Val Gln Val Asp Gln Ser Thr Val Ala  
1 5 10 15  
Ile Arg Glu Gln Phe Gly Lys Phe Asp Ser Val Leu Glu Pro Gly Cys  
20 25 30  
His Cys Met Pro Trp Phe Ala Gly Lys Arg Val Ala Gly Gln Leu Thr  
35 40 45  
Leu Arg Leu Gln Gln Leu Asp Val Arg Cys Glu Thr Lys Thr Lys Asp  
50 55 60  
Asn Val Phe Val Asn Val Val Ala Ser Ile Gln Tyr Arg Ala Leu Ala  
65 70 75 80  
Asp Lys Ala Ser Asp Ala Phe Tyr Lys Leu Ser Asn Thr Arg Ser Gln  
85 90 95  
Ile Pro Ser Leu Arg Leu  
100

(2) INFORMATION FOR SEQ ID NO:2409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..437

(D) OTHER INFORMATION: / Ceres Seq. ID 1600993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2409:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| gtgcctcttc ctaatccatc gcagagcgcc gccggcgggt agcgtactg ctagaggaga  | 60  |
| ggaagcggaa agggcggcgg cggcgcttgt ggtcagtcaa agatccaacc tccggactcg | 120 |
| cgatggggcg gcggatctc aacgatgctc tgcgcacgat ggtcaacgca gaccggcggg  | 180 |
| ggaacgcgtc ggcgcttctc cgacccatct cggcggtcat ggtctccttc ctcaacatca | 240 |
| tgaagtaccg agggatatc aaaaaatttg aggtcattga tgagaataga gttgggaaaa  | 300 |
| ttagagtgga gcttgatgga cgtcttaaag attgcaaagc tctcacctac aggcaagacc | 360 |
| tcaaagctaa ggagatagat ccgctctgoc atgggtgggc tgctatcata cgttatttat | 420 |

00669960 "101300



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2412:

(2) INFORMATION FOR SEQ ID NO:2413:

(D) OTHER INFORMATION: / Ceres Seq. ID 1601004

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:1 |             |            |            |            |            |  |     |
|----------------------------------------|-------------|------------|------------|------------|------------|--|-----|
| aacacrraac                             | cagcacacag  | ctctcgcctt | ctctctccca | tcggcacacc | cgagctcgct |  | 60  |
| cctctcttcc                             | acgtcgaggt  | ccgagtcctg | ctttgatggc | gaccgacgtg | gctgagactc |  | 120 |
| ccgcgccgtt                             | ggtggatgcg  | gccccagagg | cgcccgccga | cgcccggcg  | gcgcctgctg |  | 180 |
| ccgacgcgaa                             | gcgggccaaag | gccaagaagg | ccaccgcgcc | gaagaagcgc | gccagcccga |  | 240 |
| cccaccgcc                              | gtacgccgag  | atggtctcgg | aggcgatcac | gtcgctcaag | gagaggacgg |  | 300 |
| ggtccagcag                             | ctatgcgatt  | gccaaagttc | gtggaggaca | atcacaaaga | caagctcccg |  | 360 |
| cccaacttcc                             | gcaagcttct  | gaacgttcag | ctcaagaagc | tcgtcgccgg | cggcaagctg |  | 420 |
| accaagtgga                             | wgaactcgta  | caagctgtcg | t          |            |            |  |     |

(2) INFORMATION FOR SEQ ID NO:2414:

(B) LOCATION: 1..149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2414:

| (X17) SEQUENCE DESCRIPTION: SEQ ID NO: 1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His                                      | Xaa | Thr | Ser | Thr | Gln | Leu | Ser | Pro | Ser | Leu | Ser | His | Arg | His | Thr |
| 1                                        |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg                                      | Ala | Arg | Ser | Leu | Leu | Pro | Arg | Arg | Gly | Pro | Ser | Pro | Ala | Leu | Met |
|                                          |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala                                      | Thr | Asp | Val | Ala | Glu | Thr | Pro | Ala | Pro | Leu | Val | Asp | Ala | Ala | Pro |
|                                          |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Glu                                      | Ala | Pro | Ala | Asp | Ala | Pro | Ala | Ala | Pro | Ala | Ala | Asp | Ala | Lys | Pro |
|                                          | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ala                                      | Lys | Ala | Lys | Lys | Ala | Thr | Ala | Pro | Lys | Lys | Arg | Ala | Ser | Pro | Thr |
| 65                                       |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| His                                      | Pro | Pro | Tyr | Ala | Glu | Met | Val | Ser | Glu | Ala | Ile | Thr | Ser | Leu | Lys |
|                                          |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Glu                                      | Arg | Thr | Gly | Ser | Ser | Ser | Tyr | Ala | Ile | Ala | Lys | Val | Arg | Gly | Gly |
|                                          |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Gln                                      | Ala | Gln | Gly | Gln | Ala | Pro | Ala | Gln | Leu | Pro | Gln | Ala | Ser | Glu | Arg |

| Geographical location     |                                  |
|---------------------------|----------------------------------|
| Country                   | Spain                            |
| Region                    | Madrid                           |
| City                      | Madrid                           |
| Neighborhood              | Madrid                           |
| Address                   | Madrid                           |
| Postal code               | 28002                            |
| Phone number              | 91 414 11 11                     |
| E-mail address            | info@madrid.es                   |
| Website                   | www.madrid.es                    |
| Map reference             | Madrid                           |
| Coordinates               | 40.4168, -3.7038                 |
| Area                      | 603 km <sup>2</sup>              |
| Population                | 3,265,000                        |
| Language                  | Spanish                          |
| Currency                  | Euro (€)                         |
| Time zone                 | CET (UTC+1)                      |
| Climate                   | Temperate                        |
| Best time to visit        | Spring and Autumn                |
| Transportation            | Public transport                 |
| Attractions               | Historical sites, Museums, Parks |
| Food and drink            | Spanish cuisine, Tapas           |
| Shopping                  | Department stores, Boutiques     |
| Accommodation             | Hotels, Apartments               |
| Healthcare                | Hospitals, Clinics               |
| Education                 | Universities, Schools            |
| Religion                  | Catholicism                      |
| Government                | Autonomous community             |
| Legislation               | Spanish law                      |
| Customs                   | Travel regulations               |
| Security                  | Police, Fire department          |
| Emergency services        | 112                              |
| Language services         | English, French, German          |
| Accessibility             | Wheelchair access                |
| Environmental             | Parks, Green spaces              |
| Culture                   | Theater, Music, Festivals        |
| History                   | Historical landmarks             |
| Geography                 | Topography, Climate              |
| Demographics              | Population statistics            |
| Economy                   | Major industries                 |
| Infrastructure            | Transportation network           |
| Healthcare system         | Public healthcare                |
| Education system          | Public education                 |
| Religious institutions    | Cathedrals, Churches             |
| Government offices        | Mayor's office                   |
| Legislative bodies        | Regional assembly                |
| Customs authorities       | Border control                   |
| Security forces           | Police stations                  |
| Emergency services        | Fire stations                    |
| Language services         | Language schools                 |
| Accessibility services    | Accessibility programs           |
| Environmental agencies    | Environmental departments        |
| Cultural institutions     | Museums, Galleries               |
| Historical sites          | Historical landmarks             |
| Geographical features     | Landmarks, Parks                 |
| Demographic data          | Population statistics            |
| Economic indicators       | GDP, Unemployment                |
| Infrastructure projects   | Transportation plans             |
| Healthcare facilities     | Hospitals, Clinics               |
| Education facilities      | Schools, Universities            |
| Religious facilities      | Churches, Mosques                |
| Government facilities     | Offices, Courts                  |
| Legislative facilities    | Assembly, Council                |
| Customs facilities        | Border control                   |
| Security facilities       | Police, Fire                     |
| Emergency facilities      | First aid, Ambulance             |
| Language facilities       | Language courses                 |
| Accessibility facilities  | Accessibility programs           |
| Environmental facilities  | Parks, Green spaces              |
| Cultural facilities       | Theater, Music                   |
| Historical facilities     | Historical sites                 |
| Geographical facilities   | Landmarks, Parks                 |
| Demographic facilities    | Population statistics            |
| Economic facilities       | GDP, Unemployment                |
| Infrastructure facilities | Transportation plans             |
| Healthcare facilities     | Hospitals, Clinics               |
| Education facilities      | Schools, Universities            |
| Religious facilities      | Churches, Mosques                |
| Government facilities     | Offices, Courts                  |
| Legislative facilities    | Assembly, Council                |
| Customs facilities        | Border control                   |
| Security facilities       | Police, Fire                     |
| Emergency facilities      | First aid, Ambulance             |
| Language facilities       | Language courses                 |
| Accessibility facilities  | Accessibility programs           |
| Environmental facilities  | Parks, Green spaces              |
| Cultural facilities       | Theater, Music                   |
| Historical facilities     | Historical sites                 |
| Geographical facilities   | Landmarks, Parks                 |
| Demographic facilities    | Population statistics            |
| Economic facilities       | GDP, Unemployment                |
| Infrastructure facilities | Transportation plans             |
| Healthcare facilities     | Hospitals, Clinics               |
| Education facilities      | Schools, Universities            |
| Religious facilities      | Churches, Mosques                |
| Government facilities     | Offices, Courts                  |
| Legislative facilities    | Assembly, Council                |
| Customs facilities        | Border control                   |
| Security facilities       | Police, Fire                     |
| Emergency facilities      | First aid, Ambulance             |
| Language facilities       | Language courses                 |
| Accessibility facilities  | Accessibility programs           |
| Environmental facilities  | Parks, Green spaces              |
| Cultural facilities       | Theater, Music                   |
| Historical facilities     | Historical sites                 |
| Geographical facilities   | Landmarks, Parks                 |
| Demographic facilities    | Population statistics            |
| Economic facilities       | GDP, Unemployment                |
| Infrastructure facilities | Transportation plans             |
| Healthcare facilities     | Hospitals, Clinics               |
| Education facilities      | Schools, Universities            |
| Religious facilities      | Churches, Mosques                |
| Government facilities     | Offices, Courts                  |
| Legislative facilities    | Assembly, Council                |
| Customs facilities        | Border control                   |
| Security facilities       | Police, Fire                     |
| Emergency facilities      | First aid, Ambulance             |
| Language facilities       | Language courses                 |
| Accessibility facilities  | Accessibility programs           |
| Environmental facilities  | Parks, Green spaces              |
| Cultural facilities       | Theater, Music                   |
| Historical facilities     | Historical sites                 |
| Geographical facilities   | Landmarks, Parks                 |
| Demographic facilities    | Population statistics            |
| Economic facilities       | GDP, Unemployment                |
| Infrastructure facilities | Transportation plans             |
| Healthcare facilities     | Hospitals, Clinics               |
| Education facilities      | Schools, Universities            |
| Religious facilities      | Churches, Mosques                |
| Government facilities     | Offices, Courts                  |
| Legislative facilities    | Assembly, Council                |
| Customs facilities        | Border control                   |
| Security facilities       | Police, Fire                     |
| Emergency facilities      | First aid, Ambulance             |
| Language facilities       | Language courses                 |
| Accessibility facilities  | Accessibility programs           |
| Environmental facilities  | Parks, Green spaces              |
| Cultural facilities       | Theater, Music                   |
| Historical facilities     | Historical sites                 |
| Geographical facilities   | Landmarks, Parks                 |
| Demographic facilities    | Population statistics            |
| Economic facilities       | GDP, Unemployment                |
| Infrastructure facilities | Transportation plans             |
| Healthcare facilities     | Hospitals, Clinics               |
| Education facilities      | Schools, Universities            |
| Religious facilities      | Churches, Mosques                |
| Government facilities     | Offices, Courts                  |
| Legislative facilities    | Assembly, Council                |
| Customs facilities        | Border control                   |
| Security facilities       | Police, Fire                     |
| Emergency facilities      | First aid, Ambulance             |
| Language facilities       | Language courses                 |
| Accessibility facilities  | Accessibility programs           |
| Environmental facilities  | Parks, Green spaces              |
| Cultural facilities       | Theater, Music                   |
| Historical facilities     | Historical sites                 |
| Geographical facilities   | Landmarks, Parks                 |
| Demographic facilities    | Population statistics            |
| Economic facilities       | GDP, Unemployment                |
| Infrastructure facilities | Transportation plans             |
| Healthcare facilities     | Hospitals, Clinics               |
| Education facilities      | Schools, Universities            |
| Religious facilities      | Churches, Mosques                |
| Government facilities     | Offices, Courts                  |
| Legislative facilities    | Assembly, Council                |

115 120 125  
Ser Ala Gln Glu Ala Arg Arg Arg Arg Gln Ala Asp Gln Gly Xaa Glu  
130 135 140  
Leu Val Gln Ala Val  
145

(2) INFORMATION FOR SEQ ID NO:2415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2415:

Met Ala Thr Asp Val Ala Glu Thr Pro Ala Pro Leu Val Asp Ala Ala  
1 5 10 15  
Pro Glu Ala Pro Ala Asp Ala Pro Ala Ala Pro Ala Ala Asp Ala Lys  
20 25 30  
Pro Ala Lys Ala Lys Lys Ala Thr Ala Pro Lys Lys Arg Ala Ser Pro  
35 40 45  
Thr His Pro Pro Tyr Ala Glu Met Val Ser Glu Ala Ile Thr Ser Leu  
50 55 60  
Lys Glu Arg Thr Gly Ser Ser Ser Tyr Ala Ile Ala Lys Val Arg Gly  
65 70 75 80  
Gly Gln Ala Gln Gly Gln Ala Pro Ala Gln Leu Pro Gln Ala Ser Glu  
85 90 95  
Arg Ser Ala Gln Glu Ala Arg Arg Arg Gln Ala Asp Gln Gly Xaa  
100 105 110  
Glu Leu Val Gln Ala Val  
115

(2) INFORMATION FOR SEQ ID NO:2416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2416:

Met Arg Pro Gln Arg Arg Pro Pro Thr Pro Arg Arg Arg Leu Leu Pro  
1 5 10 15  
Thr Arg Ser Arg Pro Arg Pro Arg Arg Pro Pro Arg Arg Arg Ser Ala  
20 25 30  
Pro Ala Arg Pro Thr Arg Arg Thr Pro Arg Trp Ser Arg Arg Arg Ser  
35 40 45  
Arg Arg Ser Arg Arg Gly Arg Gly Pro Ala Ala Met Arg Leu Pro Lys  
50 55 60  
Phe Val Glu Asp Lys His Lys Asp Lys Leu Pro Pro Asn Phe Arg Lys  
65 70 75 80  
Leu Leu Asn Val Gln Leu Lys Lys Leu Val Ala Gly Gly Lys Leu Thr  
85 90 95  
Lys Val Xaa Asn Ser Tyr Lys Leu Ser  
100 105

(2) INFORMATION FOR SEQ ID NO:2417:

(i) SEQUENCE CHARACTERISTICS:

0066980 10300



- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..460
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601012
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2417:

|            |            |            |             |            |             |     |
|------------|------------|------------|-------------|------------|-------------|-----|
| cggaacccca | ttccccgccg | cctcgcgccc | ccgctcgctt  | cacttctcta | ggtgcgccacc | 60  |
| gatcagaagg | tgcttgcttc | ctcctcgctg | gcgaaaagat  | ggcggtgccg | ctgctgacga  | 120 |
| agaagatcgt | gaagaagcgg | gtcaagcagt | tcaagaggcc  | ccacctcgac | cgctacaagt  | 180 |
| gccttaagcc | aagctggcgc | aggccaaagg | gtattgattc  | ccgtgtcagg | aggaagttca  | 240 |
| agggatgcac | cttgatgcc  | aacattgggt | atggttctga  | caagtcgacc | aggcactacc  | 300 |
| tccccagcaa | gttcaagaag | tttgtggtcc | acaacgtttc  | tgagctggag | ttgctcatga  | 360 |
| tgcacaacag | gacctactgc | gctgaaattg | ctcacaacgt  | gtccaccaag | aagcgcaagg  | 420 |
| agatcgtgga | gcgtgctgca | cagctcgaca | ttgtgggtcac |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2418:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 152 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..152
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601013
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2418:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Pro | His | Ser | Pro | Pro | Arg | Ala | Pro | Ala | Arg | Phe | Thr | Ser | Leu |     |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gly | Ala | His | Arg | Ser | Glu | Gly | Ala | Cys | Leu | Leu | Leu | Val | Gly | Glu | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Ala | Val | Pro | Leu | Leu | Thr | Lys | Lys | Ile | Val | Lys | Lys | Arg | Val | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Phe | Lys | Arg | Pro | His | Leu | Asp | Arg | Tyr | Lys | Cys | Leu | Lys | Pro | Ser |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Trp | Arg | Arg | Pro | Lys | Gly | Ile | Asp | Ser | Arg | Val | Arg | Arg | Lys | Phe | Lys |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Cys | Thr | Leu | Met | Pro | Asn | Ile | Gly | Tyr | Gly | Ser | Asp | Lys | Ser | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Arg | His | Tyr | Leu | Pro | Ser | Lys | Phe | Lys | Lys | Phe | Val | Val | His | Asn | Val |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ser | Glu | Leu | Glu | Leu | Leu | Met | Met | His | Asn | Arg | Thr | Tyr | Cys | Ala | Glu |
|     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |     |
| Ile | Ala | His | Asn | Val | Ser | Thr | Lys | Lys | Arg | Lys | Glu | Ile | Val | Glu | Arg |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Ala | Ala | Gln | Leu | Asp | Ile | Val | Val |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2419:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 120 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..120
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601014

DOCKET # 08668360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2419:

Met Ala Val Pro Leu Leu Thr Lys Lys Ile Val Lys Lys Arg Val Lys  
1 5 10 15  
Gln Phe Lys Arg Pro His Leu Asp Arg Tyr Lys Cys Leu Lys Pro Ser  
20 25 30  
Trp Arg Arg Pro Lys Gly Ile Asp Ser Arg Val Arg Arg Lys Phe Lys  
35 40 45  
Gly Cys Thr Leu Met Pro Asn Ile Gly Tyr Gly Ser Asp Lys Ser Thr  
50 55 60  
Arg His Tyr Leu Pro Ser Lys Phe Lys Lys Phe Val Val His Asn Val  
65 70 75 80  
Ser Glu Leu Glu Leu Leu Met Met His Asn Arg Thr Tyr Cys Ala Glu  
85 90 95  
Ile Ala His Asn Val Ser Thr Lys Lys Arg Lys Glu Ile Val Glu Arg  
100 105 110  
Ala Ala Gln Leu Asp Ile Val Val  
115 120

(2) INFORMATION FOR SEQ ID NO:2420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..496
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2420:

aacagtgtga agcccgctaa agagagtggg tgcaaaaatc tctactccga cccccaccta 60  
aggcaccgac tcgcccgggga cagagagaga ccgacgcgcc ggcagatccc aagctcaccg 120  
gagagggggga agagggcgac cgaaggcggc gatgggtttc atcatggact tcgaggagaa 180  
tatgatcctc cgtctgatgg aggacccgga caagcgcgac caggttcggc gggagcatgt 240  
ctacaagatg aaggagcggg gcgagcgac taaggcggcg tggagcctcc ctctgcgccc 300  
ctacggcttc tggaccttcg accgcttcaa ctcgcagctc tcctgggagc cccagatcag 360  
ccaggccgcc ggccgtcggg acccctacga tgacctcacc gcccgccact ctggctcgcc 420  
gccgtcttcc tgaacaccgg ttccgatctt tgcccagaag gtctacttgg gcatcaataa 480  
gaaactcttt ccctc

(2) INFORMATION FOR SEQ ID NO:2421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2421:

Asn Ser Val Lys Pro Ala Lys Glu Ser Gly Cys Lys Asn Leu Tyr Ser  
1 5 10 15  
Asp Pro His Leu Arg His Arg Leu Ala Gly Asp Arg Glu Arg Pro Thr  
20 25 30  
Arg Arg Gln Ile Pro Ser Ser Pro Glu Arg Gly Lys Arg Ala Thr Glu  
35 40 45  
Gly Gly Asp Gly Phe His His Gly Leu Arg Gly Glu Tyr Asp Pro Pro  
50 55 60  
Ser Asp Gly Gly Pro Gly Gln Ala Arg Pro Gly Ser Ala Gly Ala Cys  
65 70 75 80  
Leu Gln Asp Glu Gly Ala Val Arg Ala His

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(2) INFORMATION FOR SEQ ID NO:2423:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..89
 (D) OTHER INFORMATION: / Ceres Seq. ID 1601018
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2423:
Met Asp Phe Ala Glu Asn Met Ile Leu Arg Leu Met Glu Asp Pro Asp
1 5 10 15
Lys Arg Asp Gln Val Arg Arg Glu His Val Tyr Lys Met Lys Glu Arg
 20 25 30
Cys Glu Arg Thr Lys Ala Ala Trp Ser Leu Pro Leu Arg Pro Tyr Gly
 35 40 45
Phe Trp Thr Phe Asp Arg Phe Asn Ser Gln Leu Ser Trp Asp Pro Gln
 50 55 60
Ile Ser Gln Ala Ala Gly Arg Arg Asp Pro Tyr Asp Asp Leu Ile Ala
65 70 75 80
Arg His Ser Gly Ser Pro Pro Ser Ser
 85

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(2) INFORMATION FOR SEQ ID NO:2424:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 436 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..436
 (D) OTHER INFORMATION: / Ceres Seq. ID 1601029
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2424:
```

(2) INFORMATION FOR SEQ ID NO:2425:

(A) LENGTH: 76 amino acids

(C) STRANDEDNESS:

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1601030

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Phe | Ser | Ser | Leu | Thr | Leu | Thr | Pro | Ser | Leu | Ala | Pro | Pro | Arg | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Arg | Tyr | Ala | Pro | His | Leu | Ala | Ser | Phe | Arg | Val | Ala | Lys | Met | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Arg | Thr | Lys | Lys | Ala | Gly | Ile | Val | Gly | Lys | Tyr | Gly | Thr | Arg | Tyr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Ala | Ser | Leu | Arg | Lys | Gln | Ile | Lys | Lys | Met | Glu | Val | Ser | Gln | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Ser | Thr | Phe | Ala | Ser | Ser | Val | Gly | Ser | Leu | Leu |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..60

(D) OTHER INFORMATION: / Ceres Seq. ID 1601031

| (X1) SEQUENCE DESCRIPTION |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met                       | Glu | Pro | Gly | Met | Val | Leu | Ala | Cys | Val | Ser | Lys | Ser | Arg | Arg | Trp |
| 1                         |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg                       | Tyr | Leu | Ser | Phe | Gln | Val | Leu | Leu | Arg | Val | Leu | Trp | Glu | Val | Cys |
|                           |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys                       | Glu | Glu | Glu | Ser | Ser | Trp | Asn | Leu | Gly | Val | Gln | Gly | Leu | Trp | Glu |
|                           |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly                       | Glu | Gly | Trp | Trp | Cys | Leu | His | His | Glu | His | Cys |     |     |     |     |
|                           | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..56

(D) OTHER INFORMATION: / Ceres Seq. ID 1601032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2427:  
Met Val Leu Ala Cys Val Ser Lys Ser Arg Arg Trp Arg Tyr Leu Ser  
1 5 10 15  
Phe Gln Val Leu Leu Arg Val Leu Trp Glu Val Cys Cys Glu Glu Glu  
20 25 30  
Ser Ser Trp Asn Leu Gly Val Gln Gly Leu Trp Glu Gly Glu Gly Trp  
35 40 45  
Trp Cys Leu His His Glu His Cys  
50 55

(2) INFORMATION FOR SEQ ID NO:2428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..497
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2428:

|                                                                       |     |
|-----------------------------------------------------------------------|-----|
| aatttccggtt tccatacttc cggcgcgggcg gagatcgaat cgagcgccccg ccacggcgcat | 60  |
| ggcgactaga gtccctgccgc cggctctgct ctctttcata ctctctctgc tgctctcgct    | 120 |
| ctcagcccgc gacaccgtcg ccgcgggcga ggatttccca cgcgacgggc gggatgatcga    | 180 |
| cctcgacgac agcaatttcg aggcggcgct gggcgccatc gactttctct tcgtcgactt     | 240 |
| ctacgcccct tgggtcgggc actgcaagag acttgcgccc gagtttagatg aagctgcacc    | 300 |
| gggtgtgtgca gggttgagtg agcctattgt tgttgccaaa gtcaacgctg ataaatacag    | 360 |
| aaaactcgga tcaaaatatg gagtggatgg gttccctacc ctcatgctct ttatccatgg     | 420 |
| tgttccaatt gaatacatg gttcgaggaa agctgaccag cttgtccgca atctgaagaa      | 480 |
| gttcgtttcg ccagatg                                                    |     |

(2) INFORMATION FOR SEQ ID NO:2429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2429:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Ile Ser Val Ser Ile Leu Pro Ala Arg Arg Arg Ser Asn Arg Ala Pro | 15  |
| 1 5 10                                                          |     |
| Ala Thr Ala Met Ala Thr Arg Val Leu Pro Pro Ala Leu Leu Ser Phe | 30  |
| 20 25                                                           |     |
| Ile Leu Leu Leu Leu Ser Leu Ser Ala Arg Asp Thr Val Ala Ala     | 45  |
| 35 40                                                           |     |
| Gly Glu Asp Phe Pro Arg Asp Gly Arg Val Ile Asp Leu Asp Asp Ser | 60  |
| 50 55 60                                                        |     |
| Asn Phe Glu Ala Ala Leu Gly Ala Ile Asp Phe Leu Phe Val Asp Phe | 80  |
| 65 70 75 80                                                     |     |
| Tyr Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala Pro Glu Leu Asp | 95  |
| 85 90                                                           |     |
| Glu Ala Ala Pro Val Leu Ser Gly Leu Ser Glu Pro Ile Val Val Ala | 110 |
| 100 105 110                                                     |     |
| Lys Val Asn Ala Asp Lys Tyr Arg Lys Leu Gly Ser Lys Tyr Gly Val | 125 |
| 115 120 125                                                     |     |
| Asp Gly Phe Pro Thr Leu Met Leu Phe Ile His Gly Val Pro Ile Glu | 140 |
| 130 135 140                                                     |     |
| Tyr Thr Gly Ser Arg Lys Ala Asp Gln Leu Val Arg Asn Leu Lys Lys |     |

096999010300



(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1601052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2432:

Arg Ser Leu Ala Leu Leu Ser Pro Ser Pro Leu Leu Ser Gly Val  
1 5 10 15  
Leu Asn Ser Asn Gln Lys Ile Lys Thr Thr Gln Arg Phe Asp Ser Arg  
20 25 30  
Arg Val Lys Arg Asp Ala Ala Ala His Gly Ser Gly Gly Asp Leu Asn  
35 40 45  
Pro Ala Ala Glu Gly Ala Pro Pro Glu Ala Ala Ala Cys Gly Val Gly  
50 55 60  
Arg Leu Arg Gly Ala Val Arg Leu Gly Ala Ala Val Val Ala Asp  
65 70 75 80  
Pro Val Arg Ala Gly Ala Gly His Pro Ala Arg Leu Cys Gln Ser Arg  
85 90 95  
Leu Ala Val Arg Ser Ala Val Arg Pro Pro Arg Pro Ala Pro Arg Arg  
100 105 110  
Pro Pro Leu Arg Pro His Arg Pro Arg Arg Phe Ala Ala Arg Ala Pro  
115 120 125  
Gln

(2) INFORMATION FOR SEQ ID NO:2433:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1601053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2433:

Val Ser Ser Ser Thr Pro Leu Pro Glu Ser Ser Pro Leu Arg Gly Ile  
1 5 10 15  
Glu Phe Glu Pro Lys Asn Gln Asn Asn Ser Ala Ile Arg Phe Ala Ala  
20 25 30  
Ser Gln Ala Gly Cys Arg Arg Ala Arg Leu Arg Arg Arg Pro Gln Pro  
35 40 45  
Arg Arg Gly Arg Cys Pro Ser Gly Ser Cys Cys Val Arg Arg Arg Ser  
50 55 60  
Pro Ala Gly Cys Ser Ser Ala Gly Arg Cys Ser Cys Arg Cys  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2434:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1601054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2434:

Met Pro Pro Arg Thr Ala Pro Ala Ala Thr Ser Thr Pro Pro Arg Lys  
1 5 10 15  
Val Pro Leu Arg Lys Leu Leu Arg Ala Ala Ser Val Ala Cys Gly Val  
20 25 30

00669960-101400

(2) INFORMATION FOR SEQ ID NO:2435:

(A) LENGTH: 509 base pairs

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..509

(D) OTHER INFORMATION: / Ceres Seq. ID 1601061

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| gagcagagca | gcagtgacca | gtgagctgct | tgtccaagaa | tcgctcccac  | tcccggctgt | 60  |
| cgggagagcg | cagcccagct | agccgcctcc | gcttcttggg | ggtcgatggc  | cgcaaggggg | 120 |
| ttgagggagg | tgaggaggag | gagggcggcg | gaggtcgggc | ggcgtgctt   | gtctggcggg | 180 |
| agcgtgggc  | cgccggcgcc | ggcggcgaag | cggaaggagg | gaggggaaggc | ggtgaacctg | 240 |
| ttcacggccg | tcaaccaggc | gtccacatc  | gccctcgaca | ccgacccccg  | cgctacgtc  | 300 |
| ttcggagagg | acgtcgggtt | cggcggcgtc | ttccgctgca | cgacaggcct  | cgccgatcgg | 360 |
| ttcggaactg | gcagagtggt | caacacgccg | ctgtgtgagc | agggatttgc  | tgattttgcc | 420 |
| atcgccctag | cagcagatgg | caatcgagct | atcgcaaaa  | tccagtttgc  | ggactacatc | 480 |
| tttccaqcc  | ttgaatcaga | ttgtccaat  |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2436:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1601062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2436:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2437:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..404
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2437:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| gaaggatgtt caccgagaaa ccctagttcg aacgcgccgc catcaccgtc gtctctcgct | 60  |
| cgttcctcgc cgctctccgc tcgtgagtac tcccacggat cggagcgaga gtaggggcgt | 120 |
| gtcggcggtg aaagcgaccg cgtcagccat ggcggacgag gagcattcgg agaggagaga | 180 |
| ggaggcctcc gagcttgccc ccttcgaccc gaccaagaag aagaaaaaga agaaggttgt | 240 |
| catccaagaa ccttctgatg aagtggacaa gcttcgagag aagacagaaa cactggcagt | 300 |
| cgcagaaccc gctgaactta acttcactgg aatgaagaag aawaagaaga agccggtgga | 360 |
| tcttgattca actcttgatg agcttggaga tggggaggac actc                  |     |

(2) INFORMATION FOR SEQ ID NO:2438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2438:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asp | Val | His | Arg | Glu | Thr | Leu | Val | Arg | Thr | Arg | His | His | Arg |     |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |     |
| Arg | Leu | Ser | Leu | Val | Pro | Ser | Arg | Ser | Pro | Leu | Val | Ser | Thr | Pro | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Asp | Arg | Ser | Glu | Ser | Arg | Gly | Val | Ser | Ala | Val | Lys | Ala | Thr | Ala | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Ala | Met | Ala | Asp | Glu | Glu | His | Ser | Glu | Arg | Arg | Glu | Glu | Ala | Ser | Glu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ala | Pro | Phe | Asp | Pro | Thr | Lys | Lys | Lys | Lys | Lys | Lys | Lys | Val | Val |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Gln | Glu | Pro | Ser | Asp | Glu | Val | Asp | Lys | Leu | Ala | Glu | Lys | Thr | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Thr | Leu | Ala | Val | Ala | Glu | Pro | Ala | Glu | Leu | Asn | Phe | Thr | Gly | Met | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Xaa | Lys | Lys | Lys | Pro | Val | Asp | Leu | Asp | Ser | Thr | Leu | Asp | Glu | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Asp | Gly | Glu | Asp | Thr |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 130 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2439:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asp | Glu | Glu | His | Ser | Glu | Arg | Arg | Glu | Glu | Ala | Ser | Glu | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |

00559930-101300



(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1601080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2442:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 472 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..472

(D) OTHER INFORMATION: / Ceres Seq. ID 1601089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2443:

| (XI) SEQUENCE DESCRIPTION: SEQ ID NO:101 |            |            |            |            |             |     |
|------------------------------------------|------------|------------|------------|------------|-------------|-----|
| gagcaacaag                               | agagagagga | catagccgca | caaagggaa  | gagaccctcg | ccaacctcga  | 60  |
| agctagtcca                               | aactagtggg | aggttgagtg | cagggatcga | tcgaggaaga | cgagacaagc  | 120 |
| ttctttctct                               | gctgcgcgcg | cgcgcagctc | tagctcacca | cgagttacta | gccaatctga  | 180 |
| caccagaccgt                              | ccatggcgcg | gggcaaggtg | caacttcggc | gcgtcgagaa | cccgggtgcac | 240 |
| cggcagctga                               | cattctgcaa | ggcgcgcgcg | gggctgctca | agaaggcccg | ggagctctcc  | 300 |
| gtcctctgcg                               | acgccagcgt | cggcatcatc | gtcttctccg | cgcacggcaa | gctctacgac  | 360 |
| ctcgccacca                               | ccgggaccat | ggaggagctg | atcgagaggt | acaaggctgc | cagcgcggga  | 420 |
| gaagcgacga                               | ccgacggctg | cggcaggcac | aacaggatgg | accccaaaca | tg          |     |

(2) INFORMATION FOR SEQ ID NO:2444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1601090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2444:

| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala                                     | Thr | Arg | Glu | Arg | Gly | His | Ser | Arg | Thr | Lys | Gly | Arg | Arg | Pro | Ser |
| 1                                       |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro                                     | Thr | Ser | Lys | Leu | Val | Gln | Thr | Ser | Gly | Arg | Leu | Ser | Ala | Gly | Ile |
|                                         |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp                                     | Arg | Gly | Arg | Arg | Asp | Lys | Leu | Leu | Leu | Leu | Leu | Pro | Pro | Pro | Pro |
|                                         |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ala                                     | Leu | Ala | His | His | Glu | Leu | Leu | Ala | Asn | Leu | Thr | Pro | Thr | Val | His |

50 55 60  
Gly Ala Gly Gln Gly Ala Thr Ser Ala Arg Arg Glu Pro Gly Ala Pro  
65 70 75 80  
Ala Gly Asp Ile Leu Gln Ala Pro Arg Gly Ala Ala Gln Glu Gly Pro  
85 90 95  
Gly Ala Leu Arg Pro Leu Arg Arg Gln Arg Arg His His Arg Leu Leu  
100 105 110  
Arg Ala Arg Gln Ala Leu Arg Pro Arg His His Arg Asp His Gly Gly  
115 120 125  
Ala Asp Arg Glu Val Gln Gly Cys Gln Arg Arg Arg Ser Asp Asp Arg  
130 135 140  
Arg Leu Arg Gln Ala Gln Gln Asp Gly Pro Gln Thr  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2445:

Met Ala Arg Gly Lys Val Gln Leu Arg Arg Val Glu Asn Pro Val His  
1 5 10 15  
Arg Gln Val Thr Phe Cys Lys Arg Arg Ala Gly Leu Leu Lys Lys Ala  
20 25 30  
Arg Glu Leu Ser Val Leu Cys Asp Ala Ser Val Gly Ile Ile Val Phe  
35 40 45  
Ser Ala His Gly Lys Leu Tyr Asp Leu Ala Thr Thr Gly Thr Met Glu  
50 55 60  
Glu Leu Ile Glu Arg Tyr Lys Ala Ala Ser Ala Gly Glu Ala Thr Thr  
65 70 75 80  
Asp Gly Cys Gly Arg His Asn Arg Met Asp Pro Lys His  
85 90

(2) INFORMATION FOR SEQ ID NO:2446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..481
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2446:

aaaaaaactc gctctcactt tactctctatc cactgcgggc tggacgcgtg cgagagactt 60  
gacaaagcag cagcagggat ggccctctg aagctgtacg ggatgccgct gtccccaac 120  
gtggtgcgcg tggcaccggt tgctcaacga gaaggccctc gacttcgaga tcgtcccggt 180  
cgacctcacc accggcgccc acaagcagcc cgacttcctc accctcaacc ctttcggcca 240  
gatcccggt ctcgtcgacg gagacgaagt cctcttcgag tcccgcgcgga tcaaccggta 300  
catcgccagc aagtacgcgt cggagggcac ggacctgctc cccgcgacgg cgtcggcggc 360  
gaagctggag gtgttgccct gggaggtgga gtcgcaccac ttccaccga acgcgtcgcc 420  
gctggtgttc cagctgctcg tgaggccgct cctgggcggc gcccgacgc gccggtggtg 480  
g

(2) INFORMATION FOR SEQ ID NO:2447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids





Ser Glu Leu Ala Ser Arg Ala Leu Ser Ile Leu Phe Ser Ala Pro Arg  
1 5 10 15  
Gly Ser Pro Val Arg Pro Val Pro His Ser Tyr Pro Leu Leu Thr Leu  
20 25 30  
Ala Ala Ala Ala Ser Pro Ala Pro Arg Ala Lys Met Asn Val Glu Lys  
35 40 45  
Leu Lys Lys Met Ala Gly Ala Val Arg Thr Gly Gly Lys Gly Ser Met  
50 55 60  
Arg Arg Lys Lys Lys Ala Val His Lys Thr Thr Thr Thr Asp Asp Lys  
65 70 75 80  
Arg Leu Gln Ser Thr Leu Lys Arg Ile Gly Val Asn Thr Ile Pro Gly  
85 90 95  
Ile Glu Glu Val Asn Ile Phe Lys Asp Asp Val Val Ile Gln Phe Val  
100 105 110  
Asn Pro Lys Val Gln Ala Ser Ile Gly Ala Asn Thr Trp Val Val Ser  
115 120 125  
Gly Thr Pro Gln Thr Lys Lys Leu Gln Asp Leu Leu Pro Ser Ile Ile  
130 135 140  
Asn Gln Leu Xaa Pro Asp Asn Leu Asp Asn Leu Arg Arg Leu Ala Glu  
145 150 155 160  
Gln Phe Gln Lys Gln Ala Pro Gly Ala Ser Arg Cys  
165 170

(2) INFORMATION FOR SEQ ID NO:2452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2452:

Met Asn Val Glu Lys Leu Lys Lys Met Ala Gly Ala Val Arg Thr Gly  
1 5 10 15  
Gly Lys Gly Ser Met Arg Arg Lys Lys Lys Ala Val His Lys Thr Thr  
20 25 30  
Thr Thr Asp Asp Lys Arg Leu Gln Ser Thr Leu Lys Arg Ile Gly Val  
35 40 45  
Asn Thr Ile Pro Gly Ile Glu Glu Val Asn Ile Phe Lys Asp Asp Val  
50 55 60  
Val Ile Gln Phe Val Asn Pro Lys Val Gln Ala Ser Ile Gly Ala Asn  
65 70 75 80  
Thr Trp Val Val Ser Gly Thr Pro Gln Thr Lys Lys Leu Gln Asp Leu  
85 90 95  
Leu Pro Ser Ile Ile Asn Gln Leu Xaa Pro Asp Asn Leu Asp Asn Leu  
100 105 110  
Arg Arg Leu Ala Glu Gln Phe Gln Lys Gln Ala Pro Gly Ala Ser Arg  
115 120 125  
Cys

(2) INFORMATION FOR SEQ ID NO:2453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

00669960

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1601121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2453:

Met Ala Gly Ala Val Arg Thr Gly Gly Lys Gly Ser Met Arg Arg Lys  
1 5 10 15  
Lys Lys Ala Val His Lys Thr Thr Thr Thr Asp Asp Lys Arg Leu Gln  
20 25 30  
Ser Thr Leu Lys Arg Ile Gly Val Asn Thr Ile Pro Gly Ile Glu Glu  
35 40 45  
Val Asn Ile Phe Lys Asp Asp Val Val Ile Gln Phe Val Asn Pro Lys  
50 55 60  
Val Gln Ala Ser Ile Gly Ala Asn Thr Trp Val Val Ser Gly Thr Pro  
65 70 75 80  
Gln Thr Lys Lys Leu Gln Asp Leu Leu Pro Ser Ile Ile Asn Gln Leu  
85 90 95  
Xaa Pro Asp Asn Leu Asp Asn Leu Arg Arg Leu Ala Glu Gln Phe Gln  
100 105 110  
Lys Gln Ala Pro Gly Ala Ser Arg Cys  
115 120

(2) INFORMATION FOR SEQ ID NO:2454:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 514 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..514

(D) OTHER INFORMATION: / Ceres Seq. ID 1601122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2454:

gaggctgagg gttgcatatt tcattgcgca agctctcgac cattgcaatg ctgagaacag 60  
gaaaatctat catgatttga atgcttatag ggtacttttt gatgaggaag gtgatccccg 120  
cttgtcaagt tttggattaa tgaagaacag ccgtgatggg aaaagttata gcactaacct 180  
ggcttacact ccaccagagt ttctacgaac tggcagagta attccggaga gtgtgatcta 240  
tagctatgga actgtcctgt tggatctttt gagcggaaaa cacattcctc ctagtcatgc 300  
cctagattta ataaggggaa agaataact gttgctgatg gattcctcct tagaagggca 360  
gtatgctaata gaagatgctt cgaaattggg tgatcttgca tcaaagtgtc tgcaatttga 420  
atctagggat agaccgaaca taaagtatct tctgtcttct gttggtcctc ttcagaatca 480  
aaaggagggt gcatacatg tggtcatggg tatt

(2) INFORMATION FOR SEQ ID NO:2455:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1601123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2455:

Arg Leu Arg Val Ala Tyr Phe Ile Ala Gln Ala Leu Asp His Cys Asn  
1 5 10 15  
Ala Glu Asn Arg Lys Ile Tyr His Asp Leu Asn Ala Tyr Arg Val Leu  
20 25 30  
Phe Asp Glu Gly Asp Pro Arg Leu Ser Ser Phe Gly Leu Met Lys  
35 40 45  
Asn Ser Arg Asp Gly Lys Ser Tyr Ser Thr Asn Leu Ala Tyr Thr Pro  
50 55 60  
Pro Glu Phe Leu Arg Thr Gly Arg Val Ile Pro Glu Ser Val Ile Tyr

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(2) INFORMATION FOR SEQ ID NO:2456:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1601124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2456:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Asn | Ser | Arg | Asp | Gly | Lys | Ser | Tyr | Ser | Thr | Asn | Leu | Ala | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Pro | Pro | Glu | Phe | Leu | Arg | Thr | Gly | Arg | Val | Ile | Pro | Glu | Ser | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Tyr | Ser | Tyr | Gly | Thr | Val | Leu | Leu | Asp | Leu | Leu | Ser | Gly | Lys | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Pro | Pro | Ser | His | Ala | Leu | Asp | Leu | Ile | Arg | Gly | Lys | Asn | Ile | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Leu | Met | Asp | Ser | Ser | Leu | Glu | Gly | Gln | Tyr | Ala | Asn | Glu | Asp | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Lys | Leu | Val | Asp | Leu | Ala | Ser | Lys | Cys | Leu | Gln | Phe | Glu | Ser | Arg |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asp | Arg | Pro | Asn | Ile | Lys | Tyr | Leu | Leu | Ser | Ser | Val | Gly | Pro | Leu | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Gln | Lys | Glu | Val | Ala | Ser | His | Val | Phe | Met | Gly | Ile |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2457:

(A) LENGTH: 474 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..474

(D) OTHER INFORMATION: / Ceres Seq. ID 1601125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2457:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| aggaagagg  | aggaccggag | cgagagcgag  | atggtagtgg | tggccgcgc  | ggccgcacgc | 60  |
| ggccgcgctg | taaagccct  | gttctctctc  | ctcgtccacc | acagccgccc | cgcgccccgc | 120 |
| ctccccgcgc | gaaccgccc  | cgcgcggccg  | ctgcgcttcc | tctctgctc  | gacctcagcg | 180 |
| ccgccgctgt | tgcgagccgt | cgcattccatg | gactcgccgc | cccagggtta | ccgcaccaac | 240 |
| gtcggcatct | gcttcgccga | cccttccctc  | accaagattt | tctcggcttc | taggatcgac | 300 |
| attcctatcg | cgtgaatcag | gcctcagggt  | ggtatagatg | cagggaaga  | accaagggcg | 360 |
| gctgctttca | gggaattgag | agaagagact  | ggtgtcacat | ccgcagagat | cgtggtcgag | 420 |
| gctccgtctg | gttaacatat | gatttcccgc  | cagatgtcag | aaccaaactg | aatg       |     |

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..144

- (D) OTHER INFORMATION: / Ceres Seq. ID 1601126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2458:

(2) INFORMATION FOR SEQ ID NO:2459:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids

- (B) TYPE: amino acid

- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..96

- (D) OTHER INFORMATION: / Ceres Seq. ID 1601127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2459:

(2) INFORMATION FOR SEQ ID NO:2460:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids

| Variable                | Mean         | SD   | Min | Max |
|-------------------------|--------------|------|-----|-----|
| Age                     | 35.2         | 12.5 | 18  | 65  |
| Gender                  | Male         | 10.5 | 0   | 20  |
| Education               | 12.5         | 1.5  | 9   | 16  |
| Income                  | 15.5         | 3.5  | 10  | 25  |
| Marital Status          | Married      | 15.5 | 0   | 20  |
| Occupation              | Professional | 10.5 | 0   | 20  |
| Religion                | Christian    | 10.5 | 0   | 20  |
| Health Status           | Good         | 10.5 | 0   | 20  |
| Stress Level            | Low          | 10.5 | 0   | 20  |
| Life Satisfaction       | High         | 10.5 | 0   | 20  |
| Work-Life Balance       | Good         | 10.5 | 0   | 20  |
| Family Support          | High         | 10.5 | 0   | 20  |
| Community Involvement   | Low          | 10.5 | 0   | 20  |
| Personal Growth         | High         | 10.5 | 0   | 20  |
| Financial Stability     | Good         | 10.5 | 0   | 20  |
| Emotional Well-being    | High         | 10.5 | 0   | 20  |
| Physical Health         | Good         | 10.5 | 0   | 20  |
| Mental Health           | Good         | 10.5 | 0   | 20  |
| Social Health           | Good         | 10.5 | 0   | 20  |
| Overall Quality of Life | High         | 10.5 | 0   | 20  |

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..134
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601128
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2460:

Met Val Val Val Ala Ala Ala Ala Arg Gly Arg Ala Val Lys Pro  
1 5 10 15  
Leu Phe Leu Val Leu Val His His Ser Arg Pro Ala Pro Arg Leu Pro  
20 25 30  
Arg Arg Thr Ala Arg Ala Arg Pro Leu Arg Phe Leu Ser Cys Ser Thr  
35 40 45  
Ser Ala Pro Pro Leu Phe Ala Ala Val Ala Ser Met Asp Ser Pro Pro  
50 55 60  
Gln Gly Tyr Arg Thr Asn Val Gly Ile Cys Leu Ala Asp Pro Ser Leu  
65 70 75 80  
Thr Lys Ile Phe Ser Ala Ser Arg Ile Asp Ile Pro Ser Ala Trp Gln  
85 90 95  
Met Pro Gln Gly Gly Ile Asp Ala Gly Glu Glu Pro Arg Ala Ala Ala  
100 105 110  
Phe Arg Glu Leu Arg Glu Glu Thr Gly Val Thr Ser Ala Glu Ile Val  
115 120 125  
Ala Glu Ala Pro Ser Gly  
130

- (2) INFORMATION FOR SEQ ID NO:2461:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 483 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..483
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1601141

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2461:

ctatctccct gtttaatacaa tcttcaagc gcaagctgcc tcctcctcgt cgtccggtcg 60  
tgagaaggga tggcgggccc tggcaaggct atcggcgctg gcgccgcgaa gaaggcaacg 120  
tcgaggagct ccaaggcccg actccagttc cccgtcgcca ggattgccag gttcctcaag 180  
gcgggcaagt acgcggagcg cgtcgcgccc ggccgccccg tgtacctcgc cgccgtcctc 240  
gagtacctcg cggtgaggt tctcgaactt gccgggaacg ccgcgaggga caacaagaag 300  
acccgcattg tgccgcgcca catccagctt gctgtgcgca acgacgagga gctgaccaa 360  
ctgttggtg gtgccaccat cgcgagcgga ggtgttatgc ctaacatcca tcagcatctg 420  
ctccccaaga aggtgcctc ctcgtcgacg atctcgtagc ggcggcgcac atggcgagcg 480  
acg

- (2) INFORMATION FOR SEQ ID NO:2462:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 84 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601142

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2462:

Ile Ser Leu Phe Asn Gln Ser Phe Lys Arg Lys Leu Pro Pro Pro Arg

005707" 08668960

1 5 10 15  
Arg Pro Val Val Arg Arg Asp Gly Gly Pro Trp Gln Gly Tyr Arg Arg  
20 25 30  
Trp Arg Arg Glu Glu Gly Asn Val Glu Glu Leu Gln Gly Arg Thr Pro  
35 40 45  
Val Pro Arg Arg Gln Asp Cys Gln Val Pro Gln Gly Gly Gln Val Arg  
50 55 60  
Gly Ala Arg Arg Arg Arg Arg Pro Arg Val Pro Arg Arg Arg Pro Arg  
65 70 75 80  
Val Pro Arg Gly

(2) INFORMATION FOR SEQ ID NO:2463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2463:

Met Ala Gly Arg Gly Lys Ala Ile Gly Ala Gly Ala Ala Lys Lys Ala  
1 5 10 15  
Thr Ser Arg Ser Ser Lys Ala Gly Leu Gln Phe Pro Val Gly Arg Ile  
20 25 30  
Ala Arg Phe Leu Lys Ala Gly Lys Tyr Ala Glu Arg Val Gly Ala Gly  
35 40 45  
Ala Pro Val Tyr Leu Ala Ala Val Leu Glu Tyr Leu Ala Ala Glu Val  
50 55 60  
Leu Glu Leu Ala Gly Asn Ala Ala Arg Asp Asn Lys Lys Thr Arg Ile  
65 70 75 80  
Val Pro Arg His Ile Gln Leu Ala Val Arg Asn Asp Glu Glu Leu Thr  
85 90 95  
Lys Leu Leu Gly Gly Ala Thr Ile Ala Ser Gly Gly Val Met Pro Asn  
100 105 110  
Ile His Gln His Leu Leu Pro Lys Lys Ala Ala Ser Ser Thr Ile  
115 120 125  
Ser

(2) INFORMATION FOR SEQ ID NO:2464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..471
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2464:

ctcctcgact gctccccctcc ttccagagtc acggtgcctc gccgtccttc cctgatctga 60  
caaccgcgttt accttgcccg gccggtccac tccgacggct ggcccgccct tctttaaccc 120  
cgccacccccg atccagccca gccgcactcc aacacggtag cagcagtcaa cagactccca 180  
ccgcaatggc cgcggcgctc ctcttgctgc tctgtccgcc cgtcggccta ctgcgcgcgc 240  
tcgcattcct caccgggccc cgcgcccggg tgcgcgtcaa agacagccac gtcttcatca 300  
cgggcggggtc cagcggcatc gggctcgcca tggccacggc cgctgcgcgg gagggcgcg 360  
gggtctccat cctggcccgc aaccttgccc gcctcgagga ggcgcgcgcc gccatccagc 420  
gcgactcggg ccgcgacgac gtgcgggtcc acgcggccga cgtgcgggac g

09689980 101300





35 40 45  
Pro Arg Pro Ala Cys Ala Ala Ala Ala Met Ala Arg Gly Asp Gly Arg  
50 55 60  
Arg Arg Gly Thr Arg Lys Gly Pro Arg Gly Thr Ser Ser Thr Ala Arg  
65 70 75 80  
Arg Arg Arg Arg Gly Arg Arg Gly Ser Gly Arg Thr Gly Ser Cys Pro  
85 90 95  
Val Thr Ser Pro Pro Ser Ser Pro Ser Ser Ser Ser Ala Ser Ala Ser  
100 105 110  
Thr Pro Ser Pro Thr Ser Arg Ser Arg Pro Gly Arg Thr Arg Arg Arg  
115 120 125  
Trp Asn Ala Ser Ser Ser  
130

(2) INFORMATION FOR SEQ ID NO:2470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..133
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2470:

Phe Pro Leu Leu Pro Arg Leu Pro Phe Pro Gln His Ser Leu His Leu  
1 5 10 15  
Pro Ile Ser Gln Ala Thr Pro Thr Arg Ser Thr Gly Gly Thr Asp Ala  
20 25 30  
Gly Asp Leu Asp Gly Arg Gly Gly His Ala Ala Arg Ala Ala Pro Leu  
35 40 45  
Leu Val Pro Arg Ala Arg Arg Arg Arg Trp Arg Gly Ala Met Asp Asp  
50 55 60  
Ala Gly Ala Arg Gly Lys Ala Gln Gly Val Pro Leu Gln Pro Pro Ala  
65 70 75 80  
Ala Ala Ala Gly Gly Asp Ala Glu Val Gly Gly Leu Gly Ala Ala Leu  
85 90 95  
Leu His His Leu Leu Pro His Arg Arg His Pro Arg Arg Arg Pro Gln  
100 105 110  
Arg Gln Ala Arg Pro His Asp Arg Asp Leu Gly Ala Arg Glu Gly Ala  
115 120 125  
Gly Thr Pro Gln Ala  
130

(2) INFORMATION FOR SEQ ID NO:2471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2471:

ccacgaagta gcgttggtgctg ttgcaaaagc aaccgtttca agtttcctcc ctagtgcacc 60  
caggaaatcg ccagcacctc ccctgttccc tctctgtctc tggctctctc tcctctccgc 120  
ccctttttat cgccgatctt cacacatttt ggaaagagga gagagagagg gagagattag 180  
agggagcgcc ctgcccagc aaagagaaac cgcggcgcga gaagagggag gaagggcaga 240  
cgggcgagca g gatgagaga gatcatcagc atccacatcg gccaggcccg gatccaggtc 300  
ggcaacgcct gctgggagct ctactgctc gagcacggca tcgagcccga tggcaccatg 360

00669980-101300





(2) INFORMATION FOR SEQ ID NO:2475:

(D) OTHER INFORMATION: / Ceres Seq. ID 1601168

(2) INFORMATION FOR SEQ ID NO:2476:

(D) OTHER INFORMATION: / Ceres Seq. ID 1601169

(2) INFORMATION FOR SEQ ID NO:2477:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

| Table 1. Demographic characteristics of the study population |                 |
|--------------------------------------------------------------|-----------------|
| Age (years)                                                  | 50.0 ± 10.0     |
| Gender                                                       |                 |
| Male                                                         | 50.0%           |
| Female                                                       | 50.0%           |
| Education (years)                                            | 12.0 ± 2.0      |
| Marital status                                               |                 |
| Married                                                      | 80.0%           |
| Single                                                       | 20.0%           |
| Occupation                                                   |                 |
| Professional                                                 | 30.0%           |
| Managerial                                                   | 20.0%           |
| Technical                                                    | 10.0%           |
| Service                                                      | 20.0%           |
| Unemployed                                                   | 20.0%           |
| Income (USD/month)                                           | 1,500.0 ± 500.0 |
| Health status                                                |                 |
| Good                                                         | 70.0%           |
| Fair                                                         | 20.0%           |
| Poor                                                         | 10.0%           |

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..179  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1601183  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2479:  
atctcaattc tcccacccgg ccgcccggcac cacacgcgcg ctccgggagc cacaacgacc 60  
gatggcgagg gcgcgcttcc ctctcctcst cctcctcctc gtggcggttc tgcgcrncac 120  
aggctccacg gcggcccgac acgcccgcgc cgcacccgcg tccgcgcccc gggcgtcgc  
(2) INFORMATION FOR SEQ ID NO:2480:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 59 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..59  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1601184  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2480:  
Ile Ser Ile Leu Pro Pro Gly Arg Arg His His Thr Arg Ala Pro Gly  
1                    5                    10                    15  
Ala Thr Thr Thr Asp Gly Glu Gly Ala Leu Pro Ser Pro Xaa Pro Pro  
                    20                    25                    30  
Pro Arg Gly Val Xaa Arg Xaa His Arg Leu His Gly Gly Pro Thr Arg  
                    35                    40                    45  
Arg Ala Arg Thr Arg Val Arg Ala Pro Gly Val  
50                    55  
(2) INFORMATION FOR SEQ ID NO:2481:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 59 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..59  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1601185  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2481:  
Ser Gln Phe Ser His Pro Ala Ala Gly Thr Thr Arg Ala Leu Arg Glu  
1                    5                    10                    15  
Pro Gln Arg Pro Met Ala Arg Ala Arg Phe Pro Leu Leu Xaa Leu Leu  
                    20                    25                    30  
Leu Val Ala Xaa Leu Ala Xaa Thr Gly Ser Thr Ala Ala Arg His Ala  
                    35                    40                    45  
Ala Pro Ala Pro Ala Ser Ala Pro Arg Ala Ser  
50                    55  
(2) INFORMATION FOR SEQ ID NO:2482:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 59 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..59  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1601186

0065980 10100

(D) OTHER INFORMATION: / Ceres Seq. ID 1601193

(2) INFORMATION FOR SEQ ID NO:2486:

(2) INFORMATION FOR SEQ ID NO:2487:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2487:

(2) INFORMATION FOR SEQ ID NO:2488:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2488:

(2) INFORMATION FOR SEQ ID NO:2489:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2489:

(2) INFORMATION FOR SEQ ID NO:2490:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2490:

(2) INFORMATION FOR SEQ ID NO:2491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..87  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601212  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2491:

Met Tyr Arg Lys Gln His Lys Lys Asp Ile His Ala Glu Ala Val Lys  
1 5 10 15  
Lys Arg Arg Arg Ala Thr Lys Lys Pro Tyr Ser Arg Ser Ile Val Gly  
20 25 30  
Ala Ser Leu Glu Val Ile Gln Lys Lys Arg Ala Glu Lys Pro Glu Val  
35 40 45  
Arg Asp Ala Ala Arg Glu Ala Ala Leu Arg Glu Ile Lys Glu Arg Ile  
50 55 60  
Lys Lys Thr Lys Asp Glu Lys Lys Ala Lys Lys Ala Glu Val Ser Lys  
65 70 75 80  
Ser Gln Glu Asp Ala Asp Lys  
85

(2) INFORMATION FOR SEQ ID NO:2492:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 483 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..483  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601224  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2492:

agcattttcct caaacaattc ggcgcgcgcgc gccgcgcgtc tccggcgtct gctactcggc 60  
tccgtgcccc ccaggcagca ggccaccacc ccaatccctc tcttcttca gagatgcaga 120  
aggtgcggct caaatgggtg aagaaccggg gcctggatca cctgatcgag cgcaccacct 180  
caatccgcgc gtcttgctg ctgctcgacc acctctcgcg cctccctggt acctcccccg 240  
tgccggcgcg ctccctcgca cgcttccaaa agccgcttgg cctgacggtg cctgtgcttc 300  
gcttccttgc ccgcctatcc acgtcttctt ccgagcaacc gcaccctcgg ttccccacgc 360  
tgctctcctt ttccctcaag gctgctgac acaccctcct gtcccgcctt gccgatgcct 420  
atgcgcacga cgcgcacctc cgcttcgcgc gctctctct cctcaccgcg tccaaggctg 480  
ctc

(2) INFORMATION FOR SEQ ID NO:2493:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 160 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..160  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601225  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2493:

Ala Phe Pro Gln Thr Ile Arg Ala Pro Pro Pro Leu Ser Gly Val  
1 5 10 15  
Cys Tyr Ser Ala Pro Cys Pro Pro Gly Ser Arg Pro Pro Pro Gln Ser  
20 25 30  
Leu Ser Ser Phe Arg Asp Ala Glu Gly Ala Ala Gln Met Gly Glu Glu  
35 40 45

00689300 101300

(2) INFORMATION FOR SEQ ID NO:2494:

(A) LENGTH: 160 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..160  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601226

| (x1) SEQUENCE DESCRIPTION: 221 AA |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| His<br>1                          | Phe | Leu | Lys | Gln | Phe | Ala | Arg | Arg | Arg | Arg | Ser | Pro | Ala | Ser |     |  |
| Ala                               | Thr | Arg | Leu | Arg | Ala | His | Gln | Ala | Ala | Gly | His | His | Pro | Asn | Pro |  |
| Ser                               | Leu | Pro | Ser | Glu | Met | Gln | Lys | Val | Arg | Leu | Lys | Trp | Val | Lys | Asn |  |
| Arg                               | Gly | Leu | Asp | His | Leu | Ile | Glu | Arg | Thr | Thr | Ser | Ile | Arg | Ala | Ser |  |
| Cys<br>65                         | Leu | Leu | Leu | Asp | His | Leu | Ser | Arg | Leu | Pro | Gly | Thr | Ser | Pro | Val |  |
| Pro                               | Ala | Arg | Ser | Leu | Ala | Arg | Leu | Gln | Lys | Pro | Leu | Gly | Leu | Thr | Val |  |
| Pro                               | Val | Leu | Arg | Phe | Leu | Arg | Arg | His | Pro | Thr | Leu | Phe | Ser | Glu | Gln |  |
| Pro                               | His | Pro | Arg | Phe | Pro | Thr | Leu | Leu | Ser | Phe | Ser | Leu | Thr | Ala | Ala |  |
| Ser                               | His | Thr | Leu | Leu | Ser | Arg | Leu | Ala | Asp | Ala | Tyr | Ala | His | Asp | Ala |  |
| His<br>145                        | Leu | Arg | Leu | Ala | Arg | Leu | Leu | Leu | Thr | Arg | Ser | Lys | Val | Ala |     |  |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..123  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601227







(2) INFORMATION FOR SEQ ID NO:2500:

(A) LENGTH: 388 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..388

(D) OTHER INFORMATION: / Ceres Seq. ID 1601272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2500:

| (x1) SEQUENCE DESCRIPTION: SEQ ID NUMBER |            |            |             |            |             |  |  |     |
|------------------------------------------|------------|------------|-------------|------------|-------------|--|--|-----|
| aagtaaaaaa                               | aagttctcgc | gcatggctcg | tctgcgactg  | cctctgaccg | cactgctctc  |  |  | 60  |
| ttctctcgtt                               | ctctctcccc | acttcgagac | ttctctccatt | cgcggtttgc | ctctctgcct  |  |  | 120 |
| ccctccctca                               | gactctcctt | aagattgcca | tggcggacca  | gctcacgcac | gaccagatcg  |  |  | 180 |
| ccgagttcaa                               | ggaagcattc | agcctcttcg | acaaggacgg  | cgacggctgc | atcaccacca  |  |  | 240 |
| aggaaattgg                               | aactgtgatg | cgctcgtttg | ggcagaacct  | tactgaggct | gagcttcagg  |  |  | 300 |
| acatgatcaa                               | cgaggttgat | gctgatggca | atggaaccat  | cgacttcctt | gagttttctca |  |  | 360 |
| acctgatgac                               | acgcaagatg | aaggacac   |             |            |             |  |  |     |

(2) INFORMATION FOR SEQ ID NO:2501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..46

(D) OTHER INFORMATION: / Ceres Seq. ID 1601273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2501:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Lys | Lys | Lys | Phe | Ser | Arg | Met | Val | Gly | Leu | Arg | Leu | Pro | Leu | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Leu | Leu | Ser | Ser | Pro | Val | Leu | Ser | Pro | His | Phe | Glu | Thr | Ser | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Arg | Gly | Leu | Pro | Leu | Cys | Leu | Pro | Pro | Ser | Asp | Pro | Pro |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2502:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1601274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2502:

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 10

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asp | Gln | Leu | Thr | Asp | Asp | Gln | Ile | Ala | Glu | Phe | Lys | Glu | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Phe | Ser | Leu | Phe | Asp | Lys | Asp | Gly | Asp | Gly | Cys | Ile | Thr | Thr | Lys | Glu |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     | 20  |     |     |     |     | 25  |     |     | 30  |     |     |     |     |     |
| Xaa | Trp | Ser | Arg | Thr | Pro | Pro | Ala | Ser | Pro | Cys | Arg | Pro | Ser | Ser | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Arg | Ser | Ala | Arg | Thr | Trp | Ser | Ala | Ser | Pro | Thr | Ser | Cys | Cys | Pro |
|     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ala | Thr | Ser | Ala | Xaa | Leu | Thr | His | Leu | Pro | Pro | Arg | Trp | Pro | Pro | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Gly | Arg | Val | Leu | Gly | Tyr | Gly | Pro | Arg | Cys | Val | Pro | Tyr | Pro | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Pro | Arg | Arg | Arg | His | Pro | Pro | Arg | Arg | Pro | Gly | Ser | Ile | Arg | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Val | Pro | Arg | Arg | Thr | His | Val | Arg | Ala | His | Gln | Asp | Leu | Ala | Gln |
|     |     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Val | Ala | Pro | Arg | Val | Asn | Val | Asn | Leu | Arg | Arg | Val | Ala | Val | Ala | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Xaa | Leu | Ala | Pro | Pro | Pro | Ser | Arg | Pro | Ser | Ser | Arg | Arg | Ala | Ala | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

(2) INFORMATION FOR SEQ ID NO:2506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1601278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2506:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Lys | His | His | Arg | Arg | Ala | Ala | Gln | Ile | Thr | Ala | Thr | Ala | Ala | Met |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ala | Ser | Ser | Arg | Pro | Xaa | Val | Ser | Val | Lys | Ala | Leu | Glu | Gly | Xaa |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| His | Gly | His | Gly | Arg | Pro | Arg | His | Arg | Leu | Ala | Ala | Arg | Leu | Arg | Cys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Asp | Pro | Pro | Gly | Arg | Gly | Pro | Leu | His | Pro | Gln | Ala | Ala | Val | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Gln | Ala | Pro | Xaa | Leu | Arg | Ile | Ser | Arg | Arg | Ala | Gly | His | Gln | Thr |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Ser | Ala | Glu | Ser | Trp | Gly | Thr | Gly | Arg | Ala | Val | Ser | Arg | Ile | Pro | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Val | Pro | Gly | Gly | Gly | Thr | His | Arg | Ala | Gly | Gln | Gly | Ala | Phe | Gly | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Met | Cys | Arg | Gly | Gly | Arg | Met | Phe | Ala | Pro | Thr | Lys | Ile | Trp | Arg | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Trp | His | Arg | Ala | Ser | Thr | Ser | Thr | Ser | Ala | Ala | Ser | Pro | Ser | Pro | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Xaa | Ser | Arg | His | Arg | Arg | Pro | Gly | Pro | Arg | Pro | Gly | Ala | Arg | Pro | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

(2) INFORMATION FOR SEQ ID NO:2507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..145  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2507:

Met Ala Ala Ser Ser Arg Pro Xaa Val Ser Val Lys Ala Leu Glu Gly  
1 5 10 15  
Xaa His Gly His Gly Arg Pro Arg His Arg Leu Ala Ala Arg Leu Arg  
20 25 30  
Cys Ala Asp Pro Pro Gly Arg Gly Pro Leu His Pro Gln Ala Ala Val  
35 40 45  
Leu Gln Gln Ala Pro Xaa Leu Arg Ile Ser Arg Arg Ala Gly His Gln  
50 55 60  
Thr Ser Ala Glu Ser Trp Gly Thr Gly Arg Ala Val Ser Arg Ile Pro  
65 70 75 80  
Arg Val Pro Gly Gly Gly Thr His Arg Ala Gly Gln Gly Ala Phe Gly  
85 90 95  
Asn Met Cys Arg Gly Gly Arg Met Phe Ala Pro Thr Lys Ile Trp Arg  
100 105 110  
Lys Trp His Arg Ala Ser Thr Ser Thr Ser Ala Ala Ser Pro Ser Pro  
115 120 125  
Arg Xaa Ser Arg His Arg Arg Pro Gly Pro Arg Pro Gly Ala Arg Pro  
130 135 140  
Pro  
145

(2) INFORMATION FOR SEQ ID NO:2508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..502  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2508:

gttcccctcc gctgtctcgc ctctcccttg gttcctcgcg gcgacgactg ggcgagcgcc 60  
tcctcccctc cctcactccc tccgtgagct cctcgccggc ggcgagcgcc gccgcccgtc 120  
gccacgtctt ctccgctgac gtgggctcac cagatccaat gaaggctgcc aacttgacgc 180  
aaggggaata aagatccaaa taagtttttg acattgatct gtagccagta ctgcaatggc 240  
tatgaagctt gtggttctcg gtatcccctg ggatgttgac actgaagggt tacgagagta 300  
catggccaag tttggacccc tagacgattg tgctgctatg aaggagcggt cttctgggcg 360  
atctcgcggg tttggctatg taacattcgc ctcagctgac gatgcaaaga atgttcttga 420  
ttgcgagcat gttcttgga gccgtacatt agaagtgaag gtagctactc caaaggaaga 480  
aatgaaatca caaggatcaa ag

(2) INFORMATION FOR SEQ ID NO:2509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..89  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2509:

Met Ala Met Lys Leu Val Val Leu Gly Ile Pro Trp Asp Val Asp Thr  
1 5 10 15  
Glu Gly Leu Arg Glu Tyr Met Ala Lys Phe Gly Pro Leu Asp Asp Cys  
20 25 30

00000000 00000000



(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..496
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2512:

|                                                                      |     |
|----------------------------------------------------------------------|-----|
| agcggtcgaa gaaagaaatt aatgaaacgg cagtcgcaac tcgcaagcaa atcgaacgaa    | 60  |
| cccagccgaa gcgcgagctg agcaaggcgg aggcggcgagg accggcgatg gagcggctgc   | 120 |
| agcggatctt tggcgccctcc ggcattggggc agccgcgcgac ggactcgccg ctgctcgact | 180 |
| cctccgagca ggtctacatc tcctccctcg cgcttctcaa gatgctcaag cacgggaggg    | 240 |
| ccggcggtgcc catggagggtc atgggtctca tgctcggcga gttcgctgat gactacaccg  | 300 |
| tcagggtcgt cgacgtcttc gccatgccgc agagcgggac tggggtcagc gtcgaggccg    | 360 |
| tcgaccacgt cttccagaca aacatgcttg acatgctcaa gcagaccggc aggccagaaa    | 420 |
| tggttgtagg ctggtatcac tcacatcctg gcttcggttg ctggctatca ggcgttgata    | 480 |
| tcaatactca gcagag                                                    |     |

(2) INFORMATION FOR SEQ ID NO:2513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601289

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2513:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Arg Ser Lys Lys Glu Ile Asn Glu Thr Ala Val Ala Thr Arg Lys Gln |  |
| 1 5 10 15                                                       |  |
| Ile Glu Arg Thr Gln Pro Lys Arg Glu Leu Ser Lys Ala Glu Ala Ala |  |
| 20 25 30                                                        |  |
| Gly Pro Ala Met Glu Arg Leu Gln Arg Ile Phe Gly Ala Ser Gly Met |  |
| 35 40 45                                                        |  |
| Gly Gln Pro Pro Thr Asp Ser Pro Leu Leu Asp Ser Ser Glu Gln Val |  |
| 50 55 60                                                        |  |
| Tyr Ile Ser Ser Leu Ala Leu Leu Lys Met Leu Lys His Gly Arg Ala |  |
| 65 70 75 80                                                     |  |
| Gly Val Pro Met Glu Val Met Gly Leu Met Leu Gly Glu Phe Val Asp |  |
| 85 90 95                                                        |  |
| Asp Tyr Thr Val Arg Val Val Asp Val Phe Ala Met Pro Gln Ser Gly |  |
| 100 105 110                                                     |  |
| Thr Gly Val Ser Val Glu Ala Val Asp His Val Phe Gln Thr Asn Met |  |
| 115 120 125                                                     |  |
| Leu Asp Met Leu Lys Gln Thr Gly Arg Pro Glu Met Val Val Gly Trp |  |
| 130 135 140                                                     |  |
| Tyr His Ser His Pro Gly Phe Gly Cys Trp Leu Ser Gly Val Asp Ile |  |
| 145 150 155 160                                                 |  |
| Asn Thr Gln Gln                                                 |  |

(2) INFORMATION FOR SEQ ID NO:2514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2514:

Met Glu Arg Leu Gln Arg Ile Phe Gly Ala Ser Gly Met Gly Gln Pro

09669980-10100







(2) INFORMATION FOR SEO ID NO:2519:

(A) LENGTH: 471 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1601303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2519:

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| aaccocctcgg | acagaccagc | cttcaaaacta | gggtttactc | ctcccgtctc | gagaaagcaa | 60  |
| acaagcgctca | gctccgcgcg | cggcctcggg  | ctctctcccc | cgcgcacct  | tctctacgcc | 120 |
| aggactgcca  | agatgaagct | cgtcagattc  | cttatgaagc | taaacaatga | gacggtcacc | 180 |
| atcgagctca  | agaacggcac | ggttggtcac  | ggcaccatca | ccggtgttga | cataagcatg | 240 |
| aacactcato  | tgaagacagt | gaagcttaca  | ctgaaaggga | agaacctgt  | aacgctggac | 300 |
| cacctcagcg  | tgcgagagaa | caacatccgc  | tattacattc | ttcctgacag | cttaaacttg | 360 |
| gagactttgc  | tggtgagaga | aacccctagg  | gttaagccta | aaagccgac  | tacaggaaag | 420 |
| cttttggggc  | gtgggcgcgg | ccdtggtcgt  | ggacgtgttc | ggggacgggg | g          |     |

(2) INFORMATION FOR SEQ ID NO:2520:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1601304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2520:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Pro | Ser | Asp | Arg | Pro | Ala | Phe | Lys | Leu | Gly | Phe | Thr | Pro | Pro | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Arg | Lys | Gln | Thr | Ser | Val | Ser | Ser | Ala | Gly | Gly | Leu | Ala | Leu | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Pro | Pro | His | Leu | Leu | Tyr | Ala | Arg | Thr | Ala | Lys | Met | Lys | Leu | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Phe | Leu | Met | Lys | Leu | Asn | Asn | Glu | Thr | Val | Thr | Ile | Glu | Leu | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Gly | Thr | Val | Val | His | Gly | Thr | Ile | Thr | Gly | Val | Asp | Ile | Ser | Met |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asn | Thr | His | Leu | Lys | Thr | Val | Lys | Leu | Thr | Leu | Lys | Gly | Lys | Asn | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Thr | Leu | Asp | His | Leu | Ser | Val | Arg | Gly | Asn | Asn | Ile | Arg | Tyr | Tyr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Leu | Pro | Asp | Ser | Leu | Asn | Leu | Glu | Thr | Leu | Leu | Val | Glu | Glu | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Arg | Val | Lys | Pro | Lys | Lys | Pro | Thr | Thr | Gly | Lys | Pro | Leu | Gly | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Arg | Gly | Arg | Gly | Arg | Gly | Arg | Gly | Arg | Gly | Arg | Gly |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2521:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..113  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1601305  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2521:  
Met Lys Leu Val Arg Phe Leu Met Lys Leu Asn Asn Glu Thr Val Thr  
1                  5                  10                  15  
Ile Glu Leu Lys Asn Gly Thr Val Val His Gly Thr Ile Thr Gly Val  
                  20                  25                  30  
Asp Ile Ser Met Asn Thr His Leu Lys Thr Val Lys Leu Thr Leu Lys  
                  35                  40                  45  
Gly Lys Asn Pro Val Thr Leu Asp His Leu Ser Val Arg Gly Asn Asn  
                  50                  55                  60  
Ile Arg Tyr Tyr Ile Leu Pro Asp Ser Leu Asn Leu Glu Thr Leu Leu  
65                  70                  75                  80  
Val Glu Glu Thr Pro Arg Val Lys Pro Lys Lys Pro Thr Thr Gly Lys  
                  85                  90                  95  
Pro Leu Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg  
                  100                  105                  110  
Gly

(2) INFORMATION FOR SEQ ID NO:2522:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 106 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..106  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1601306  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2522:  
Met Lys Leu Asn Asn Glu Thr Val Thr Ile Glu Leu Lys Asn Gly Thr  
1                  5                  10                  15  
Val Val His Gly Thr Ile Thr Gly Val Asp Ile Ser Met Asn Thr His  
                  20                  25                  30  
Leu Lys Thr Val Lys Leu Thr Leu Lys Gly Lys Asn Pro Val Thr Leu  
                  35                  40                  45  
Asp His Leu Ser Val Arg Gly Asn Asn Ile Arg Tyr Tyr Ile Leu Pro  
50                  55                  60  
Asp Ser Leu Asn Leu Glu Thr Leu Leu Val Glu Glu Thr Pro Arg Val  
65                  70                  75                  80  
Lys Pro Lys Lys Pro Thr Thr Gly Lys Pro Leu Gly Arg Gly Arg Gly  
                  85                  90                  95  
Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly  
                  100                  105

(2) INFORMATION FOR SEQ ID NO:2523:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 389 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..389

09599990 101300

(ix) FEATURE:



Arg Asp Pro Thr Ala Leu Pro Ser Thr Ser Thr Pro Leu Pro Ser Gly  
115 120 125  
Thr Arg Phe Arg Ile Ser Arg Pro Ser Thr Met Pro Met Gly Arg  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2529:

Met Gln Ala Cys Asn Leu Met Cys Leu Pro Glu Asn Tyr Gln Met Lys  
1 5 10 15  
Tyr Tyr Phe Tyr His Met Leu Ser Trp Pro Gln Leu Leu Phe Val Ala  
20 25 30  
Glu Asp Tyr Gly Gly Ser Ile Val Gly Tyr Val Leu Ala Lys Met Glu  
35 40 45  
Glu Asp Pro Ser Glu Pro Cys His Gly His Ile Thr Ser Leu Ala Val  
50 55 60  
Leu Arg Ser His Arg Lys Leu Gly Leu Ala Thr Lys Leu Met Ser Ala  
65 70 75 80  
Ala Gln Ala Ala Met Asp Gln Val Phe Gly Ala Glu Tyr Val Ser Leu  
85 90 95  
His Val Arg Asp Pro Thr Ala Leu Pro Ser Thr Ser Thr Pro Leu Pro  
100 105 110  
Ser Gly Thr Arg Phe Arg Ile Ser Arg Pro Ser Thr Met Pro Met Gly  
115 120 125

Arg

(2) INFORMATION FOR SEQ ID NO:2530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2530:

Met Cys Leu Pro Glu Asn Tyr Gln Met Lys Tyr Tyr Phe Tyr His Met  
1 5 10 15  
Leu Ser Trp Pro Gln Leu Leu Phe Val Ala Glu Asp Tyr Gly Gly Ser  
20 25 30  
Ile Val Gly Tyr Val Leu Ala Lys Met Glu Glu Asp Pro Ser Glu Pro  
35 40 45  
Cys His Gly His Ile Thr Ser Leu Ala Val Leu Arg Ser His Arg Lys  
50 55 60  
Leu Gly Leu Ala Thr Lys Leu Met Ser Ala Ala Gln Ala Ala Met Asp  
65 70 75 80  
Gln Val Phe Gly Ala Glu Tyr Val Ser Leu His Val Arg Asp Pro Thr  
85 90 95  
Ala Leu Pro Ser Thr Ser Thr Pro Leu Pro Ser Gly Thr Arg Phe Arg  
100 105 110  
Ile Ser Arg Pro Ser Thr Met Pro Met Gly Arg

- 115 120  
(2) INFORMATION FOR SEQ ID NO:2531:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 508 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..508  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2531:  
aacacaggca ccacagctga gagacgatag aagcacgcag cagctgaaag ggaggggaac 60  
taggaatgaa ggggagcaag gtccacgagc acgaggcaga cgtccccgcc tccgacctct 120  
gggcgatcta cggtccctc cgcgcgcgg aactcctgcc ggagctgctc ccgcacgtgc 180  
ttgccaaggt ggagctcgtc agcggcgacg gcggtgttg taccatcttg cagctaatat 240  
ttcctcccg gattcctggg ctacagagtt acaaggagaa gttcatcaaa gttgacaacg 300  
agaactatat caaggaggca gaagccattg atggcgacat tttgaagctg gggttcgagg 360  
catacatgat acggtttgag atcattccaa aaggggcca ttcgtctgtc atcaggtcga 420  
ctatcgagta tgtgattgct gatgcgcacc cggagctcga agctatggtg agcacagcaa 480  
ctttggctga aactgctcag aaattttc

(2) INFORMATION FOR SEQ ID NO:2532:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 97 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..97  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2532:

Thr Gln Ala Pro Gln Leu Arg Asp Asp Arg Ser Thr Gln Gln Leu Lys  
1 5 10 15  
Gly Arg Gly Thr Arg Asn Glu Gly Glu Gln Gly Pro Arg Ala Arg Gly  
20 25 30  
Arg Arg Pro Arg Leu Arg Pro Leu Gly Asp Leu Arg Leu Pro Pro Arg  
35 40 45  
Arg Gly Thr Pro Ala Gly Ala Ala Pro Ala Arg Ala Cys Gln Gly Gly  
50 55 60  
Ala Arg Gln Arg Arg Arg Arg Cys Trp Tyr His Leu Ala Ala Asn Ile  
65 70 75 80  
Ser Ser Arg Asp Ser Trp Ala Thr Glu Leu Gln Gly Glu Val His Gln  
85 90 95  
Ser

(2) INFORMATION FOR SEQ ID NO:2533:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 147 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..147  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2533:

Met Lys Gly Ser Lys Val His Glu His Glu Ala Asp Val Pro Ala Ser

CONFIDENTIAL 08563950



1 5 10 15  
Asp Leu Trp Ala Ile Tyr Gly Ser Leu Arg Ala Ala Glu Leu Leu Pro  
20 25 30  
Glu Leu Leu Pro His Val Leu Ala Lys Val Glu Leu Val Ser Gly Asp  
35 40 45  
Gly Gly Val Gly Thr Ile Leu Gln Leu Ile Phe Pro Pro Gly Ile Pro  
50 55 60  
Gly Leu Gln Ser Tyr Lys Glu Lys Phe Ile Lys Val Asp Asn Glu Asn  
65 70 75 80  
Tyr Ile Lys Glu Ala Glu Ala Ile Asp Gly Asp Ile Leu Lys Leu Gly  
85 90 95  
Phe Glu Ala Tyr Met Ile Arg Phe Glu Ile Ile Pro Lys Gly Ala Asn  
100 105 110  
Ser Ser Val Ile Arg Ser Thr Ile Glu Tyr Val Ile Ala Asp Ala His  
115 120 125  
Pro Glu Leu Glu Ala Met Val Ser Thr Ala Thr Leu Ala Glu Thr Ala  
130 135 140  
Gln Lys Phe  
145

(2) INFORMATION FOR SEQ ID NO:2534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..475
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2534:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aatccacaca | cacacaacac | agcagagaga | ttactacgat | ccaacagttc | tagagcaaga | 60  |
| gagaggaaga | cacaccgcag | agttagcagg | ctaataactt | gcaggagcag | caggaatggc | 120 |
| ggcgacgcgt | cgctctctt  | gccttctcct | cgccgtgctt | ctggcaggag | tgccgcgtgc | 180 |
| caccgccttc | gacgaagcgg | ctgctgccgg | cttcgggctt | ggccacggcg | cgcgtttcgc | 240 |
| gcgcaagcat | ggacgagctg | ccgctgagat | gcccagcccg | gagccacaac | ctaaaactaa | 300 |
| gccggagccc | catatgcagc | cactgcncca | gccagaacct | aaaccgaaac | ctatgccaca | 360 |
| tccagagcca | aagcctgaac | ctcaaccaa  | gccaacct   | gaacctcaac | caatgcccaa | 420 |
| gcctctacca | aatccaaac  | cagagccatt | gcctacacng | aagccagaac | ctaag      |     |

(2) INFORMATION FOR SEQ ID NO:2535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2535:

Asn Pro His Thr His Asn Thr Ala Glu Arg Leu Leu Arg Ser Asn Ser  
1 5 10 15  
Ser Arg Ala Arg Glu Arg Lys Thr His Arg Arg Val Ser Arg Leu Ile  
20 25 30  
Thr Cys Arg Ser Ser Arg Asn Gly Asp Ala Ser Pro Leu Leu Pro  
35 40 45  
Ser Pro Arg Arg Ala Ser Gly Arg Ser Gly Arg Cys His Arg Leu Arg  
50 55 60  
Arg Ser Gly Cys Cys Arg Leu Arg Ala Trp Pro Arg Arg Ala Phe Arg  
65 70 75 80

00000000 101300



(B) LOCATION: 1..499

(D) OTHER INFORMATION: / Ceres Seq. ID 1601351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2538:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| ggaccgcacc | cgctgtagcc  | gccatgtcgt | ccgccgcgcg | cacagccttt | gccggagtct | 60  |
| ccgtcgccac | cccgaaacctc | accactccat | ttcgcggtcg | cgtgcgcctt | ccgctacgcg | 120 |
| gggtctccgc | tgcaccaagc  | cgcgcgcgtc | cttcgatggc | cgtgtccgcc | cccaggtccg | 180 |
| gcgcgcgcgc | ctcgttcttg  | gagcgccgcg | agtcgcgagc | cgctctccac | ttcgtcaagt | 240 |
| accagggcct | cggcaatgac  | ttcattatgg | tggacaacag | ggattcgtcg | gtgccgaagg | 300 |
| tgacgccgga | ggaggcgcgc  | aagctgtgcg | accgaaactt | cggcattggg | gccgacggcg | 360 |
| tcatcttcgt | catgccaggg  | gtcaatgatg | ccgactacac | catgaggatc | ttcaactctg | 420 |
| acggcagcga | gccagagatg  | tgtggtaatg | gagtcgcgtt | ctttgctcgg | tttataggcg | 480 |
| aacttgaaaa | atctgcagg   |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1601352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2539:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Ala | Pro | Ala | Val | Ala | Ala | Met | Ser | Ser | Ala | Ala | Ala | Thr | Ala | Phe |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Ala | Gly | Val | Ser | Val | Ala | Thr | Pro | Asn | Leu | Thr | Thr | Pro | Phe | Arg | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg | Val | Arg | Leu | Pro | Leu | Arg | Gly | Val | Ser | Ala | Ala | Pro | Arg | Arg | Ala |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Ala | Ser | Met | Ala | Val | Ser | Ala | Pro | Arg | Ser | Gly | Ala | Ala | Ala | Ser |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Phe | Leu | Glu | Arg | Arg | Glu | Ser | Glu | Arg | Ala | Leu | His | Phe | Val | Lys | Tyr |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Gln | Gly | Leu | Gly | Asn | Asp | Phe | Ile | Met | Val | Asp | Asn | Arg | Asp | Ser | Ser |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Val | Pro | Lys | Val | Thr | Pro | Glu | Glu | Ala | Lys | Leu | Cys | Asp | Arg | Asn |     |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |  |
| Phe | Gly | Ile | Gly | Ala | Asp | Gly | Val | Ile | Phe | Val | Met | Pro | Gly | Val | Asn |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Asp | Ala | Asp | Tyr | Thr | Met | Arg | Ile | Phe | Asn | Ser | Asp | Gly | Ser | Glu | Pro |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |  |
| Glu | Met | Cys | Gly | Asn | Gly | Val | Arg | Cys | Phe | Ala | Arg | Phe | Ile | Gly | Glu |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Leu | Glu | Lys | Ser | Ala |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2540:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1601353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2540:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Ser | Ala | Ala | Ala | Thr | Ala | Phe | Ala | Gly | Val | Ser | Val | Ala | Thr |  |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |  |
| Pro | Asn | Leu | Thr | Thr | Pro | Phe | Arg | Gly | Arg | Val | Arg | Leu | Pro | Leu | Arg |  |







- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 119 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..119  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1601380  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2548:

Leu Ser Ile Thr Ser Gly Gln Pro Asn Pro Thr Gln Pro Thr Thr Ala  
1                    5                    10                    15  
Val Pro Pro Arg Ser Pro Val Pro Thr Ala Asp Arg Leu Leu Leu Leu  
                    20                    25                    30  
Leu Ser Pro Arg His Pro Arg Gly Ile Thr Gly Ala Ala Thr Ser Leu  
                    35                    40                    45  
Arg Arg Lys Pro Ala Pro Ala Pro Asp Pro Met Ala Asn Ser Asn Leu  
                    50                    55                    60  
Pro Arg Arg Ile Ile Lys Glu Thr Gln Arg Leu Leu Ser Glu Pro Ala  
65                    70                    75                    80  
Pro Gly Ile Xaa Ala Ser Pro Ser Glu Glu Asn Xaa Arg Tyr Phe Asn  
                    85                    90                    95  
Val Met Ile Leu Gly Pro Ala Gln Ser Xaa Tyr Glu Gly Gly Val Phe  
                    100                    105                    110  
Lys Leu Glu Leu Xaa Phe Thr  
                    115

(2) INFORMATION FOR SEQ ID NO:2549:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 61 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..61  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1601381  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2549:

Met Ala Asn Ser Asn Leu Pro Arg Arg Ile Ile Lys Glu Thr Gln Arg  
1                    5                    10                    15  
Leu Leu Ser Glu Pro Ala Pro Gly Ile Xaa Ala Ser Pro Ser Glu Glu  
                    20                    25                    30  
Asn Xaa Arg Tyr Phe Asn Val Met Ile Leu Gly Pro Ala Gln Ser Xaa  
                    35                    40                    45  
Tyr Glu Gly Gly Val Phe Lys Leu Glu Leu Xaa Phe Thr  
                    50                    55                    60

(2) INFORMATION FOR SEQ ID NO:2550:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 484 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..484  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1601386  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2550:

gtcatccgcg cgccgaggat cttctaccca gccatcaacg ccctcctcca tcaacggaag 60  
gtggccgagg atccgccccca ccctcctccc cagcgcgctg tcgatggaag gtgcgatctc 120

00000000 101300





|            |            |            |            |            |            |           |            |            |           |            |           |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----------|------------|------------|-----------|------------|-----------|------------|------------|------------|-----|
| His<br>1   | Pro        | Arg        | Ala        | Glu<br>5   | Asp        | Leu       | Leu        | Pro        | Ser<br>10 | His        | Gln       | Arg        | Pro        | Pro<br>15  | Pro |
| Ser        | Thr        | Glu        | Gly<br>20  | Gly        | Arg        | Gly       | Ser        | Ala<br>25  | Pro       | Pro        | Ser       | Ser        | Pro<br>30  | Arg        | Arg |
| Arg        | Arg        | Trp<br>35  | Lys        | Val        | Arg        | Ser       | Pro<br>40  | Thr        | Pro       | Leu        | Leu       | His<br>45  | His        | Gln        | Arg |
| Pro        | Pro<br>50  | Pro        | Ser        | Pro        | Ser        | Ile<br>55 | Val        | Ala        | Ala       | Pro        | Pro<br>60 | Pro        | His        | His        | Val |
| Ser<br>65  | Gln        | Thr        | Arg        | Arg        | Ser<br>70  | Glu       | Asp        | Pro        | Pro       | Ser<br>75  | Thr       | Pro        | Arg        | Pro<br>80  | Pro |
| Ser        | Ser        | Pro        | Ser        | Ala<br>85  | Pro        | Arg       | Arg        | Gln<br>90  | Gly       | Ser        | Glu       | Ala        | Ala<br>95  | Ile        | Asn |
| Ala        | Leu        | Leu        | Pro<br>100 | Thr        | Pro        | Ser       | Met        | Ala<br>105 | Arg       | Ala        | Asp       | Pro        | Val<br>110 | Ser        | Phe |
| Arg        | Gln        | His<br>115 | Arg        | Ala        | Ile        | Ser       | Gly<br>120 | Ile        | Ser       | Phe        | Arg       | His<br>125 | Gln        | Gln        | Lys |
| Val        | Leu<br>130 | Arg        | Ile        | Leu        | Gly<br>135 | Lys       | Gln        | Glu        | Arg       | Gly<br>140 | Arg       | Gly<br>145 | Gly        | Gln        | Gly |
| His<br>145 | Asn        | Arg        | Glu        | Ala<br>150 | Asn        | Ser       | Ser        | Asn        | Pro       | Val<br>155 | Pro       | Ser        | Val        | Gly<br>160 | Arg |

|            |            |             |            |            |             |     |
|------------|------------|-------------|------------|------------|-------------|-----|
| aagaaaaaac | attcttttgc | ctctttctcct | ccgctcccca | tttctcttgc | taggggtttct | 60  |
| accctccat  | atcctcgtct | cacgggtcatg | gcgaagacga | agcagggaaa | taaggacgtg  | 120 |
| gattcgtaca | ccatcggcgg | caccaacaag  | gtcgtctatg | tgggagactg | cgtgctgatg  | 180 |
| cggcgctcgg | actcggacaa | ccagccgtat  | gtggcgcggg | tggagaagat | ggagggcgac  | 240 |
| ggcgct     |            |             |            |            |             |     |

(B) LOCATION: 1..82



(A) NAME/KEY: -  
(B) LOCATION: 1..401  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601400

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| cgcaccaaga | accagcatga | agccactggg | ggcgcgctg  | ctcctctgct | actcctgct  | 60  |
| ctggctggcg | cccgcggcag | ccccgctacg | cctgcagcac | gatcatgtcc | ggggccacgg | 120 |
| ccacggccat | gcccacccgc | ctccgtacgc | gcgtaacgcg | acggcgtagc | gcgtctcggc | 180 |
| ggcgctgtgc | ccgggctgcg | gcgcggtggc | ggacgcgctc | gagttcctct | actaccacaa | 240 |
| cctggtgctg | ctggcgctgc | tggagccgcg | gctggcgctg | tccccgcgcc | tggcgctgta | 300 |
| cgcggtctgg | tggggcggcg | agccgcggcg | ggactgcgcg | ctgcgccact | ccttccccga | 360 |
| cggccagttc | gcgctcgggg | agaacgtctt | ctggggcggg | c          |            |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(A) NAME/KEY: peptide  
(B) LOCATION: 1..133  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601401

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(A) NAME/KEY: peptide  
(B) LOCATION: 1..128  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601402

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Pro | Leu | Val | Ala | Arg | Leu | Leu | Leu | Cys | Tyr | Ser | Leu | Leu | Trp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ala | Pro | Ala | Ala | Ala | Pro | Leu | Arg | Leu | Gln | His | Asp | His | Val | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | His | Gly | His | Gly | His | Ala | His | Pro | Pro | Pro | Tyr | Ala | Arg | Asn | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Ala | Tyr | Gly | Val | Ser | Ala | Ala | Leu | Cys | Pro | Gly | Cys | Gly | Ala | Trp |



- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..130
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601409
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2563:

Ile Tyr Val Thr Asp Val Gly Gln Gln Gln His Phe Asp Met Phe Phe  
1 5 10 15  
Ser Ala Ala Lys Met Ala Gly Trp Leu Pro Gly Pro Asn Glu Lys Lys  
20 25 30  
Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Val Leu Gly Ser Asp  
35 40 45  
Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg Leu Val Glu  
50 55 60  
Leu Leu Asp Glu Ala Lys Ser Arg Ser Lys Ser Glu Leu Leu Gln Arg  
65 70 75 80  
Leu Thr Glu Asn Gly Lys Ile Val Asp Trp Thr Asp Glu Glu Leu Glu  
85 90 95  
Gln Thr Ser Glu Ala Val Gly Tyr Gly Ala Val Lys Tyr Ala Asp Leu  
100 105 110  
Lys Asn Asn Arg Leu Thr Asn Tyr Thr Phe Ser Phe Glu Gln Ile Ala  
115 120 125  
Glu Arg  
130

(2) INFORMATION FOR SEQ ID NO:2564:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 117 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2564:

Met Phe Phe Ser Ala Ala Lys Met Ala Gly Trp Leu Pro Gly Pro Asn  
1 5 10 15  
Glu Lys Lys Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Val Leu  
20 25 30  
Gly Ser Asp Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg  
35 40 45  
Leu Val Glu Leu Leu Asp Glu Ala Lys Ser Arg Ser Lys Ser Glu Leu  
50 55 60  
Leu Gln Arg Leu Thr Glu Asn Gly Lys Ile Val Asp Trp Thr Asp Glu  
65 70 75 80  
Glu Leu Glu Gln Thr Ser Glu Ala Val Gly Tyr Gly Ala Val Lys Tyr  
85 90 95  
Ala Asp Leu Lys Asn Asn Arg Leu Thr Asn Tyr Thr Phe Ser Phe Glu  
100 105 110  
Gln Ile Ala Glu Arg  
115

(2) INFORMATION FOR SEQ ID NO:2565:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 110 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

00569980 101300

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..110  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1601411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2565:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Trp | Leu | Pro | Gly | Pro | Asn | Glu | Lys | Lys | Phe | Pro | Lys | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | His | Val | Gly | Phe | Gly | Leu | Val | Leu | Gly | Ser | Asp | Gly | Lys | Arg | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Thr | Arg | Ser | Thr | Glu | Val | Val | Arg | Leu | Val | Glu | Leu | Leu | Asp | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Lys | Ser | Arg | Ser | Lys | Ser | Glu | Leu | Leu | Gln | Arg | Leu | Thr | Glu | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gly | Lys | Ile | Val | Asp | Trp | Thr | Asp | Glu | Glu | Leu | Glu | Gln | Thr | Ser | Glu |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Ala | Val | Gly | Tyr | Gly | Ala | Val | Lys | Tyr | Ala | Asp | Leu | Lys | Asn | Asn | Arg |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Thr | Asn | Tyr | Thr | Phe | Ser | Phe | Glu | Gln | Ile | Ala | Glu | Arg |     |     |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:2566:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 363 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..363  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1601416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2566:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| accaggcacc | agcatagatc | tctgtctcgc | cactattatt | ctgcacagca | acgcatcagc | 60  |
| cttctggaac | catctcgccg | ccgccacacc | acaatccaca | acccgtcgaa | gcgaagcaag | 120 |
| caatggccgg | agtcggatcg | aaggccctcg | ccgttgccgc | cgttctggcg | gccgtctcct | 180 |
| tctcggtggc | cgccgcggcc | gaggcgccc  | cgcccagccc | cgtctccgcc | gccgtcgccg | 240 |
| cgtegtcgcc | cttcgcgcgc | gctctcgtcg | cctccgcgcg | cgccttcctc | ttcgccgcgc | 300 |
| tccgcactga | gccgatgggg | cctcgtgcct | gcaggctacc | tagcagtact | tccccgcgcg | 360 |

(2) INFORMATION FOR SEQ ID NO:2567:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 121 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..121  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1601417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2567:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Arg | His | Gln | His | Arg | Ser | Arg | Ala | Arg | His | Tyr | Tyr | Ser | Ala | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gln | Arg | Ile | Ser | Leu | Leu | Glu | Pro | Ser | Arg | Arg | Arg | His | Thr | Thr | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Asn | Pro | Ser | Lys | Arg | Ser | Lys | Gln | Trp | Pro | Glu | Ser | Asp | Arg | Arg |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Pro | Ser | Pro | Leu | Pro | Pro | Phe | Trp | Arg | Pro | Ser | Pro | Ser | Arg | Trp | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Arg | Pro | Arg | Arg | Pro | Arg | Pro | Ala | Pro | Ser | Pro | Pro | Pro | Ser | Arg |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |







(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2572:

Thr Ala Pro Arg Leu Gln Tyr Gln Gln Ser Arg Ala Gly Gln Ile Tyr  
1 5 10 15  
Arg Asp Pro Arg His Arg Gly Glu Arg Asp Arg His Gly Gly Gly Ala  
20 25 30  
Gly Thr Arg Pro Val Leu Arg Gln Arg Pro Ala Glu Ala Thr Leu Leu  
35 40 45  
Pro Gly Arg Pro Arg Gly Pro Ala Gly Val Arg His Arg Pro Ala Pro  
50 55 60  
Arg Leu Gly Ala Arg Gly Ala Leu Val His Gly Arg Leu Arg Arg Glu  
65 70 75 80  
Ala Pro Pro Pro Ala Gly Pro His Arg Gly Leu His Arg Gln Ala Pro  
85 90 95  
Pro Pro Arg Ala Pro Arg Cys Gln Gly Gln Asp Gln Gly Pro Leu Arg  
100 105 110  
Trp Pro Arg Ala Arg Leu Ala Val Pro Ala Arg Leu Arg Gly Arg Gly  
115 120 125  
Gly Gly Gly Gly Gly Ala Gly Ala Gly Ala Arg Arg Arg Arg Gly  
130 135 140  
Leu Glu Arg Val Arg Arg Val Gly Gly Gly Gly Gly Arg Ala Leu  
145 150 155 160  
Ala Ala Ile Val

(2) INFORMATION FOR SEQ ID NO:2573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2573:

Met Val Val Ala Leu Gly Pro Gly Arg Phe Tyr Gly Ser Gly Leu Pro  
1 5 10 15  
Arg Pro Arg Phe Phe Pro Gly Asp Arg Val Asp Pro Pro Ala Ser Val  
20 25 30  
Thr Asp Pro Leu Leu Asp Trp Ala Arg Glu Ala His Trp Ser Met Gly  
35 40 45  
Gly Phe Gly Val Lys Arg Leu Arg Leu Gln Gly Arg Ile Glu Gly Ser  
50 55 60  
Ile Asp Lys Leu Arg Arg Arg Ala Arg Arg Asp Ala Arg Ala Lys Thr  
65 70 75 80  
Lys Ala Arg Ser Ala Gly His Val Pro Ala Ser Leu Ser Pro Leu Gly  
85 90 95  
Ser Glu Asp Glu Ala Glu Glu Val Ala Ala Pro Glu Arg Gly Leu Val  
100 105 110  
Val Asp Asp Val Gly Ser Asn Gly Ser Asp Glu Ser Glu Gly Glu Glu  
115 120 125  
Glu Asp Glu Pro Ser Leu Leu Ser  
130 135

(2) INFORMATION FOR SEQ ID NO:2574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

DOCKET "08669960

- (A) NAME/KEY: -  
(B) LOCATION: 1..454  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2574:

|                                       |            |            |            |             |            |     |
|---------------------------------------|------------|------------|------------|-------------|------------|-----|
| cttaaccgca                            | tcataccttc | cctcgcgccg | ccgccaacgc | aacccttgca  | gccccaatcc | 60  |
| ctcacagcaa                            | ccatggctgg | cgcgcaggag | tccctctctc | tggtggggcac | gatgcgcggc | 120 |
| cacaacggcg                            | aggtgacggc | gacgcgcacc | ccgatcgaca | actcgccggt  | catcgtttcc | 180 |
| tcctcccgcg                            | acaagtccct | scgtgtgtgg | gacctgacca | acccggtcca  | ctccaccccg | 240 |
| gaatccggcg                            | ccaccgcgga | ctacggcgtc | cccttcggcc | gcctcaccgg  | ccactcccac | 300 |
| ttcgccagg                             | acgtcgctct | cagttccgac | ggccagttcg | ccctttccgg  | ctcctgggat | 360 |
| ggagagctcc                            | gcctctggga | cctctccacc | ggcctcacca | cccgcgcgtt  | cgtcggccac | 420 |
| gagaaggatg tcctctccgt tgccttctcc gttg |            |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..151  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2575:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Asn | Arg | Ile | Ile | Leu | Ser | Leu | Ala | Pro | Pro | Pro | Thr | Gln | Pro | Leu |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Gln | Pro | Gln | Ser | Leu | Thr | Ala | Thr | Met | Ala | Gly | Ala | Gln | Glu | Ser | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Leu | Val | Gly | Thr | Met | Arg | Gly | His | Asn | Gly | Glu | Val | Thr | Ala | Ile |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Ala | Thr | Pro | Ile | Asp | Asn | Ser | Pro | Phe | Ile | Val | Ser | Ser | Ser | Arg | Asp |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Lys | Ser | Xaa | Leu | Val | Trp | Asp | Leu | Thr | Asn | Pro | Val | His | Ser | Thr | Pro |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Glu | Ser | Gly | Ala | Thr | Ala | Asp | Tyr | Gly | Val | Pro | Phe | Arg | Arg | Leu | Thr |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Gly | His | Ser | His | Phe | Val | Gln | Asp | Val | Val | Leu | Ser | Ser | Asp | Gly | Gln |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Phe | Ala | Leu | Ser | Gly | Ser | Trp | Asp | Gly | Glu | Leu | Arg | Leu | Trp | Asp | Leu |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Ser | Thr | Gly | Leu | Thr | Thr | Arg | Arg | Phe | Val | Gly | His | Glu | Lys | Asp | Val |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Leu | Ser | Val | Ala | Phe | Ser | Val |     |     |     |     |     |     |     |     |     |  |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..127  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2576:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Gly | Ala | Gln | Glu | Ser | Leu | Ser | Leu | Val | Gly | Thr | Met | Arg | Gly |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| His | Asn | Gly | Glu | Val | Thr | Ala | Ile | Ala | Thr | Pro | Ile | Asp | Asn | Ser | Pro |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Phe | Ile | Val | Ser | Ser | Ser | Arg | Asp | Lys | Ser | Xaa | Leu | Val | Trp | Asp | Leu |  |

DOCKET# 08668960

35 40 45  
Thr Asn Pro Val His Ser Thr Pro Glu Ser Gly Ala Thr Ala Asp Tyr  
50 55 60  
Gly Val Pro Phe Arg Arg Leu Thr Gly His Ser His Phe Val Gln Asp  
65 70 75 80  
Val Val Leu Ser Ser Asp Gly Gln Phe Ala Leu Ser Gly Ser Trp Asp  
85 90 95  
Gly Glu Leu Arg Leu Trp Asp Leu Ser Thr Gly Leu Thr Thr Arg Arg  
100 105 110  
Phe Val Gly His Glu Lys Asp Val Leu Ser Val Ala Phe Ser Val  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1601427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2577:

Met Arg Gly His Asn Gly Glu Val Thr Ala Ile Ala Thr Pro Ile Asp  
1 5 10 15  
Asn Ser Pro Phe Ile Val Ser Ser Ser Arg Asp Lys Ser Xaa Leu Val  
20 25 30  
Trp Asp Leu Thr Asn Pro Val His Ser Thr Pro Glu Ser Gly Ala Thr  
35 40 45  
Ala Asp Tyr Gly Val Pro Phe Arg Arg Leu Thr Gly His Ser His Phe  
50 55 60  
Val Gln Asp Val Val Leu Ser Ser Asp Gly Gln Phe Ala Leu Ser Gly  
65 70 75 80  
Ser Trp Asp Gly Glu Leu Arg Leu Trp Asp Leu Ser Thr Gly Leu Thr  
85 90 95  
Thr Arg Arg Phe Val Gly His Glu Lys Asp Val Leu Ser Val Ala Phe  
100 105 110  
Ser Val

(2) INFORMATION FOR SEQ ID NO:2578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..292

(D) OTHER INFORMATION: / Ceres Seq. ID 1601428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2578:

atccgaagtt ccgaacccaa gccaagcccc aggggtccgac cgcagaaccg acccaaaatg 60  
tcgcccgcct gctccatgct caccaccgcg tcgctctcct ccccgctccc agccccgcgc 120  
ctccgcgcgc ccgcgcgcctt cgctccgcgc cgccgcgcgc cagtcacact cgtcgtgcgc 180  
gcggcgtccg catcttccaa gtcccctgcc acggcggagg cggccccgaa gaagaagagg 240  
gcgaccggca tcaccagcc gaagtccgtg tcgcccgcgc tgcaggcaat cg

(2) INFORMATION FOR SEQ ID NO:2579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:





(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1601447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2584:

```
Met Ala Leu Thr Ser Arg Ala Leu Val Gly Lys Pro Ala Thr Ser Thr
 1 5 10 15
Arg Asp Val Phe Gly Glu Gly Arg Ile Thr Met Arg Lys Thr Ala Gly
 20 25 30
Lys Pro Lys Pro Ala Ala Ser Gly Ser Pro Trp Tyr Gly Ala Asp Arg
 35 40 45
Val Leu Tyr Leu Gly Pro Cys Pro Ala Ser Pro Gln Ala Thr
 50 55 60
```

(2) INFORMATION FOR SEQ ID NO:2585:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..37

(D) OTHER INFORMATION: / Ceres Seq. ID 1601448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2585:

```
Met Leu Gly Ala Leu Gly Cys Val Phe Pro Glu Leu Leu Ala Arg Asn
 1 5 10 15
Gly Val Lys Phe Gly Glu Ala Val Trp Phe Lys Ala Gly Ser Arg Ser
 20 25 30
Ser Ala Arg Ala Gly
 35
```

(2) INFORMATION FOR SEQ ID NO:2586:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 499 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..499

(D) OTHER INFORMATION: / Ceres Seq. ID 1601453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2586:

```
aaaaaacctt atcgccctc ccgcgcagcc accagcgaag cagcggggca cgcggacgag 60
ccgagcgagg cggaggcgga gagatggcgc gcggcggtgt ggctggggcg aagggtggtg 120
cgcccggcgg cggcggaag aagaagggtt ccgtcacgtt cacgatcgac tgcaccaagc 180
ccgtcgagga caagatcatg gagatcgcca cgctcgagaa gttcctgcag gagcgcatca 240
aggtcgctgg aggcaaggcc ggccagctcg gcgaggcggt caccgtcacc cgcgataagt 300
ccaaggtcac cgtcacctcc gacgggcctt tctctaagag gtacctgaaa tacttgacca 360
agaagtacct gaagaagcac aatgtgctgt actggctccg agttgtagcg gcaagcaagg 420
accgcagtgt astatgagct acggtacttc aacattgctg agaacgagga ggaataggcg 480
gcttagacct tatagacgc
```

(2) INFORMATION FOR SEQ ID NO:2587:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

00689980 08668960







| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2393: |             |             |             |            |            |     |
|--------------------------------------------|-------------|-------------|-------------|------------|------------|-----|
| gttttctgga                                 | ggcttctctgc | gcgtaggagag | acgggagaaac | gaagcagcag | cagcagcagg | 60  |
| cgccatccgc                                 | tcgttctctt  | ccccccaccg  | ccagcgtcgc  | ctctccgtgt | gcgcgccccg | 120 |
| ccgggggttg                                 | cgtaactgca  | ccctttggga  | gcgggcgcct  | acctacctac | gtgcgggggg | 180 |
| agccacacgc                                 | ctccctctcg  | ctctttggca  | tggacgccgg  | cggagagaag | tgcggcgaac | 240 |
| cggcggcgga                                 | gggcggggag  | ggtggcggag  | acctctacgc  | ggttctcggg | ctcaagaagg | 300 |
| agtgcctcca                                 | cgccgagctt  | aaggtcgctt  | accggaagct  | cgccaagaaa | tggcaccocg | 360 |

acaaatgctc gtcctccagc agcgtgaagc acatggagga agccaaggag aagttccaag 420  
agatccaggg cgctattcc gtactctccg acgccaataa acggctcctc tacgatgtgg 480  
gagt

(2) INFORMATION FOR SEQ ID NO:2594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2594:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Trp | Arg | Leu | Pro | Ala | Arg | Gly | Glu | Thr | Gly | Glu | Arg | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ser | Ser | Arg | Arg | His | Pro | Leu | Ala | Ser | Phe | Pro | Pro | Pro | Pro | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Pro | Leu | Arg | Val | Arg | Ala | Pro | Gly | Val | Ala | Ser | Leu | His | Pro |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Trp | Ala | Ala | Gly | Ala | Tyr | Leu | Pro | Thr | Cys | Gly | Gly | Ser | His | Thr | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Ser | Arg | Leu | Leu | Ala | Trp | Thr | Pro | Ala | Glu | Arg | Ser | Ala | Ala | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Arg | Arg | Arg | Ala | Gly | Arg | Val | Ala | Glu | Thr | Ser | Thr | Arg | Phe | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Ser | Arg | Arg | Ser | Ala | Pro | Thr | Pro | Ser | Leu | Arg | Ser | Leu | Thr | Gly |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Ser | Pro | Arg | Asn | Gly | Thr | Arg | Thr | Asn | Ala | Arg | Pro | Pro | Ala | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2595:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ser | Gly | Gly | Phe | Leu | Arg | Val | Glu | Arg | Glu | Asn | Glu | Ala | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ala | Ala | Gly | Ala | Ile | Arg | Ser | Leu | Pro | Ser | Pro | His | Arg | Gln |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Arg | Leu | Ser | Val | Cys | Ala | Pro | Arg | Arg | Gly | Trp | Arg | His | Cys | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Gly | Gln | Arg | Ala | His | Thr | Tyr | Leu | Arg | Ala | Gly | Gly | Ala | Thr | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Pro | Leu | Ala | Ser | Trp | His | Gly | Arg | Arg | Arg | Arg | Glu | Val | Arg | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Gly | Gly | Gly | Arg | Gly | Gly | Trp | Arg | Arg | Pro | Leu | Arg | Gly | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Gln | Glu | Gly | Val | Leu | Arg | Arg | Arg | Ala |     |     |     |     |     |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2596:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..160  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1601479  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2596:  
Phe Leu Glu Ala Ser Cys Ala Trp Arg Asp Gly Arg Thr Lys Gln Gln  
1                  5                  10                  15  
Gln Gln Gln Ala Pro Ser Ala Arg Phe Leu Pro Pro Thr Ala Ser Val  
                  20                  25                  30  
Ala Ser Pro Cys Ala Arg Pro Ala Gly Gly Gly Val Thr Ala Pro Leu  
                  35                  40                  45  
Gly Ser Gly Arg Ile Pro Thr Tyr Val Arg Gly Glu Pro His Ala Ser  
50                  55                  60  
Leu Ser Pro Leu Gly Met Asp Ala Gly Gly Glu Lys Cys Gly Asp Ala  
65                  70                  75                  80  
Ala Ala Glu Gly Gly Glu Gly Gly Gly Asp Leu Tyr Ala Val Leu Gly  
                  85                  90                  95  
Leu Lys Lys Glu Cys Ser Asp Ala Glu Leu Lys Val Ala Tyr Arg Lys  
                  100                  105                  110  
Leu Ala Lys Lys Trp His Pro Asp Lys Cys Ser Ser Ser Ser Ser Val  
                  115                  120                  125  
Lys His Met Glu Glu Ala Lys Glu Lys Phe Gln Glu Ile Gln Gly Ala  
130                  135                  140  
Tyr Ser Val Leu Ser Asp Ala Asn Lys Arg Leu Leu Tyr Asp Val Gly  
145                  150                  155                  160

(2) INFORMATION FOR SEQ ID NO:2597:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 491 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..491  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1601480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2597:

```
acgtagtaag ctgggattct tcgtatagac cggattaaaa ccctaggccc tagccaccgc 60
ccaccgtcgc ctcagcaaat cctcctcccg tttcaccatg ccgccctgct gctcccccac 120
cacctccgcc gtcaccgctg cggcggcacg tcccggcgcc tcgcgcagcg ggggcctcct 180
gcgcgcgctc cgcccagccc ccgccgcggt gaattgtaaa aagattgatt ctctgaggtc 240
aatcaatgga gcaccacctt gcattccggt gtccaacagg tcgttattga ctctgtaac 300
cttgccagtt ttccgggatc caaacatgag gaacgacacg aggctgcgca tcttctcagg 360
cacagccaat ccttcctttt ccaggagat agcaagttac ttggggctag aacttgggaa 420
gataaccata aagaggtttg ctgatggtga aatatatgtt cagttgcaag aaagtgtacg 480
gggctgtgat g
```

(2) INFORMATION FOR SEQ ID NO:2598:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 131 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

00669980 "10300

(A) NAME/KEY: peptide  
(B) LOCATION: 1..131  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2598:

Met Pro Pro Cys Cys Ser Pro Thr Thr Ser Ala Val Thr Ala Ala Ala  
1 5 10 15  
Ala Ser Pro Gly Ala Ser Arg Ser Gly Gly Leu Leu Arg Arg Ser Arg  
20 25 30  
Pro Ala Pro Ala Ala Val Asn Cys Lys Lys Ile Asp Ser Leu Arg Ser  
35 40 45  
Ile Asn Gly Ala Pro Pro Cys Ile Pro Val Ser Asn Arg Ser Leu Leu  
50 55 60  
Thr Pro Val Thr Leu Pro Val Phe Arg Asp Pro Asn Met Arg Asn Asp  
65 70 75 80  
Thr Arg Leu Arg Ile Phe Ser Gly Thr Ala Asn Pro Ser Leu Ser Gln  
85 90 95  
Glu Ile Ala Ser Tyr Leu Gly Leu Glu Leu Gly Lys Ile Thr Ile Lys  
100 105 110  
Arg Phe Ala Asp Gly Glu Ile Tyr Val Gln Leu Gln Glu Ser Val Arg  
115 120 125  
Gly Cys Asp  
130

(2) INFORMATION FOR SEQ ID NO:2599:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 408 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..408  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2599:

aatctactcc tccattctcc accgcgcccc aacctcgaag agttccgaag tttccacacc 60  
ctcaaagcga agcagcatga gttccaccgg aggcagcggc cgtgggaagg cgaagccagc 120  
gaccaagtct gtgtcgcggt cttccaaggc tgggctccag ttcccgcgtcg gccgcacgcg 180  
gcggtacctc aaggccggca agtaacggga gcgcgtaggc gccggggctc ccgtgtacct 240  
ctccgcgctc ctcgagtacc tcgcgcgcga ggtgctggag ctggccggga acgctgctcg 300  
ggacaacaag aagaaccgga tcgtgccgcg ccacattcag ctggcgggtg ggaacgacga 360  
ggagctgagc aagcttctgg gcactgtgac gatcgcggcc gccggcgt

(2) INFORMATION FOR SEQ ID NO:2600:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..136  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601484

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2600:

Asn Leu Leu Leu His Ser Pro Pro Arg Pro Asn Leu Glu Glu Phe Arg  
1 5 10 15  
Ser Phe His Thr Leu Lys Ala Lys Gln His Glu Phe His Arg Arg Gln  
20 25 30  
Arg Pro Trp Glu Gly Glu Ala Ser Asp Gln Val Cys Val Ala Val Phe  
35 40 45  
Gln Gly Trp Ala Pro Val Pro Arg Arg Pro His Arg Ala Val Pro Gln  
50 55 60

00000000 101400



(2) INFORMATION FOR SEQ ID NO:2603:

(A) LENGTH: 482 base pairs

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(D) OTHER INFORMATION: / Ceres Seq. ID 1601495

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| acacgatcaa | aaacaaaacc  | aagctccaag | caccatagc  | cacacaccac | accaagtcaa  | 60  |
| gcaaggagct | cgatcgacag  | caacaacggc | catcatgaac | tccagcttca | tcgggctcaa  | 120 |
| gcccgtctcg | gcagcagccc  | aggccaccgc | ggctgcctcg | tcgccgatga | agcagcagca  | 180 |
| ggtgcaggtc | gcgcccaga   | gccgcgcgc  | cgctgtgtc  | ggcctggcgg | ccgtcttcgc  | 240 |
| cgtcaccgcc | accacggccg  | gatcagccaa | ggctggggtc | ttcgacgagt | acctcgagaa  | 300 |
| gagcaaggct | aacaaggagc  | tgaacgacaa | gaagaggatg | gccaccagcg | ctgccaaactt | 360 |
| tgcgcgcgcc | tacacagtcg  | agttcggcag | ctgccagttc | ccctacaact | tactgggtg   | 420 |
| ccaggacctc | gccaaagcaga | agaaagtccc | tttcttcagc | gacgacctcg | agatcgagtg  | 480 |
| cc         |             |            |            |            |             |     |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1601496

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Asp | Gln | Lys | Gln | Asn | Gln | Ala | Pro | Ser | Thr | His | Ser | His | Thr | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Gln | Val | Lys | Gln | Gly | Ala | Arg | Ser | Thr | Ala | Thr | Thr | Ala | Ile | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Ser | Ser | Phe | Ile | Gly | Leu | Lys | Pro | Ala | Ala | Ala | Ala | Ala | Gln | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Thr | Ala | Ala | Ala | Ser | Ser | Pro | Met | Lys | Gln | Gln | Gln | Val | Gln | Val | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Gln | Ser | Arg | Arg | Ala | Ala | Leu | Leu | Gly | Leu | Ala | Ala | Val | Phe | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Thr | Ala | Thr | Thr | Ala | Gly | Ser | Ala | Lys | Ala | Gly | Val | Phe | Asp | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Leu | Glu | Lys | Ser | Lys | Ala | Asn | Lys | Glu | Leu | Asn | Asp | Lys | Lys | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Met | Ala | Thr | Ser | Ala | Ala | Asn | Phe | Ala | Arg | Ala | Tyr | Thr | Val | Glu | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Ser | Cys | Gln | Phe | Pro | Tyr | Asn | Phe | Thr | Gly | Cys | Gln | Asp | Leu | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Gln | Lys | Lys | Val | Pro | Phe | Leu | Ser | Asp | Asp | Leu | Glu | Ile | Glu | Cys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

(2) INFORMATION FOR SEO ID NO:2605:







- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 539 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..539  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1601502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2610:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aaaccctcat | ttttctctct | ctgcgccgc  | gacgtccctc | gccttcgccg | ccgaatccga | 60  |
| gactccgata | tcgggttcac | cgcagcgcac | agagcagcct | cgactcccgg | cccgatccgc | 120 |
| gctctcctct | ccgtcgcttc | agtcattgca | ggaatggcac | ctgaggggtc | tcagttcgat | 180 |
| gctaagcact | atgattctaa | gatgcaggag | ctgctgagca | ccggtgagac | tgaggagttc | 240 |
| ttcacttcat | atgatgaagt | ttttgagagt | tttgatgata | tgggcctcca | agagaatctt | 300 |
| ctgagaggca | tttatgctta | tgttttgag  | aagccatctg | caattcagca | gagaggaatt | 360 |
| gttcccttct | gcaagggctc | tgatgtcatt | cagcaagcac | aatctggtac | aggaaagaca | 420 |
| gcaaccttct | gttctgggat | cttgacagag | ctggactatg | gcctggttga | atgccaggcc | 480 |
| ctggtccttg | ctcccacccc | gtgagcttgc | acagcaaata | gagaaagta  | tgcgcgcg   |     |

(2) INFORMATION FOR SEQ ID NO:2611:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 167 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..167  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1601503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2611:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Pro | Ser | Phe | Phe | Ser | Leu | Leu | Arg | Arg | Asp | Val | Pro | Arg | Leu | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Arg | Ile | Arg | Asp | Ser | Asp | Leu | Gly | Phe | Thr | Ala | Ala | His | Arg | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ser | Thr | Pro | Gly | Pro | Ile | Arg | Ala | Leu | Leu | Ser | Val | Ala | Ser | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Met | Ala | Gly | Met | Ala | Pro | Glu | Gly | Ser | Gln | Phe | Asp | Ala | Lys | His | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asp | Ser | Lys | Met | Gln | Glu | Leu | Leu | Ser | Thr | Gly | Glu | Thr | Glu | Glu | Phe |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |     |
| Phe | Thr | Ser | Tyr | Asp | Glu | Val | Phe | Glu | Ser | Phe | Asp | Asp | Met | Gly | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gln | Glu | Asn | Leu | Leu | Arg | Gly | Ile | Tyr | Ala | Tyr | Gly | Phe | Glu | Lys | Pro |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ser | Ala | Ile | Gln | Gln | Arg | Gly | Ile | Val | Pro | Phe | Cys | Lys | Gly | Leu | Asp |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Val | Ile | Gln | Gln | Ala | Gln | Ser | Gly | Thr | Gly | Lys | Thr | Ala | Thr | Phe | Cys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Gly | Ile | Leu | Gln | Gln | Leu | Asp | Tyr | Gly | Leu | Val | Glu | Cys | Gln | Ala |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Val | Leu | Ala | Pro | Thr | Pro |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2612:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 119 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2612:

Met Ala Gly Met Ala Pro Glu Gly Ser Gln Phe Asp Ala Lys His Tyr  
1 5 10 15  
Asp Ser Lys Met Gln Glu Leu Leu Ser Thr Gly Glu Thr Glu Glu Phe  
20 25 30  
Phe Thr Ser Tyr Asp Glu Val Phe Glu Ser Phe Asp Asp Met Gly Leu  
35 40 45  
Gln Glu Asn Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro  
50 55 60  
Ser Ala Ile Gln Gln Arg Gly Ile Val Pro Phe Cys Lys Gly Leu Asp  
65 70 75 80  
Val Ile Gln Gln Ala Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Cys  
85 90 95  
Ser Gly Ile Leu Gln Gln Leu Asp Tyr Gly Leu Val Glu Cys Gln Ala  
100 105 110  
Leu Val Leu Ala Pro Thr Pro  
115

(2) INFORMATION FOR SEQ ID NO:2613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2613:

Met Ala Pro Glu Gly Ser Gln Phe Asp Ala Lys His Tyr Asp Ser Lys  
1 5 10 15  
Met Gln Glu Leu Leu Ser Thr Gly Glu Thr Glu Glu Phe Phe Thr Ser  
20 25 30  
Tyr Asp Glu Val Phe Glu Ser Phe Asp Asp Met Gly Leu Gln Glu Asn  
35 40 45  
Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro Ser Ala Ile  
50 55 60  
Gln Gln Arg Gly Ile Val Pro Phe Cys Lys Gly Leu Asp Val Ile Gln  
65 70 75 80  
Gln Ala Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Cys Ser Gly Ile  
85 90 95  
Leu Gln Gln Leu Asp Tyr Gly Leu Val Glu Cys Gln Ala Leu Val Leu  
100 105 110  
Ala Pro Thr Pro  
115

(2) INFORMATION FOR SEQ ID NO:2614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..472
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2614:

00669990-101300







(2) INFORMATION FOR SEQ ID NO:2622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2622:

Met Val Asn Val Pro Lys Thr Lys Lys Thr Tyr Cys Lys Asn Lys Glu  
1 5 10 15  
Cys Arg Lys His Thr Leu His Lys Val Thr Gln Tyr Lys Lys Gly Lys  
20 25 30  
Asp Ser Leu Ser Ala Gln Gly Lys Arg Arg Tyr Asp Arg Lys Gln Ser  
35 40 45  
Gly Tyr Gly Gly Gln Thr Lys Pro Val Phe His Lys Lys Ala Lys Thr  
50 55 60  
Thr Lys Lys Ile Val Leu Lys Leu Gln Cys Gln Ser Cys Lys His Tyr  
65 70 75 80  
Ser Gln His Pro Ile Lys Arg Cys Lys His Phe Glu Ile Gly Gly Asp  
85 90 95  
Lys Lys Gly Lys Gly Thr Ser Leu Phe  
100 105

(2) INFORMATION FOR SEQ ID NO:2623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..382
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2623:

agaacatcct aatcgaacac caatggcatt cttgcattga aggaaccttc cctccacctc 60  
caccgcccga gagcgagcgg ccggacgggg ttttggttg gcattggctgc cccggcgatg 120  
ctccaagtgg tgatcctcgc cgcggctctc cttctcccg tctcagcgt gccggcgcc 180  
gaggcacaga ccaagaagtt ctgcctcacg cagttcgcca tcgctagcca ggcctgcgcc 240  
atcctgccac ccaccagtcc tgagcaccac caccatcatc acgatgacga ggacaatgac 300  
gaggacaacg acgaagatga ggacgaagac gaggacaacg atgaagatga agacgaggac 360  
aatgacgacg atagcggcgg tg

(2) INFORMATION FOR SEQ ID NO:2624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2624:

Asn Ile Leu Ile Glu His Gln Trp His Ser Cys Ile Glu Gly Thr Phe  
1 5 10 15  
Pro Pro Pro Pro Pro Pro Glu Ser Glu Arg Pro Asp Gly Val Leu Val

00669980 "101400"



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gln | Tyr | Cys | Cys | Ala | Leu | Ala | Val | Ala | Leu | Ala | Leu | Pro | Leu | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Gln | His | Ala | Thr | Ala | Ala | Ala | Ala | Pro | Pro | Arg | Ala | Arg | Ile | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Cys | Asp | Leu | Ala | Arg | Gly | Tyr | Arg | Gly | Trp | Cys | Ala | Cys | Ser | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Arg | Glu | Ala | Pro | Arg | Asp | Gly | Arg | Gly | Arg | Arg | Arg | Arg | Cys | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |



(2) INFORMATION FOR SEQ ID NO:2630:

(A) LENGTH: 109 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(A) NAME/KEY: peptide  
(B) LOCATION: 1..109

| Met | Ala | Gly | Gly | Gly | Gly | Gly | Gly | Ala | Ala | Pro | Lys | His | Asp | Asp | Phe |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Pro | His | Pro | Val | Lys | Asp | Gln | Leu | Pro | Gly | Val | Ser | Tyr | Cys | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ser | Pro | Pro | Pro | Trp | Pro | Glu | Ala | Val | Leu | Leu | Gly | Phe | Gln | His |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Tyr | Leu | Val | Met | Leu | Gly | Thr | Thr | Val | Ile | Ile | Pro | Thr | Ala | Leu | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Gln | Met | Gly | Gly | Asn | Asn | Glu | Asp | Lys | Ala | Val | Val | Ile | Gln | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Leu | Phe | Val | Ala | Gly | Ile | Asn | Thr | Leu | Leu | Gln | Ser | Phe | Phe | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Met | Leu | Pro | Ala | Val | Ile | Gly | Gly | Ser | Tyr | Thr | Phe |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(A) LENGTH: 423 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

| (x1) SEQUENCE DESCRIPTION: SEQ ID NO:1001 |            |            |             |            |            |  |     |  |
|-------------------------------------------|------------|------------|-------------|------------|------------|--|-----|--|
| atccatctat                                | ccatcatcac | cagctagcac | ctcctttcc   | acgactccc  | agcgtctgc  |  | 60  |  |
| gtgtggcgcg                                | cggcagcatg | gcgactgcga | acggggagcag | caaggggtcg | ttcgaggtgc |  | 120 |  |
| ccaaggtgga                                | ggtcaggttc | accaagctct | tcatcgacgg  | caagttcgtc | gacgcgctct |  | 180 |  |
| ccggcaagac                                | gttcgagacc | cgggacctc  | gcaccggcga  | ggtgatcgcc | agcatcgcg  |  | 240 |  |
| agggagacaa                                | ggccgacgtc | gacctcgccg | tcaaggccgc  | ccgggaggcc | ttcgacaacg |  | 300 |  |
| ggccctggcc                                | caggatgacg | ggatacgagc | gtggtcggat  | ctccacacgg | ttcgcgacc  |  | 360 |  |
| tgatcgacga                                | gcacgtggag | gagctggcgg | cgctggacac  | ggtggacgcc | ggcaagctgt |  | 420 |  |
| tcg                                       |            |            |             |            |            |  |     |  |

(A) LENGTH: 140 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(D) OTHER INFORMATION: / Ceres Seq. ID 1601541

| (X1) SEQUENCE DESCRIPTION |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser                       | Ile | Tyr | Pro | Ser | Ser | Pro | Ala | Ser | Thr | Ser | Phe | Pro | Thr | Thr | Pro |
| 1                         |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu                       | Arg | Ser | Ala | Cys | Gly | Ala | Arg | Gln | His | Gly | Asp | Cys | Glu | Arg | Glu |
|                           |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln                       | Gln | Gly | Val | Val | Arg | Gly | Ala | Gln | Gly | Gly | Gly | Gln | Val | His | Gln |
|                           |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ala                       | Leu | His | Arg | Arg | Gln | Val | Arg | Arg | Arg | Arg | Leu | Arg | Gln | Asp | Val |
|                           | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg                       | Asp | Pro | Gly | Pro | Ser | His | Arg | Arg | Gly | Asp | Arg | Gln | His | Arg | Gly |
| 65                        |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Gly                       | Arg | Gln | Gly | Arg | Arg | Arg | Pro | Arg | Arg | Gln | Gly | Arg | Pro | Gly | Gly |
|                           |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu                       | Arg | Gln | Arg | Ala | Leu | Ala | Gln | Asp | Asp | Gly | Ile | Arg | Ala | Trp | Ser |
|                           |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Asp                       | Pro | Pro | Gln | Val | Arg | Gly | Pro | Asp | Arg | Arg | Ala | Arg | Gly | Gly | Ala |
|                           |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly                       | Gly | Ala | Gly | His | Gly | Gly | Arg | Arg | Gln | Ala | Val |     |     |     |     |
|                           | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..140  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601542

| SEQUENCE DESCRIPTION: 522 12 100 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|----------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Pro                              | Ser | Ile | His | His | His | Gln | Leu | Ala | Pro | Pro | Phe | Pro | Arg | Leu | Pro |  |
| 1                                |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser                              | Ala | Leu | Arg | Val | Ala | Arg | Gly | Ser | Met | Ala | Thr | Ala | Asn | Gly | Ser |  |
|                                  |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser                              | Lys | Gly | Ser | Phe | Glu | Val | Pro | Lys | Val | Glu | Val | Arg | Phe | Thr | Lys |  |
|                                  |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Leu                              | Phe | Ile | Asp | Gly | Lys | Phe | Val | Asp | Ala | Val | Ser | Gly | Lys | Thr | Phe |  |
|                                  | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Glu                              | Thr | Arg | Asp | Pro | Arg | Thr | Gly | Glu | Val | Ile | Ala | Ser | Ile | Ala | Glu |  |
| 65                               |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Gly                              | Asp | Lys | Ala | Asp | Val | Asp | Leu | Ala | Val | Lys | Ala | Ala | Arg | Glu | Ala |  |
|                                  |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Phe                              | Asp | Asn | Gly | Pro | Trp | Pro | Arg | Met | Thr | Gly | Tyr | Glu | Arg | Gly | Arg |  |
|                                  |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ile                              | Leu | His | Arg | Phe | Ala | Asp | Leu | Ile | Asp | Glu | His | Val | Glu | Glu | Leu |  |
|                                  |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ala                              | Ala | Leu | Asp | Thr | Val | Asp | Ala | Gly | Lys | Leu | Phe |     |     |     |     |  |
|                                  | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |  |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..115  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2634:

[illegible]

| (A1) SEQUENCE DESCRIPTION: 221-11 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu                               | Pro | Phe | Arg | Pro | Leu | Leu | Gln | Ser | Ser | Pro | Ser | Leu | Ser | Pro | Pro |  |
| 1                                 |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Pro                               | Ser | Gln | Pro | Glu | Gly | Arg | Gly | Arg | Lys | Ala | Met | Pro | Cys | Cys | Gln |  |
|                                   |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Thr                               | Val | Leu | Ser | Ala | Ala | Ala | Ala | Ala | Ala | Ala | Ser | Arg | Thr | Pro | Ser |  |
|                                   |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Trp                               | Leu | His | Arg | Leu | His | Ala | Lys | Gly | Gly | Leu | Ser | Phe | Pro | Ser | His |  |
|                                   | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |  |
| Leu                               | Asn | Ile | Asp | Asp | Leu | Leu | Tyr | Gly | Gly | Arg | Gln | Ala | Gln | Thr | Pro |  |
| 65                                |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Pro                               | Pro | Pro | Pro | Ser | Pro | Leu | Pro | Pro | Ser | Ser | Ser | Asn | Asp | His | Asn |  |
|                                   |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Asp                               | Leu | Val | Val | Val | Val | Arg | Glu | Ser | Pro | Thr | Lys | Ala | Ala | Ala | Lys |  |

[illegible]

100 105 110  
Pro Lys Pro Pro Pro Ala Ala Gln Arg Pro Pro Arg Asn Pro Ser Arg  
115 120 125  
Pro Asn Pro Ser Ser Ser Asn Ser Ser Gln Pro Pro Pro Gln Pro Gln  
130 135 140  
Leu Gln Leu Val Ala Val Ile Ser Asp Val Phe Ala Val  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1601549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2637:

Phe Leu Phe Val Leu Phe Ser Ser Arg Pro Pro Val Ser Val His His  
1 5 10 15  
Arg Arg Ser Arg Arg Gly Glu Asp Gly Arg Gln Cys Arg Ala Ala Arg  
20 25 30  
Leu Cys Ser Val Pro Arg Arg Pro Pro Pro Pro Ala Glu Arg Arg His  
35 40 45  
Gly Ser Ile Gly Cys Thr Pro Lys Gly Val Tyr Pro Ser Pro Pro Thr  
50 55 60  
Ser Thr Leu Thr Thr Ser Ser Thr Gly Ala Asp Arg Pro Lys Leu Pro  
65 70 75 80  
Leu Pro Leu Pro Arg Pro Cys His Leu Leu Pro Met Ile Thr Thr  
85 90 95  
Thr Ser Ser Leu Leu Ser Gly Ser Arg Leu Gln Arg Pro Pro Leu Ser  
100 105 110  
Pro Ser Arg Arg Arg Arg Leu Ser Val Arg Pro Ala Thr Leu Arg Asp  
115 120 125  
Gln Thr Leu Ala Leu Ala Ile Pro Arg Ser Arg Arg Arg Asn His Ser  
130 135 140  
Phe Ser Ser Leu Pro  
145

(2) INFORMATION FOR SEQ ID NO:2638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1601550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2638:

Met Pro Cys Cys Gln Thr Val Leu Ser Ala Ala Ala Ala Ala Ala  
1 5 10 15  
Ser Arg Thr Pro Ser Trp Leu His Arg Leu His Ala Lys Gly Gly Leu  
20 25 30  
Ser Phe Pro Ser His Leu Asn Ile Asp Asp Leu Leu Tyr Gly Gly Arg  
35 40 45  
Gln Ala Gln Thr Pro Pro Pro Pro Pro Ser Pro Leu Pro Pro Ser Ser  
50 55 60  
Ser Asn Asp His Asn Asp Leu Val Val Val Val Arg Glu Ser Pro Thr  
65 70 75 80

DOCKET "08668860"

Lys Ala Ala Ala Lys Pro Lys Pro Pro Pro Ala Ala Gln Arg Pro Pro  
85 90 95  
Arg Asn Pro Ser Arg Pro Asn Pro Ser Ser Asn Ser Ser Gln Pro  
100 105 110  
Pro Pro Gln Pro Gln Leu Gln Leu Val Ala Val Ile Ser Asp Val Phe  
115 120 125  
Ala Val  
130

(2) INFORMATION FOR SEQ ID NO:2639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..485
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2639:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| cgcccactcc | cagaggctct | tctcctcctc | gcctcctctc | cctagcctcc | acgacgcaag | 60  |
| ggagagtgc  | ggaagcgac  | gcggcgcgag | cgaggagggc | caaggggaag | aggggaagca | 120 |
| cgcaccagg  | acccttggtc | gcgcgcgcgc | cctctgatct | ccgcgagggt | gtcaggattc | 180 |
| aatatgtcg  | ccagcacatt | cgctacttcc | tgcacgctgt | tgggcaatgt | tagaacaacg | 240 |
| caggcctccc | agacagcggg | gaagagccct | tcgtctctaa | gcttcttcag | ccaagttacg | 300 |
| aaggttccaa | gcctgaagac | ctccaagaaa | ctggatgtct | ccgccatggc | tgtataaca  | 360 |
| gtgaagcttg | tcgggcctga | aggtgaagag | cacgagtttg | atgctccaga | cgacgcctac | 420 |
| atccttgacg | cagccgagac | tgcggtgtgg | agttgccata | ctcgtgccgt | gctggggcct | 480 |
| gytcc      |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2640:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | His | Ser | Gln | Arg | Leu | Phe | Ser | Ser | Ser | Pro | Pro | Leu | Pro | Ser | Leu |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| His | Asp | Ala | Arg | Glu | Ser | Asp | Gly | Lys | Arg | Arg | Gly | Ala | Ser | Glu | Glu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Gln | Gly | Glu | Glu | Gly | Lys | His | Arg | Thr | Arg | Thr | Leu | Val | Arg | Arg |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Arg | Arg | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 50  |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2641:

DOCKET "08663960"

Pro Thr Pro Arg Gly Ser Ser Pro Pro Arg Leu Leu Ser Leu Ala Ser  
1 5 10 15  
Thr Thr Gln Gly Arg Val Thr Glu Ser Asp Ala Ala Arg Ala Arg Arg  
20 25 30  
Ala Lys Gly Lys Arg Gly Ser Thr Ala Pro Gly Pro Leu Phe Ala Ala  
35 40 45  
Ala Ala Ser Asp Leu Arg Glu Val Val Arg Ile Gln Tyr Val Asp Gln  
50 55 60  
His Ile Arg Tyr Phe Leu His Ala Val Gly Gln Cys  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2642:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1601562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2642:

Met Ser Thr Ser Thr Phe Ala Thr Ser Cys Thr Leu Leu Gly Asn Val  
1 5 10 15  
Arg Thr Thr Gln Ala Ser Gln Thr Ala Val Lys Ser Pro Ser Ser Leu  
20 25 30  
Ser Phe Phe Ser Gln Val Thr Lys Val Pro Ser Leu Lys Thr Ser Lys  
35 40 45  
Lys Leu Asp Val Ser Ala Met Ala Val Tyr Lys Val Lys Leu Val Gly  
50 55 60  
Pro Glu Gly Glu Glu His Glu Phe Asp Ala Pro Asp Asp Ala Tyr Ile  
65 70 75 80  
Leu Asp Ala Ala Glu Thr Ala Val Trp Ser Cys His Thr Arg Ala Val  
85 90 95  
Leu Gly Leu

(2) INFORMATION FOR SEQ ID NO:2643:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..437

(D) OTHER INFORMATION: / Ceres Seq. ID 1601567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2643:

acacataacc agcacacagc tctcgcttc tctctcccat cggcacaccc gagctcgctc 60  
cctccttcca cgtcgaggtc cgagtcctgc tttgatggcg accgacgtgg ctgagactcc 120  
cgcgccgttg gtggatgcgg cccagaggc gcccgccgta cgccgagatg gtctcgagg 180  
cgatcacgtc gctcaaggag aggacggggt ccagcagcta tgcgattgcc aagttcgtgg 240  
aggacaagca caaggacaag ctcccgcca acttccgcaa gttctgaac gttcagctca 300  
agaagctcgt cgccggcggc aagctgacca aggtgaagaa ctcgtaacag ctgtcgctccg 360  
ccgccaccaa gccgaatccc aagcccaagg ccgccccgaa gaagcccaag accggcgcta 420  
agaagccaag gccgctg

(2) INFORMATION FOR SEQ ID NO:2644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..139  
(D) OTHER INFORMATION: / Ceres Seq. ID 1601568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2644:

His Ile Thr Ser Thr Gln Leu Ser Pro Ser Leu Ser His Arg His Thr  
1                  5                  10                  15  
Arg Ala Arg Ser Leu Leu Pro Arg Arg Gly Pro Ser Pro Ala Leu Met  
                  20                  25                  30  
Ala Thr Asp Val Ala Glu Thr Pro Ala Pro Leu Val Asp Ala Ala Pro  
                  35                  40                  45  
Glu Ala Pro Ala Val Arg Arg Asp Gly Leu Gly Gly Asp His Val Ala  
50                  55                  60  
Gln Gly Glu Asp Gly Val Gln Gln Leu Cys Asp Cys Gln Val Arg Gly  
65                  70                  75                  80  
Gly Gln Ala Gln Gly Gln Ala Pro Ala Gln Leu Pro Gln Ala Ser Glu  
                  85                  90                  95  
Arg Ser Ala Gln Glu Ala Arg Arg Arg Gln Ala Asp Gln Gly Glu  
                  100                 105                 110  
Glu Leu Val Gln Ala Val Val Arg Arg His Gln Ala Glu Ser Gln Ala  
115                 120                 125  
Gln Gly Arg Pro Glu Glu Ala Gln Asp Arg Arg  
130                 135

(2) INFORMATION FOR SEQ ID NO:2645:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 108 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..108  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1601569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2645:

Met Ala Thr Asp Val Ala Glu Thr Pro Ala Pro Leu Val Asp Ala Ala  
1                  5                  10                  15  
Pro Glu Ala Pro Ala Val Arg Arg Asp Gly Leu Gly Gly Asp His Val  
                  20                  25                  30  
Ala Gln Gly Glu Asp Gly Val Gln Gln Leu Cys Asp Cys Gln Val Arg  
35                  40                  45  
Gly Gly Gln Ala Gln Gly Gln Ala Pro Ala Gln Leu Pro Gln Ala Ser  
50                  55                  60  
Glu Arg Ser Ala Gln Glu Ala Arg Arg Arg Arg Gln Ala Asp Gln Gly  
65                  70                  75                  80  
Glu Glu Leu Val Gln Ala Val Val Arg Arg His Gln Ala Glu Ser Gln  
                  85                  90                  95  
Ala Gln Gly Arg Pro Glu Glu Ala Gln Asp Arg Arg  
100                 105

(2) INFORMATION FOR SEQ ID NO:2646:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 101 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..101

00669980 101300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2646:

(2) INFORMATION FOR SEQ ID NO:2647:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2647:

(2) INFORMATION FOR SEQ ID NO:2648:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2648:

| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val                                       | Lys | Ala | Glu | Ser | Ala | Pro | Pro | Arg | Ala | Val | Leu | Phe | Gly | Ser | Pro |  |
| 1                                         |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Leu                                       | Pro | Ser | Pro | Arg | Arg | Arg | Arg | Asn | Pro | Gln | Met | Glu | Val | Val | Val |  |
|                                           |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ala                                       | Ala | Lys | Gln | Lys | Ala | Lys | Lys | His | Ile | His | Leu | Phe | Tyr | Cys | Ser |  |
|                                           |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Glu                                       | Cys | Glu | Glu | Leu | Ala | Leu | Lys | Ile | Ala | Ala | Ser | Ser | Asp | Ala | Ile |  |
|                                           | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Glu                                       | Leu | Gln | Ser | Ile | Asn | Trp | Arg | Ser | Phe | Asp | Asp | Gly | Phe | Pro | Asn |  |
| 65                                        |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Leu                                       | Phe | Ile | Asn | Lys | Ala | His | Asp | Ile | Arg | Gly | Gln | His | Val | Ala | Phe |  |
|                                           |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |



Leu Ala Ser Phe Ser Ser Pro Ser Val Ile Phe Glu Gln Ile Ser Val  
100 105 110  
Ile Phe Ala Leu Pro Lys Leu Phe Ile Ala Ser Phe Thr Leu Val Leu  
115 120 125  
Pro Phe Phe Pro Thr Gly Ser Phe Glu Arg Val Glu Glu Glu Gly Asp  
130 135 140  
Val Ala Thr Ala Phe Thr Leu Ala Arg Ile Leu Ser Xaa Ile Pro Lys  
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:2649:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1601573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2649:

Ser Lys Gln Ser Leu Pro Leu Pro Ala Pro Phe Phe Leu Val Pro His  
1 5 10 15  
Ser Pro Val Pro Ala Ala Ala Glu Thr Arg Arg Trp Arg Ser Ser Ser  
20 25 30  
Pro Arg Ser Arg Arg Arg Arg Asn Thr Tyr Thr Ser Ser Thr Ala Gln  
35 40 45  
Asn Ala Arg Ser Ser Pro Leu Arg Ser Pro Pro Ala Pro Thr Pro Ser  
50 55 60  
Ser Ser Asn Pro Ser Thr Gly Gly Ala Ser Thr Thr Gly Ser Arg Thr  
65 70 75 80  
Cys Ser Ser Thr Arg Arg Thr Thr Ser Val Gly Ser Thr Trp Arg Ser  
85 90 95  
Trp Pro Pro Ser Ala Arg Arg Arg Ser Tyr Ser Ser Arg Ser Pro Ser  
100 105 110  
Ser Ser Arg Cys Pro Ser Tyr Ser Leu Pro His Ser Leu Ser Cys Cys  
115 120 125  
Leu Ser Ser Pro Arg Ala His Ser Ser Ala Leu Arg Arg Arg Ala Met  
130 135 140  
Ser Pro Pro Arg Ser Pro Ser Arg Ala Phe Ser Arg Xaa Ser Pro Ser  
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:2650:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1601574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2650:

Met Glu Val Val Val Ala Ala Lys Gln Lys Ala Lys Lys His Ile His  
1 5 10 15  
Leu Phe Tyr Cys Ser Glu Cys Glu Glu Leu Ala Leu Lys Ile Ala Ala  
20 25 30  
Ser Ser Asp Ala Ile Glu Leu Gln Ser Ile Asn Trp Arg Ser Phe Asp

00669990 03669990

(i) SEQUENCE CHARACTERISTICS:

| General information |                                                                                                                                                                                                                                           |
|---------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Study ID            | 1001                                                                                                                                                                                                                                      |
| Study title         | Investigation of the effects of a new drug on blood pressure                                                                                                                                                                              |
| Study type          | Randomized controlled trial                                                                                                                                                                                                               |
| Study location      | University Hospital, Department of Medicine                                                                                                                                                                                               |
| Study dates         | January 2018 to December 2019                                                                                                                                                                                                             |
| Study population    | Adults aged 18-75 with hypertension                                                                                                                                                                                                       |
| Study objectives    | To evaluate the efficacy and safety of the new drug compared to the standard treatment.                                                                                                                                                   |
| Study design        | Parallel, randomized, double-blind, placebo-controlled trial                                                                                                                                                                              |
| Study arms          | Experimental group (New Drug) and Control group (Standard Treatment)                                                                                                                                                                      |
| Study outcomes      | Primary outcome: Change in systolic blood pressure. Secondary outcomes: Change in diastolic blood pressure, adverse effects, and patient satisfaction.                                                                                    |
| Study results       | The experimental group showed a significantly greater reduction in systolic blood pressure compared to the control group. No significant differences were observed in diastolic blood pressure, adverse effects, or patient satisfaction. |
| Study conclusions   | The new drug is effective in reducing systolic blood pressure in adults with hypertension. Further studies are needed to evaluate its long-term safety and efficacy.                                                                      |
| Study limitations   | Short duration of the study, limited sample size, and potential bias due to self-reporting of outcomes.                                                                                                                                   |
| Study funding       | Grants from the National Institutes of Health and the pharmaceutical company.                                                                                                                                                             |
| Study ethics        | The study was approved by the Institutional Review Board and all participants gave informed consent.                                                                                                                                      |
| Study registration  | Registered at ClinicalTrials.gov (NCT03456789)                                                                                                                                                                                            |
| Study contact       | Dr. John Doe, Principal Investigator, Email: john.doe@university.edu                                                                                                                                                                      |

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..83
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601577
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2653:

Met Gly Gln Asn Leu Ala Leu Asn Ile Ala Glu Lys Gly Phe Pro Ile  
1 5 10 15  
Ser Val Tyr Asn Arg Thr Thr Ser Lys Val Asp Glu Thr Val Gln Arg  
20 25 30  
Ala Lys Ala Glu Gly Asn Leu Pro Val Tyr Gly Phe His Asp Pro Ala  
35 40 45  
Ser Phe Val Asn Ser Ile Gln Lys Pro Arg Val Val Ile Met Leu Val  
50 55 60  
Lys Ala Gly Ala Pro Val Asp Gln Thr Ser Arg Arg Ser Gln Leu Thr  
65 70 75 80  
Trp Ser Arg

- (2) INFORMATION FOR SEQ ID NO:2654:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 490 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..490
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601582
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2654:

gcaacgycgt tgcttcaact cgactccage atccctcgtc cccgcatcac cgcgcgcgccg 60  
asactccgct cgctttcgct cccgagaccc gggcctgccg tagccgccgc catggacgag 120  
gagtacgacg tgatcgttct gggcacgggg ctcaaggagt gcatoctcag cggctctcctc 180  
ytctgtcgac ggctcaagg ttctacacat ggatagaaat gattactaog gaggagattc 240  
cacctcccta aacctgaacc ayctctggaa tgakgttttag ggggkaagac aagccaccgg 300  
cacatctagg tgcaagcaga gattacaatk tagacatggt tccaaagttt atgatggcaa 360  
acgggacttt ggttcgact ctcatcaca ctgatgtgac aaaatatttg tcattcaaag 420  
ctgttgatgg aagctatgtc tycagcaaac ggaagattca caaggttct gcnaccgata 480  
tggaggctct

- (2) INFORMATION FOR SEQ ID NO:2655:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 71 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..71
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1601583
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2655:

Ala Thr Xaa Leu Leu Gln Leu Asp Ser Ser Ile Pro Arg Pro Arg Ile  
1 5 10 15  
Thr Ala Pro Pro Xaa Leu Arg Ser Leu Ser Leu Pro Arg Pro Gly Pro  
20 25 30  
Ala Val Ala Ala Ala Met Asp Glu Tyr Asp Val Ile Val Leu Gly  
35 40 45

00E101" 08668960

(2) INFORMATION FOR SEQ ID NO:2656:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2656:

(2) INFORMATION FOR SEQ ID NO:2657:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2657:

(2) INFORMATION FOR SEQ ID NO:2658:

- ```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 492 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
    (A) NAME/KEY: -
    (B) LOCATION: 1..492
    (D) OTHER INFORMATION: / Ceres Seq. ID 1601586
```

(X1) SEQUENCE DESCRIPTION: SEQ ID NUMBER:						
ctcaggatga	atcggaagag	agaatcctac	caaacctagc	taccaactcg	atcgtcgtca	60
tcacgctcga	ccgcacaact	gcaccaaggg	gggaggagac	ctaaaaacta	ctacatcttt	120
tagctacaca	tctagctaaa	gatcgagagg	ggtaaaataag	gacgagcggg	cgcgagctag	180
aagagcagct	gcaggtacta	ccatcatcgt	cgtcgtcgtc	gccaggatga	ccgtcgtcga	240
cgccgtcgtc	tctctcaacg	atgccggcgc	ccctgctgcc	gccgccaccg	cgttaccggc	300
ggggaacggg	cagaccgtgt	gcgtgaccgg	cgcggccggg	tacatcgcc	cgtggttggt	360
gaagctgctg	ctcgagaagg	gatacactgt	gaagggcacc	gtcaggaacc	cagatgaccc	420
gaagaacgcg	cacctcaagg	cgctggacgg	cgccgccgag	cggctgatcc	tctgcaaggc	480
ccgatctgct	gg					

(i) SEQUENCE CHARACTERISTICS:

- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: / Ceres Seq. ID 1601587

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: / Ceres Seq. ID 1601596

(X1)	SEQUENCE	DESCRIPTION	SEQ ID NO	LENGTH		
acattccatc	ggtcgtgaaa	agaaaaaagg	aaacaaacca	agctagagaa	aagaagaagg	60
tactacatac	tagctagcta	gcttagctat	gggcaccatc	gtcgacgctg	acgtcgggtt	120
cgcggtgaag	aggacgagca	ggtcgtctgt	gccgcctgcg	tcggcgacgc	cgcgggagac	180
gctgcggctg	tcggtgatcg	accgcgtggc	ggggctgcgc	cacctggtgc	ggtcgttgca	240
cgtgttcgcc	gcggggcgcg	acaagaagcg	gcagcaggcg	acggcgacgc	cggccaaggc	300
gctgcgggag	gcgctgggga	aggcgctggt	ggactactac	ccgttcgcgg	ggcggttcgt	360
ggtggtggac	gcggagggcg	gcggggagac	gcgggtggcg	tgaccgcgcg	agggcgctcg	420
gttcgtggag	gccaacgcgc	cgtgtctcgt	cgaggaggcc	cgccacctcg	accaccccat	480
gctcat						

(i) SEQUENCE CHARACTERISTICS:

- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2661:

(2) INFORMATION FOR SEQ ID NO:2662:

(A) LENGTH: 381 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..381

(D) OTHER INFORMATION: / Ceres Seq. ID 1601598

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2662:

(2) INFORMATION FOR SEQ ID NO:2663:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1601599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2663:

Ile	Thr	Val	Ala	Ile	Thr	Thr	Pro	Leu	Leu	Ser	Leu	Ile	Gly	Ser	Asn
1				5					10					15	
Gly	Gly	Arg	Arg	Arg	Gln	Val	Pro	Ala	Ala	Arg	Arg	Arg	Gly	Ile	Pro
			20					25					30		
Gly	Cys	Leu	Asp	Leu	Leu	Pro	Leu	Leu	Pro	Arg	Arg	Arg	Arg	Arg	Arg
		35					40					45			

Arg Gly Arg Arg Gly Arg Xaa Ser Arg Ser Ser Ser Pro Ala Trp Ala
50 55 60
Ser Pro Ser Pro Val Gly Ser Pro Ser His Arg Asp Gly Thr Met Ala
65 70 75 80
Pro Tyr Gln Ser Pro Ser Arg Pro Met Ser Leu Ser Ala Val Met Arg
85 90 95
Val Pro Ala Arg Ser Arg Gly Arg Trp Arg Arg Arg Arg Leu Gly Arg
100 105 110
Trp Met

(2) INFORMATION FOR SEQ ID NO:2664:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1601600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2664:

Ser Pro Ser Pro Ser Leu Pro Leu Ser Ser Leu Ser Ser Ala Pro Met
1 5 10 15
Ala Asp Ala Asp Ala Lys Ser Gln Pro Pro Asp Ala Ala Ala Ser Pro
20 25 30
Asp Ala Ser Ile Ser Ser Pro Ser Ser Leu Gly Gly Gly Gly Asp
35 40 45
Ala Ala Asp Ala Asp Ala Xaa Arg Glu Ala Ala Arg Arg Pro Gly His
50 55 60
Arg Arg Arg Arg Trp Val Pro Arg Ala Ile Gly Met Gly Arg Trp Pro
65 70 75 80
Arg Thr Ser Pro His Pro Gly Arg Cys Pro Cys Arg Arg
85 90

(2) INFORMATION FOR SEQ ID NO:2665:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1601601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2665:

Met Ala Asp Ala Asp Ala Lys Ser Gln Pro Pro Asp Ala Ala Ala Ser
1 5 10 15
Pro Asp Ala Ser Ile Ser Ser Pro Ser Ser Leu Gly Gly Gly Gly Gly
20 25 30
Asp Ala Ala Asp Ala Asp Ala Xaa Arg Glu Ala Ala Arg Arg Pro Gly
35 40 45
His Arg Arg Arg Arg Trp Val Pro Arg Ala Ile Gly Met Gly Arg Trp
50 55 60
Pro Arg Thr Ser Pro His Pro Gly Arg Cys Pro Cys Arg Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:2666:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

09689900 101300

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..289
 (D) OTHER INFORMATION: / Ceres Seq. ID 1601602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2666:
ccccaaagcg gatcaaacc tagatctcgt cttgtcgccc cggttcctccg atcccatcct 60
atccgatcct catggattcc tccctmwgtcc agcctcagcc agcagcccga gttcgactac 120
ctcttcaagc tactycttat cggcgactcc ggcgtcggca agagcagcct cctcctccgc 180
ttcaccgccc actccttcga tgacctctcc cctaccatag gtgttgactt caaggtgaag 240
atggttagca ttggtggcaa aaaaaactca agcttgccat ctgggacac

(2) INFORMATION FOR SEQ ID NO:2667:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..96
 (D) OTHER INFORMATION: / Ceres Seq. ID 1601603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2667:

Pro Gln Ser Gly Ser Asn Pro Arg Ser Arg Leu Val Ala Pro Phe Leu
1 5 10 15
Arg Ser His Pro Ile Arg Ser Ser Trp Ile Pro Pro Xaa Ser Ser Leu
 20 25 30
Ser Gln Gln Pro Glu Phe Asp Tyr Leu Phe Lys Leu Xaa Leu Ile Gly
 35 40 45
Asp Ser Gly Val Gly Lys Ser Ser Leu Leu Leu Arg Phe Thr Ala Asp
 50 55 60
Ser Phe Asp Asp Leu Ser Pro Thr Ile Gly Val Asp Phe Lys Val Lys
65 70 75 80
Met Val Ser Ile Gly Gly Lys Lys Asn Ser Ser Leu Pro Ser Gly Thr
 85 90 95

(2) INFORMATION FOR SEQ ID NO:2668:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..72
 (D) OTHER INFORMATION: / Ceres Seq. ID 1601604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2668:

Pro Lys Ala Asp Gln Thr Leu Asp Leu Val Leu Ser Pro Arg Ser Ser
1 5 10 15
Asp Pro Ile Leu Ser Asp Pro His Gly Phe Leu Xaa Xaa Pro Ala Ser
 20 25 30
Ala Ser Ser Pro Ser Ser Thr Thr Ser Ser Ser Tyr Xaa Leu Ser Ala
 35 40 45
Thr Pro Ala Ser Ala Arg Ala Ala Ser Ser Ser Ala Ser Pro Pro Thr
 50 55 60
Pro Ser Met Thr Ser Pro Leu Pro
65 70

(2) INFORMATION FOR SEQ ID NO:2669:

00663900 101000

Gly Pro Ile Arg Gly Pro Arg His Arg Ala Arg Pro Trp Cys
65 70 75

(2) INFORMATION FOR SEQ ID NO:2675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1601611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2675:

Leu Asp Arg Ser Ser Gly Val Val Ser Gly Leu Ala Cys Arg Ser Leu
1 5 10 15
Leu Phe Ser Gly Ser Val Ala Arg Gln Arg Glu Gln Arg Arg Val Phe
20 25 30
Lys Pro Lys Thr Met Asp Pro Val Arg Lys Ser Val Cys Val Thr Gly
35 40 45
Ala Gly Gly Phe Val Ala Ser Glu Leu Val Lys Leu Leu Ser Arg
50 55 60
Gly Gln Tyr Ala Val Arg Gly Thr Val Arg Asp Pro Gly Ala Ser Lys
65 70 75 80
Asn Ala His Leu Lys Val Leu Glu Gly Ala Glu Glu Arg Leu Gln Leu
85 90 95
Leu Lys Ala Asp Leu Met Asp Tyr Asp Ser Ile Ala Ser Ala Val Ala
100 105 110
Gly Cys Glu Gly Val Phe His Val Ala Ser Pro Val Leu Ser His Arg
115 120 125
Pro Ser Asn Pro Glu Val Glu Val Ile Ala Pro Ala Val Ile Gly Thr
130 135 140
Thr Asn Val Leu Lys Ala Cys
145 150

(2) INFORMATION FOR SEQ ID NO:2676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1601612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2676:

Met Asp Pro Val Arg Lys Ser Val Cys Val Thr Gly Ala Gly Gly Phe
1 5 10 15
Val Ala Ser Glu Leu Val Lys Leu Leu Leu Ser Arg Gly Gln Tyr Ala
20 25 30
Val Arg Gly Thr Val Arg Asp Pro Gly Ala Ser Lys Asn Ala His Leu
35 40 45
Lys Val Leu Glu Gly Ala Glu Glu Arg Leu Gln Leu Lys Ala Asp
50 55 60
Leu Met Asp Tyr Asp Ser Ile Ala Ser Ala Val Ala Gly Cys Glu Gly
65 70 75 80
Val Phe His Val Ala Ser Pro Val Leu Ser His Arg Pro Ser Asn Pro
85 90 95
Glu Val Glu Val Ile Ala Pro Ala Val Ile Gly Thr Thr Asn Val Leu
100 105 110
Lys Ala Cys

00668980 104300

115

(2) INFORMATION FOR SEQ ID NO:2677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..513
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2677:

aataatctac tactaccgcc cccatggagg ccggggggca gttttctctc tcgctcgctc	60
tcgtctcgtc tcttccaaaa gctcgtatatt ttagctctcc ctagctctct ctctctctct	120
ctcacgacca agctctcgcc atggccaaaa gcacatgcaa gctatgctcc cgccgcttcg	180
ccagcccccg cgccctcgcc ggccacatgc gcgcccactc catggcctcc gcaaagtcgc	240
agatctcatc ggctcgtcg gcttcgacat ccatcacggc tagcggcatc gacgccgaca	300
agaagcgcgg ccccgctccg gggcacgcgc tgcgggagaa tcccaagcgc cgcgcccgcc	360
tcgacgactc ggatcgcgag agcgagacga cggactacta ctctccgctc cgggacgcca	420
agcgctcgca cgccggatcg ggggacgcgc agcccggtga gctcgggtctc cgacgcggcc	480
acgccggagg aggacgtcgc gctgtcyctg atg	

(2) INFORMATION FOR SEQ ID NO:2678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2678:

Asn Asn Leu Leu Leu Pro Pro Pro Trp Arg Pro Gly Gly Ser Phe Leu	
1 5 10 15	
Ser Arg Ser Leu Ser Ser Arg Leu Leu Gln Lys Leu Val Phe Leu Ala	
20 25 30	
Leu Pro Ser Ser Leu Ser Leu Ser Leu Thr Thr Lys Leu Ser Pro Trp	
35 40 45	
Pro Lys Ala His Ala Ser Tyr Ala Pro Ala Ala Ser Pro Ala Pro Ala	
50 55 60	
Pro Ser Pro Ala Thr Cys Ala Pro Thr Pro Trp Pro Pro Gln Ser Arg	
65 70 75 80	
Arg Ser His Arg Pro Arg Arg Leu Arg His Pro Ser Arg Leu Ala Ala	
85 90 95	
Ser Thr Pro Thr Arg Ser Ala Ala Pro Ser Gly Gly Thr Arg Cys Gly	
100 105 110	
Arg Ile Pro Ser Ala Ala Ala Ala Ser Thr Thr Arg Ile Ala Arg Ala	
115 120 125	
Arg Arg Arg Thr Thr Thr Leu Arg Arg Arg Thr Pro Ser Ala Arg Thr	
130 135 140	
Pro Asp Arg Gly Thr Arg Ser Pro Val Ser Ser Val Ser Asp Ala Ala	
145 150 155 160	
Thr Pro Glu Glu Asp Val Ala Leu Xaa Leu Met	
165 170	

(2) INFORMATION FOR SEQ ID NO:2679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

DOE FOR "03668960

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1601618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2679:

Met Ala Lys Ser Thr Cys Lys Leu Cys Ser Arg Arg Phe Ala Ser Pro
1 5 10 15
Arg Ala Leu Ala Gly His Met Arg Ala His Ser Met Ala Ser Ala Lys
20 25 30
Ser Gln Ile Ser Ser Ala Ser Ser Ala Ser Thr Ser Ile Thr Ala Ser
35 40 45
Gly Ile Asp Ala Asp Lys Lys Arg Gly Pro Val Arg Gly His Ala Leu
50 55 60
Arg Glu Asn Pro Lys Arg Arg Gly Arg Leu Asp Asp Ser Asp Arg Glu
65 70 75 80
Ser Glu Thr Thr Asp Tyr Tyr Ser Pro Ser Pro Asp Ala Lys Arg Ser
85 90 95
His Ala Gly Ser Gly Asp Ala Glu Pro Gly Glu Leu Gly Leu Arg Arg
100 105 110
Gly His Ala Gly Gly Gly Arg Arg Ala Val Xaa Asp
115 120

(2) INFORMATION FOR SEQ ID NO:2680:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1601619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2680:

Met Arg Ala His Ser Met Ala Ser Ala Lys Ser Gln Ile Ser Ser Ala
1 5 10 15
Ser Ser Ala Ser Thr Ser Ile Thr Ala Ser Gly Ile Asp Ala Asp Lys
20 25 30
Lys Arg Gly Pro Val Arg Gly His Ala Leu Arg Glu Asn Pro Lys Arg
35 40 45
Arg Gly Arg Leu Asp Asp Ser Asp Arg Glu Ser Glu Thr Thr Asp Tyr
50 55 60
Tyr Ser Pro Ser Pro Asp Ala Lys Arg Ser His Ala Gly Ser Gly Asp
65 70 75 80
Ala Glu Pro Gly Glu Leu Gly Leu Arg Arg Gly His Ala Gly Gly Gly
85 90 95
Arg Arg Ala Val Xaa Asp
100

(2) INFORMATION FOR SEQ ID NO:2681:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 413 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..413

(D) OTHER INFORMATION: / Ceres Seq. ID 1601636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2681:

DOCKET# 08558960

1 5 10 15
Ala Ala Ala Ala Asp Gly Gly Gly Asp Val Gly Ala Ala Ser Ala Arg
20 25 30
Arg Arg Arg Arg Leu Gly Arg Ala Thr Glu Gly Pro Ala Pro Thr Lys
35 40 45
Arg Ile Arg Ser Gly Ser Gln Arg Ser Pro Tyr Asp Ser Ser Leu Glu
50 55 60
Thr Ala Thr Asp Gly Cys Cys Trp Pro Ala Arg Leu Ser His Gly Ala
65 70 75 80
Val Ser Val Ile Gly Arg Arg Arg Glu Met Glu Asp Ala Phe Ala Val
85 90 95
Ala Leu Ser Phe Leu Ala Ser Glu Ala Val Gly Gly Glu Gln Glu Gln
100 105 110
Glu Leu Asp Phe Phe Ala Val Tyr Asp Gly His Gly Gly Ala Arg Val
115 120 125
Ala Glu Ala Cys Arg Glu Arg Ile Ala Arg Gly Ala
130 135 140

(2) INFORMATION FOR SEQ ID NO:2692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..409
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2692:

ctaattcgaaa aaaaacacga gcgagcacaa aaaaaaatc ccaatatccg caacggcaat	60
gtctccgctg cccgcacatg tgcctctcgc cgctcgccgc gccgcgcgcg cagcggtcac	120
ggcgtcagcc acgtcgctca ggggcgcggc gaacgacctt ctccccaagt acggcctccc	180
gaaggggctc atcccggaact cgcgcgcctc ctacagcttc gacgaggcca cgggcgcctt	240
cgagatccac ctgcgcggca cctgctacgt ccacttcggc tcccaacctg tctactacga	300
gaggaccata accggcaagc tctccaaggg cgccatctcg gacctctcgc gcgtccaggg	360
caagaaactc ttcctctggg tctacgtcac gggatggctg cgcacccccg	

(2) INFORMATION FOR SEQ ID NO:2693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2693:

Leu Ile Glu Lys Lys His Glu Arg Ala Gln Lys Lys Asn Pro Asn Ile
1 5 10 15
Arg Asn Gly Asn Val Ser Ala Ala Pro His Arg Ala Pro Arg Arg Arg
20 25 30
Arg Arg Arg Arg Arg Ser Gly His Gly Val Ser His Val Ala Gln Arg
35 40 45
Arg Gly Glu Arg Pro Thr Pro Gln Val Arg Pro Pro Glu Gly Ala His
50 55 60
Pro Gly Leu Arg Arg Leu Leu Gln Leu Arg Arg Gly His Gly Arg Leu
65 70 75 80
Arg Asp Pro Pro Arg Arg His Leu Leu Arg Pro Leu Arg Leu Pro Pro
85 90 95
Arg Leu Leu Arg Glu Asp His Asn Arg Gln Ala Leu Gln Gly Arg His

CONFIDENTIAL

100 105 110
Leu Gly Pro Leu Arg Arg Pro Gly Gln Glu Thr Leu Pro Leu Gly Leu
115 120 125
Arg His Gly Met Val Ala His Pro
130 135

(2) INFORMATION FOR SEQ ID NO:2694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2694:

Asn Arg Lys Lys Thr Arg Ala Ser Thr Lys Lys Lys Ser Gln Tyr Pro
1 5 10 15
Gln Arg Gln Cys Leu Arg Cys Pro Ala Ser Cys Ser Ser Pro Ser Pro
20 25 30
Pro Pro Pro Pro Gln Arg Ser Arg Arg Gln Pro Arg Arg Ser Ala Ala
35 40 45
Arg Arg Thr Thr Tyr Ser Pro Ser Thr Ala Ser Arg Arg Gly Ser Ser
50 55 60
Arg Thr Pro Ser Pro Pro Thr Ala Ser Thr Arg Pro Arg Ala Pro Ser
65 70 75 80
Arg Ser Thr Ser Pro Ala Pro Ala Thr Ser Thr Ser Ala Pro Thr Ser
85 90 95
Ser Thr Thr Arg Gly Pro
100

(2) INFORMATION FOR SEQ ID NO:2695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2695:

Met Ser Pro Leu Pro Arg Ile Val Leu Leu Ala Val Ala Ala Ala
1 5 10 15
Ala Ala Ala Val Thr Ala Ser Ala Thr Ser Leu Ser Gly Ala Ala Asn
20 25 30
Asp Leu Leu Pro Lys Tyr Gly Leu Pro Lys Gly Leu Ile Pro Asp Ser
35 40 45
Val Ala Ser Tyr Ser Phe Asp Glu Ala Thr Gly Ala Phe Glu Ile His
50 55 60
Leu Ala Gly Thr Cys Tyr Val His Phe Gly Ser His Leu Val Tyr Tyr
65 70 75 80
Glu Arg Thr Ile Thr Gly Lys Leu Ser Lys Gly Ala Ile Ser Asp Leu
85 90 95
Ser Gly Val Gln Ala Lys Lys Leu Phe Leu Trp Val Tyr Val Thr Gly
100 105 110
Trp Ser Arg Thr Pro
115

(2) INFORMATION FOR SEQ ID NO:2696:

(i) SEQUENCE CHARACTERISTICS:

1 5 10 15
Pro Gln Ser Ser Arg Leu Arg Gly Glu Asp Val Gly Ala Arg Gln Gly
20 25 30
Arg Gln Gly Pro Gly Gln Gly Arg Arg Glu Ala Ser Pro Glu Gly Ala
35 40 45
Ala Arg Gln His Pro Gly Asp His Glu Ala Gly Asp Pro Glu Ala Gly
50 55 60
Ala Ala Gly Arg Arg Glu Ala His Leu Gly Ala His Leu Arg Gly Asp
65 70 75 80
Pro Arg Arg Ala Gln Asp Leu Pro Gly Glu Arg His Pro Arg Arg Arg
85 90 95
His Leu His Arg Ala Arg Ala Pro
100

(2) INFORMATION FOR SEQ ID NO:2699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2699:

Met Ser Gly Arg Gly Lys Gly Gly Lys Gly Leu Gly Lys Gly Gly Ala
1 5 10 15
Lys Arg His Arg Lys Val Leu Arg Asp Asn Ile Gln Gly Ile Thr Lys
20 25 30
Pro Ala Ile Arg Arg Leu Ala Arg Arg Gly Gly Val Lys Arg Ile Ser
35 40 45
Gly Leu Ile Tyr Glu Glu Thr Arg Gly Val Leu Lys Ile Phe Leu Glu
50 55 60
Asn Val Ile Arg Asp Ala Val Thr Tyr Thr Glu His Ala Arg Arg Lys
65 70 75 80
Thr Val Thr Ala Met Asp Val Val Tyr Ala Leu Lys Arg Gln Gly Arg
85 90 95
Thr Leu Tyr Gly Phe Gly Gly
100

(2) INFORMATION FOR SEQ ID NO:2700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..440
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2700:

aagccgattt cgtgtccctg cagccacggc caccgccaat ctccaattct ttatcttctc 60
cgaggaaagt aggtcgagga tgccccgcag cggcttctcg gggtccttca ggtcgccc aa 120
gatcgacgtc gtcacgcaca tgggaaaccc cttcctcaac cgcaccgtcg acggcttcct 180
caagatcggc gccgtcgggc cctgcaaggt ggctgccgag gagaccttcg agtgcctcca 240
caggggggat gtttcgaagc acaaggttga gcatgccctg aggaagatgt gcaaggaggg 300
cgcatattgg ggcactgttg ctggagttta tgtgggcatg gtgtacggcg tggaaagggt 360
ccgtggccgc agtgactgga agaacgcgat gatcgggggc gccttgtcog gcgccctgat 420
ctccggcgcc agcaacagcg

(2) INFORMATION FOR SEQ ID NO:2701:

(i) SEQUENCE CHARACTERISTICS:

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..110
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2708:

Met Ala Lys Asn Tyr Pro Thr Val Ser Ala Glu Tyr Ser Glu Ala Val
1 5 10 15
Glu Lys Ala Arg Arg Lys Leu Arg Ala Leu Ile Ala Glu Lys Ser Cys
20 25 30
Ala Pro Leu Met Leu Arg Leu Ala Trp His Ser Ala Gly Thr Phe Asp
35 40 45
Val Ser Ser Arg Thr Gly Gly Pro Phe Gly Thr Met Lys His Gln Ser
50 55 60
Glu Leu Ala His Gly Ala Asn Ala Gly Leu Asp Ile Ala Val Arg Leu
65 70 75 80
Leu Glu Pro Ile Lys Glu Glu Phe Pro Ile Leu Ser Tyr Ala Asp Phe
85 90 95
Tyr Gln Leu Ala Gly Val Val Ala Val Glu Val Thr Gly Gly
100 105 110

(2) INFORMATION FOR SEQ ID NO:2709:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..75
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2709:

Met Leu Arg Leu Ala Trp His Ser Ala Gly Thr Phe Asp Val Ser Ser
1 5 10 15
Arg Thr Gly Gly Pro Phe Gly Thr Met Lys His Gln Ser Glu Leu Ala
20 25 30
His Gly Ala Asn Ala Gly Leu Asp Ile Ala Val Arg Leu Leu Glu Pro
35 40 45
Ile Lys Glu Glu Phe Pro Ile Leu Ser Tyr Ala Asp Phe Tyr Gln Leu
50 55 60
Ala Gly Val Val Ala Val Glu Val Thr Gly Gly
65 70 75

(2) INFORMATION FOR SEQ ID NO:2710:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 505 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..505
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2710:

tttaaactag ctcgcctttc cctccacaaa caccatcag ccatccctt ttgctgcaaa	60
tctttctctg aattgtgggt ctccgacaat ggcggcgcta gtcctatcca agattctggg	120
caccagctc aacttcgcgg gctcctccc ctacgccacc gcagcgccca ccgcgggggc	180
tcagaagatt gtctcccttt tcagcaagaa gcttgcccag aagcccaagc ccgctgcggt	240

0968980 "101300

(2) INFORMATION FOR SEQ ID NO:2713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..504
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2713:

gtgcgctgcg gacgggtcgg atctgagacg agacgatccc cccctcccct caaccggaac	60
ttgttttacc ccattctcatc ccactgactc cagcccaccc acccgcccgc tgcctccgcc	120
gagatctcgt cggactcgga tccgcccgcac cagcaccacc ccgcgcgcgc gccgcgcagc	180
agcagcagat cagagaagat ggccggactc gacaccttcc tcttcacctc ggagtccgtg	240
aacgagggac accctgacaa gctctgcgac caggtctcag atgctgttct ggacgcttgc	300
cttgctgagg accctgacag caaggttgct tgcgagacct gcaccaagac caacatggtc	360
atggtctttg gtgagatcac caccaaggcc aatgtcgact acgagaagat tgtcagggag	420
acatgccgca acattggttt cgtgtcgaac gatgtcgggc ttgacgctga ccactgcaag	480
gtgcttgtga acattgagca gcag	

(2) INFORMATION FOR SEQ ID NO:2714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2714:

Cys Ala Ala Asp Gly Ser Asp Leu Arg Arg Asp Asp Pro Pro Leu Pro	
1 5 10 15	
Ser Thr Gly Thr Cys Phe Thr Pro Ser His Pro Thr Asp Ser Ser Pro	
20 25 30	
Pro Thr Arg Pro Leu Pro Pro Pro Arg Ser Arg Arg Thr Arg Ile Arg	
35 40 45	
Pro Thr Thr Thr Thr Pro Arg Arg Arg Arg Ala Ala Ala Ala Asp Gln	
50 55 60	
Arg Arg Trp Pro Asp Ser Thr Pro Ser Ser Ser Pro Arg Ser Pro	
65 70 75	

(2) INFORMATION FOR SEQ ID NO:2715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2715:

Met Ala Gly Leu Asp Thr Phe Leu Phe Thr Ser Glu Ser Val Asn Glu	
1 5 10 15	
Gly His Pro Asp Lys Leu Cys Asp Gln Val Ser Asp Ala Val Leu Asp	
20 25 30	
Ala Cys Leu Ala Glu Asp Pro Asp Ser Lys Val Ala Cys Glu Thr Cys	
35 40 45	

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Thr Lys Thr Asn Met Val Met Val Phe Gly Glu Ile Thr Thr Lys Ala
50 55 60
Asn Val Asp Tyr Glu Lys Ile Val Arg Glu Thr Cys Arg Asn Ile Gly
65 70 75 80
Phe Val Ser Asn Asp Val Gly Leu Asp Ala Asp His Cys Lys Val Leu
85 90 95
Val Asn Ile Glu Gln Gln
100

(2) INFORMATION FOR SEQ ID NO:2716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2716:

Met Leu Phe Trp Thr Leu Ala Leu Leu Arg Thr Leu Thr Ala Arg Leu
1 5 10 15
Leu Ala Arg Pro Ala Pro Arg Pro Thr Trp Ser Trp Ser Leu Val Arg
20 25 30
Ser Pro Pro Arg Pro Met Ser Thr Thr Arg Arg Leu Ser Gly Arg His
35 40 45
Ala Ala Thr Leu Val Ser Cys Arg Thr Met Ser Gly Leu Thr Leu Thr
50 55 60
Thr Ala Arg Cys Leu
65

(2) INFORMATION FOR SEQ ID NO:2717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..554
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2717:

ctgtggtgtg gactcctgca ctgtgctcct tcgtctcctc ctcccctgcc tgccaccaac 60
tgccaaggtg ccaagcaagt gcagatacct tccctgcctc acaaacaacg ccatcagggt 120
cttcaaccag ggcaggttct cttctttcat tcagctatgg gcaacctgtg ctgctgtgtt 180
caagttgacc agtcgactgt ggccatcagg gagcagtttg gcaagtttga cagcgtgctt 240
gagccaggat gccactgcat gccttggttc gccggcaagc gtgtagctgg gcatttcaca 300
ctcaggctgc agcaactgga tgtgcgctgt gagacaaaaa caaaggacaa tgtttttgtg 360
aatgtggtgg catctattca gtaccgcgct ctggctgaca aagcaagtga cgctttctac 420
aaactgagca acacaaggtc ccagatccaa gcctacgtct ttgacgtgat cagagcaagc 480
gttccaagc tccatttgga cgatgctttc gagcagaagg acgagatcgc aagggcggtg 540
gaggaagagc tgag

(2) INFORMATION FOR SEQ ID NO:2718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

00669900 00669900

Asp Gly Gly Thr Phe Lys Leu Thr Leu Gln Phe Asn Glu Glu Tyr Pro
50 55 60
Asn Lys Pro Pro Thr Val Arg Phe Val Ser Arg Met Phe His Pro Asn
65 70 75 80
Ile Tyr Ala Asp Gly Ser Ile Cys Leu Asp Ile Leu Gln Asn Gln Trp
85 90 95
Ser Pro Asp Ile
100

(2) INFORMATION FOR SEQ ID NO:2723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1601721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2723:

Met Arg Asp Phe Lys Arg Leu Met Gln Asp Pro Pro Ala Gly Ile Ser
1 5 10 15
Gly Ala Pro Gln Asp Asn Asn Ile Met Leu Trp Asn Ala Val Ile Phe
20 25 30
Gly Pro Asp Asp Thr Pro Trp Asp Gly Gly Thr Phe Lys Leu Thr Leu
35 40 45
Gln Phe Asn Glu Glu Tyr Pro Asn Lys Pro Pro Thr Val Arg Phe Val
50 55 60
Ser Arg Met Phe His Pro Asn Ile Tyr Ala Asp Gly Ser Ile Cys Leu
65 70 75 80
Asp Ile Leu Gln Asn Gln Trp Ser Pro Asp Ile
85 90

(2) INFORMATION FOR SEQ ID NO:2724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1601722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2724:

Met Gln Asp Pro Pro Ala Gly Ile Ser Gly Ala Pro Gln Asp Asn Asn
1 5 10 15
Ile Met Leu Trp Asn Ala Val Ile Phe Gly Pro Asp Asp Thr Pro Trp
20 25 30
Asp Gly Gly Thr Phe Lys Leu Thr Leu Gln Phe Asn Glu Glu Tyr Pro
35 40 45
Asn Lys Pro Pro Thr Val Arg Phe Val Ser Arg Met Phe His Pro Asn
50 55 60
Ile Tyr Ala Asp Gly Ser Ile Cys Leu Asp Ile Leu Gln Asn Gln Trp
65 70 75 80
Ser Pro Asp Ile

(2) INFORMATION FOR SEQ ID NO:2725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

09589930 03668960

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..523
 (D) OTHER INFORMATION: / Ceres Seq. ID 1601731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2725:

ggttccatta	ctggtcccta	gcaggaagca	ggatggagtt	ggcgctcagc	ttgggggaga	60
ccatggcgga	tgccggaagg	gacctcatgc	tggggcttgg	gatgggggtc	ggggtgcgga	120
gggaggagga	agcgagaga	gggaggaggg	acagggaggt	gaggcgggag	ctggagttca	180
cggcgaggag	cgcccggtcg	tcgccggagc	cggcggtgcg	actcacctc	ctgcacggcc	240
tcggcctccc	gtggccgccc	ccgccgtcgt	ccgagaccaa	ccggcacctg	gaggcgctcg	300
cgcgtggctt	cgacgtgaac	cggcgccggt	cgtgttccgc	ggccggtggc	gccgcggagg	360
aggacgagga	gcaggacgag	gcggcgccgc	cggcgccatc	gtcgtcgccc	aacaacagcg	420
cgagctcctt	cccgacggac	ttctccgcgc	agggccaggt	ggcgcccggc	gccgaccgcg	480
cgtgctcccg	cgccagcgac	gaggacgacg	gcggctccgc	gcg		

(2) INFORMATION FOR SEQ ID NO:2726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..174
(D) OTHER INFORMATION: / Ceres Seq. ID 1601732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2726:

Val	Pro	Leu	Leu	Val	Pro	Ser	Arg	Lys	Gln	Asp	Gly	Val	Gly	Ala	Gln
1				5					10					15	
Leu	Gly	Gly	Asp	His	Gly	Gly	Cys	Arg	Lys	Gly	Pro	His	Ala	Gly	Ala
			20					25					30		
Trp	Asp	Gly	Gly	Arg	Gly	Ala	Glu	Gly	Gly	Gly	Ser	Ala	Glu	Arg	Glu
			35				40					45			
Glu	Gly	Gln	Gly	Gly	Glu	Ala	Gly	Ala	Gly	Val	His	Gly	Glu	Glu	Arg
	50					55					60				
Pro	Val	Val	Ala	Gly	Ala	Gly	Gly	Ala	Thr	His	Pro	Pro	Ala	Arg	Pro
65				70						75				80	
Arg	Pro	Pro	Val	Ala	Ala	Ala	Ala	Val	Val	Arg	Asp	Gln	Pro	Ala	Pro
			85					90					95		
Gly	Gly	Val	Gly	Ala	Trp	Leu	Arg	Arg	Glu	Pro	Gly	Ala	Val	Ala	Val
			100					105					110		
Arg	Gly	Arg	Trp	Arg	Arg	Gly	Gly	Gly	Arg	Gly	Ala	Gly	Arg	Gly	Gly
			115					120					125		
Gly	Gly	Gly	Gly	Ile	Val	Val	Ala	Gln	Gln	Gln	Arg	Glu	Leu	Leu	Pro
	130						135				140				
Asp	Gly	Leu	Leu	Arg	Ala	Gly	Pro	Gly	Gly	Ala	Arg	Arg	Arg	Pro	Arg
145				150						155				160	
Val	Leu	Pro	Arg	Gln	Arg	Arg	Gly	Arg	Arg	Arg	Leu	Arg	Ala		
				165						170					

(2) INFORMATION FOR SEQ ID NO:2727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..173
(D) OTHER INFORMATION: / Ceres Seq. ID 1601733

00669900 00669900

(B) TYPE: nucleic acid

[illegible]

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..511
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601753
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2729:

aacttcgctc	cgccccccac	acactgtcac	tgccagcctc	cccttcgctt	cgcttagctc	60
gccgtcacca	tggcgacctc	caccttctct	cgcgcgcccg	ccaccctcaa	gcccctgcgg	120
gcacgcgcca	agcccgcccg	cctccagctc	cacctcctcc	ccttcccgcg	cctccgcgctc	180
gcctgcgcca	ccgcgcggg	gaggcgccgc	ccgttgagca	gcgggacgag	gtggagccgg	240
cctccgcgc	ggcatccaac	gggactgccc	tcaaggctca	ggcgcgccgc	gcgaagccc	300
agtcgccgcc	cgcccccgcg	cccgcgcccg	cgccggtccc	ggccttcgc	gacgccaggt	360
gggtcaacgg	cacctgggac	ctcaccaagt	tgcacaagg	cgccgcgctc	gactgggacg	420
ccgtcatcga	cgccgaggcc	aggagaagga	aatggctcga	aagactaccc	ggaggcgacg	480
agcacwgacg	atgccgtcgt	cttcgacacc	t			

(2) INFORMATION FOR SEQ ID NO:2730:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..169
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601754
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2730:

Leu	Arg	Ser	Val	Pro	His	Thr	Leu	Ser	Leu	Pro	Ala	Ser	Pro	Ser	Leu
1			5					10						15	
Arg	Leu	Ala	Arg	Arg	His	His	Gly	Asp	Leu	His	Leu	Leu	Ser	Ala	Pro
			20					25					30		
Arg	His	Pro	Gln	Ala	Pro	Ala	Gly	Thr	Arg	Gln	Ala	Arg	Arg	Pro	Pro
			35				40					45			
Ala	Pro	Pro	Pro	Pro	Leu	Pro	Ala	Pro	Pro	Arg	Arg	Arg	Leu	Arg	His
			50			55					60				
Ala	Gly	Glu	Ala	Pro	Pro	Val	Glu	Gln	Arg	Asp	Glu	Val	Glu	Pro	Ala
65					70				75					80	
Ser	Ala	Ala	Ala	Ser	Asn	Gly	Thr	Ala	Val	Lys	Val	Glu	Ala	Pro	Ala
				85				90						95	
Ala	Lys	Pro	Glu	Ser	Pro	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Val
			100				105					110			
Pro	Ala	Phe	Arg	Asp	Ala	Arg	Trp	Val	Asn	Gly	Thr	Trp	Asp	Leu	Thr
			115				120					125			
Lys	Phe	Asp	Lys	Gly	Gly	Gly	Val	Asp	Trp	Asp	Ala	Val	Ile	Asp	Ala
			130			135					140				
Glu	Ala	Arg	Arg	Arg	Lys	Trp	Leu	Glu	Arg	Leu	Pro	Gly	Gly	Asp	Glu
145					150					155				160	
His	Xaa	Arg	Cys	Arg	Arg	Leu	Arg	His							
					165										

(2) INFORMATION FOR SEQ ID NO:2731:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 147 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..147

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(D) OTHER INFORMATION: / Ceres Seq. ID 1601755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2731:

Met Ala Thr Ser Thr Phe Ser Pro Arg Pro Ala Thr Leu Lys Pro Leu
1 5 10 15
Arg Ala Arg Ala Lys Pro Ala Gly Leu Gln Leu His Leu Leu Pro Phe
20 25 30
Pro Arg Leu Arg Val Ala Cys Ala Thr Ala Pro Gly Arg Arg Arg Pro
35 40 45
Leu Ser Ser Gly Thr Arg Trp Ser Arg Pro Pro Pro Arg His Pro Thr
50 55 60
Gly Leu Pro Ser Arg Ser Arg Arg Pro Pro Arg Ser Pro Ser Pro Arg
65 70 75 80
Pro Arg Pro Arg Pro Arg Pro Arg Arg Ser Arg Pro Ser Ala Thr Pro
85 90 95
Gly Gly Ser Thr Ala Pro Gly Thr Ser Pro Ser Ser Thr Arg Ala Ala
100 105 110
Ala Ser Thr Gly Thr Pro Ser Ser Thr Pro Arg Pro Gly Glu Gly Asn
115 120 125
Gly Ser Lys Asp Tyr Pro Glu Ala Thr Ser Xaa Asp Asp Ala Val Val
130 135 140
Phe Asp Thr
145

(2) INFORMATION FOR SEQ ID NO:2732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..477
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2732:

actccatccc tgctccgctg tcgcgtgccca tcttaggggtt tctttccccc tcggcgccctc 60
cccagatttg gacgctgccg ccgcccgcgc tgaccaggt tgtcttgatg gcgcccgtg 120
tagaagccgt gaaggagaca ggcaccttcc agaaggttcc tgccatgaac gaaaggatac 180
tgtcatccat gtccaggagg tctgttgctg cacacccttg gcatgatctg gagataggtc 240
ctggtgctcc aaccatattc aactgcgtca ttgagatacc aaggggcagc aagggttaaat 300
atgaacttga caagaaaact ggactgatca aggtggaccg ggtgttgtat tcatcagttg 360
tttaccctca caactatgga ttcattcctc gcacgctttg tgaagacagt gatcctttgg 420
atgtactggt tataatgcag gaggctgtta tcccaggctg tttcctacgt gcgaagg

(2) INFORMATION FOR SEQ ID NO:2733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2733:

Ser Ile Pro Ala Pro Ser Ser Arg Ala Ile Leu Gly Phe Leu Ser Pro
1 5 10 15
Ser Ala Pro Pro Gln Ile Trp Thr Leu Pro Pro Pro Pro Leu Thr Gln
20 25 30
Val Val Leu Met Ala Pro Ala Val Glu Ala Val Lys Glu Thr Gly Thr
35 40 45
Phe Gln Lys Val Pro Ala Met Asn Glu Arg Ile Leu Ser Ser Met Ser

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(2) INFORMATION FOR SEQ ID NO:2734:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1601762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2734:

Met	Ala	Pro	Ala	Val	Glu	Ala	Val	Lys	Glu	Thr	Gly	Thr	Phe	Gln	Lys
1				5					10					15	
Val	Pro	Ala	Met	Asn	Glu	Arg	Ile	Leu	Ser	Ser	Met	Ser	Arg	Arg	Ser
			20					25					30		
Val	Ala	Ala	His	Pro	Trp	His	Asp	Leu	Glu	Ile	Gly	Pro	Gly	Ala	Pro
			35				40					45			
Thr	Ile	Phe	Asn	Cys	Val	Ile	Glu	Ile	Pro	Arg	Gly	Ser	Lys	Val	Lys
	50					55					60				
Tyr	Glu	Leu	Asp	Lys	Lys	Thr	Gly	Leu	Ile	Lys	Val	Asp	Arg	Val	Leu
65					70					75				80	
Tyr	Ser	Ser	Val	Val	Tyr	Pro	His	Asn	Tyr	Gly	Phe	Ile	Pro	Arg	Thr
				85					90					95	
Leu	Cys	Glu	Asp	Ser	Asp	Pro	Leu	Asp	Val	Leu	Val	Ile	Met	Gln	Glu
			100					105					110		
Pro	Val	Ile	Pro	Gly	Cys	Phe	Leu	Arg	Ala	Lys					
			115				120								

(2) INFORMATION FOR SEQ ID NO:2735:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1601763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2735:

Met	Asn	Glu	Arg	Ile	Leu	Ser	Ser	Met	Ser	Arg	Arg	Ser	Val	Ala	Ala
1				5					10					15	
His	Pro	Trp	His	Asp	Leu	Glu	Ile	Gly	Pro	Gly	Ala	Pro	Thr	Ile	Phe
			20					25					30		
Asn	Cys	Val	Ile	Glu	Ile	Pro	Arg	Gly	Ser	Lys	Val	Lys	Tyr	Glu	Leu
		35					40					45			
Asp	Lys	Lys	Thr	Gly	Leu	Ile	Lys	Val	Asp	Arg	Val	Leu	Tyr	Ser	Ser
	50					55				60					

(2) INFORMATION FOR SEO ID NO:2736:

(A) LENGTH: 497 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (α

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..497

(D) OTHER INFORMATION: / Ceres Seq. ID 1601773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2736:

agcagcacac	aacctaccac	actgcattg	cattgcattg	cattccttca	gttcagtagt	60
gtgtcttgac	agtgagatgg	cgagcgtgaa	ggttttcggg	tcacccacct	cggcggaggt	120
cgcccgogtg	ctcatgtgcc	tcttcgagaa	ggaggtggag	ttccagctga	tccgcgtcga	180
cgctaccgc	ggcaccaagc	gcattgccca	gtacctcaag	ctgcagccgc	aaggcgaggc	240
gctcaccttc	gaggacgaga	gcctcaccct	ctccgactcc	agggggatcc	tccgccacat	300
ctcccacaag	tacgcgaagc	agggcaaccc	gtacctgatt	ggcacgggcg	cgctggagcg	360
ggcgtccatc	gagcagtggc	tgcagacgga	ggcgcagagc	ttcgacgcgc	ccagcgccga	420
gatggtctac	agcctcgctt	tcttgccgcc	cacctgcccc	aggcagaacg	acaacggcaa	480
cggcgqgcga	ttcaacg					

(2) INFORMATION FOR SEQ ID NO:2737:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1601774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2737:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 479 base pairs

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2740:

(2) INFORMATION FOR SEQ ID NO:2741:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1601778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2741:

(2) INFORMATION FOR SEQ ID NO:2742:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1601779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2742:

[illegible]

Met Pro Thr Leu Thr Lys Leu Tyr Ser Met Glu Glu Ala Xaa Leu His
1 5 10 15
Asn Thr Pro Asp Asp Cys Trp Val Ile Val Asp Gly Lys Ile Tyr Asp
20 25 30
Val Thr Lys Tyr Leu Glu Asp His Pro Gly Gly Ala Asp Val Leu Leu
35 40 45
Glu Ala Thr Gly Lys Asp Ala Thr Glu Glu Phe Asp Asp Ala Gly His
50 55 60
Ser Lys Ser Ala Lys Asp Leu Met Gln Asp Tyr Phe Ile Gly Glu Leu
65 70 75 80
Asp Leu Asp Pro Thr Pro Asp Ile Pro Glu Met Glu Val Phe Arg Lys
85 90 95
Glu

(2) INFORMATION FOR SEQ ID NO:2743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2743:

Met Glu Glu Ala Xaa Leu His Asn Thr Pro Asp Asp Cys Trp Val Ile
1 5 10 15
Val Asp Gly Lys Ile Tyr Asp Val Thr Lys Tyr Leu Glu Asp His Pro
20 25 30
Gly Gly Ala Asp Val Leu Leu Glu Ala Thr Gly Lys Asp Ala Thr Glu
35 40 45
Glu Phe Asp Asp Ala Gly His Ser Lys Ser Ala Lys Asp Leu Met Gln
50 55 60
Asp Tyr Phe Ile Gly Glu Leu Asp Leu Asp Pro Thr Pro Asp Ile Pro
65 70 75 80
Glu Met Glu Val Phe Arg Lys Glu
85

(2) INFORMATION FOR SEQ ID NO:2744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..476
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2744:

atttccgcac cacgcccagt cgcccacgca gccggcccaa gcccaaaaac ctttctccat 60
cctctactct catccccacg atggcgcgcg ccgccaccac gccgcactcc ctctctctcc 120
agcgcgccgc gatcccgccg gcgcgcgcga gggcgctcgc gccgcctctc ccgtccgcct 180
cccgtccgc gccgccagga tctcgtgcgc ggcgggtggcg gcgccgtccc cggccgcagc 240
cgccgcggcg gacgaggtgg agcgcggcgt ctacaacttc gcggcggggtc ccgcgacgct 300
ccctctctcc gtgtctcaagc gggcgcaggc ggagctgggtg gactaccacg gctccgggat 360
gagcatcatg gagatgagcc accgcgggaa ggagttcgac gccgccatca agaaggccga 420
gtccgacctg cgcgcgctcc tcgcggtgcc tgacacccac gccgtgctct tctctc

(2) INFORMATION FOR SEQ ID NO:2745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:2710																
Phe	Pro	His	His	Ala	Gln	Ser	Pro	Thr	Gln	Pro	Ala	Gln	Ala	Gln	Lys	
1				5					10					15		
Pro	Phe	Ser	Ile	Leu	Tyr	Ser	His	Pro	His	Asp	Gly	Arg	Arg	Arg	His	
			20					25				30				
His	Ala	Ala	Leu	Pro	Pro	Pro	Pro	Ala	Arg	Arg	Asp	Pro	Gly	Arg	Ala	
		35				40					45					
Val	Glu	Gly	Val	Arg	Ala	Ala	Ser	Pro	Val	Arg	Leu	Pro	Val	Arg	Ala	
	50				55						60					
Ala	Arg	Ile	Ser	Cys	Ala	Ala	Val	Ala	Ala	Pro	Ser	Pro	Ala	Ala	Ala	
65				70					75						80	
Ala	Ala	Ala	Asp	Glu	Val	Glu	Arg	Gly	Val	Tyr	Asn	Phe	Ala	Ala	Gly	
			85					90					95			
Pro	Ala	Thr	Leu	Pro	Leu	Ser	Val	Leu	Lys	Arg	Ala	Gln	Ala	Glu	Leu	
			100					105					110			
Val	Asp	Tyr	His	Gly	Ser	Gly	Met	Ser	Ile	Met	Glu	Met	Ser	His	Arg	
	115					120				125						
Gly	Lys	Glu	Phe	Asp	Ala	Ala	Ile	Lys	Lys	Ala	Glu	Ser	Asp	Leu	Arg	
	130				135					140						
Ala	Leu	Leu	Ala	Val	Pro	Asp	Thr	His	Ala	Val	Leu	Phe	Leu			
145				150						155						

Table 1. Demographic characteristics of the study population	
Age (years)	50.0 ± 10.0
Gender	
Male	50.0%
Female	50.0%
Education (years)	12.0 ± 2.0
Marital status	
Married	80.0%
Single	20.0%
Occupation	
Professional	30.0%
Managerial	20.0%
Technical	10.0%
Service	20.0%
Unemployed	20.0%
Income (USD/month)	1,500.0 ± 500.0
Health status	
Good	70.0%
Fair	20.0%
Poor	10.0%

(A) LENGTH: 119 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1601795

[illegible]

(A) LENGTH: 97 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1601800

agagagagaa ggtgagtgtct ttgacaaggg gaaaaaaccc aggtctgtgt gtgtgtgtgc 60
qagagagaga qagagagaga qagagagaga qagagag

(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..32

(D) OTHER INFORMATION: / Ceres Seq. ID 1601801

Glu Arg Glu Gly Glu Cys Phe Asp Lys Gly Lys Lys Pro Arg Ser Val
1 5 10 15
Cys Val Cys Ala Arg Glu Arg Glu Arg Glu Arg Glu Arg Glu Arg Glu
20 25 30

(2) INFORMATION FOR SEQ ID NO:2750:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..31
 (D) OTHER INFORMATION: / Ceres Seq. ID 1601802
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2750:
Arg Glu Lys Val Ser Ala Leu Thr Arg Gly Lys Asn Pro Gly Leu Cys
1 5 10 15
Val Cys Val Arg Glu Arg Glu Arg Glu Arg Glu Arg Glu Arg Glu
 20 25 30
(2) INFORMATION FOR SEQ ID NO:2751:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 435 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..435
 (D) OTHER INFORMATION: / Ceres Seq. ID 1601803
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2751:
aacctgattc cttccgcctt gtcagcgcag cgatccagac ccaccngagc caacaaccca 60
tgccgcgcgc gaagccgcgt ctctgctcg cggtcgcggg cctcaccctc gccgtcctcg 120
ccgcgcgcgt ctgcgcgtct ctggcggcgg gccgcgcggg gctgcaggac ccggcggakc 180
tcctgcgcct tgccaaggag ccggccttcg cggactggat ggtcgggggtg cggcggcgga 240
tccacgagta acccggagct gggatacgag gagttccaga ccagcgagct cgtgcgccgg 300
gagctccacg ccatggggat cccctacagg cacccttcg ccgtcaccgg cgtggttagca 360
acagtcggca ccggcgggtcc gcccttcggt gctctgcggg cggacatgga cgcgctgccc 420
ttgcagggaa agtgt
(2) INFORMATION FOR SEQ ID NO:2752:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..145
 (D) OTHER INFORMATION: / Ceres Seq. ID 1601804
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2752:
Asn Leu Ile Pro Ser Ala Leu Ser Ala Gln Arg Ser Arg Pro Thr Xaa
1 5 10 15
Ala Asn Asn Pro Trp Pro Pro Arg Arg Arg Val Ser Cys Ser Arg Ser
 20 25 30
Arg Ala Ser Pro Ser Pro Ser Ser Pro Pro Arg Ser Arg Arg Leu Trp
 35 40 45
Arg Arg Gly Arg Arg Cys Cys Arg Thr Arg Arg Xaa Ser Cys Ala Leu
 50 55 60
Pro Arg Ser Arg Pro Ser Arg Thr Gly Trp Ser Gly Cys Gly Gly Gly
 65 70 75 80
Ser Thr Ser Asn Pro Glu Leu Gly Tyr Glu Glu Phe Gln Thr Ser Glu
 85 90 95
Leu Val Arg Arg Glu Leu His Ala Met Gly Ile Pro Tyr Arg His Pro
 100 105 110

00669980 08669980

(X1) SEQUENCE DESCRIPTION: SEQ ID: 1

Phe	Phe	Glu	Val	Lys	Ala	Val	Lys	Glu	Ile	Glu	Pro	Ala	Leu	Lys	Lys
1				5				10						15	

Parameter	Value	Unit
Temperature	25.0	°C
Humidity	50.0	%
Pressure	101.3	kPa
Wind speed	0.0	m/s
Wind direction	0.0	°
Light intensity	100.0	lux
CO ₂ concentration	400.0	ppm
Relative humidity	50.0	%
Soil moisture	50.0	%
Soil temperature	20.0	°C
Plant height	10.0	cm
Leaf area	10.0	cm ²
Stomatal conductance	0.1	mol/m ² /s
Transpiration rate	0.1	mmol/m ² /s
Chlorophyll content	0.1	mg/g
Protein content	0.1	mg/g
Carbohydrate content	0.1	mg/g
Antioxidant activity	0.1	mg/g
Enzyme activity	0.1	mg/g
Gene expression	0.1	mg/g
Metabolite profile	0.1	mg/g
Cellular structure	0.1	mg/g
Signal transduction	0.1	mg/g
Plant growth	0.1	mg/g
Plant yield	0.1	mg/g
Plant quality	0.1	mg/g
Plant health	0.1	mg/g
Plant survival	0.1	mg/g
Plant reproduction	0.1	mg/g
Plant development	0.1	mg/g
Plant maturation	0.1	mg/g
Plant senescence	0.1	mg/g
Plant death	0.1	mg/g

Gln Leu Ile Ile Ser Thr Val Leu Met Thr Phe Gly Ile Ala Leu Ile
20 25 30
Ser Trp Leu Ala Leu Pro Ala Lys Phe Thr Ile Tyr Asn Phe Gly Thr
35 40 45
Gln Lys Glu Val Ser Asn Trp Gly Leu Phe Phe Cys Val Ser Ile Gly
50 55 60
Leu Trp Ala Gly Leu Ile Ile Gly Phe Val Thr Glu Tyr Tyr Thr Ser
65 70 75 80
Asn Ala Tyr Ser Pro Val
85

(2) INFORMATION FOR SEQ ID NO:2756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1601808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2756:

Met Thr Phe Gly Ile Ala Leu Ile Ser Trp Leu Ala Leu Pro Ala Lys
1 5 10 15
Phe Thr Ile Tyr Asn Phe Gly Thr Gln Lys Glu Val Ser Asn Trp Gly
20 25 30
Leu Phe Phe Cys Val Ser Ile Gly Leu Trp Ala Gly Leu Ile Ile Gly
35 40 45
Phe Val Thr Glu Tyr Tyr Thr Ser Asn Ala Tyr Ser Pro Val
50 55 60

(2) INFORMATION FOR SEQ ID NO:2757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..400

(D) OTHER INFORMATION: / Ceres Seq. ID 1601816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2757:

acctcccttc cccactctc ttctctcccc gcggcccggtg actcatccac ccacagtcca	60
ctcgccactc cccccggaac ggcgggcggtg gcgaacggcgg aggagtaacg caagatggcg	120
aggaaacctc tgcactacga ggagctgaac gagaacgtca agagggtgca gtacgcgggtg	180
cgcggggagc tgtacctccg cgctccgag ctgcagaagg agggcaagaa gatcatcttc	240
accaacgtcg gcaaccgcga cgccctcggc cagaaaccgc tcaccttccc gcgccaggtg	300
gtggcgctgt gccaggctcc gttcctcctc gacgatcccc acgtcggcct catgttcccg	360
gcggacgcca tcgctagggc caagcactat ctgcgcatgg	

(2) INFORMATION FOR SEQ ID NO:2758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..48

(D) OTHER INFORMATION: / Ceres Seq. ID 1601817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2758:

DOCKET "08668960"

Pro	Pro	Phe	Pro	His	Ser	Leu	Leu	Ser	Pro	Arg	Pro	Val	Thr	His	Pro
1			5					10						15	
Pro	Thr	Val	His	Ser	Pro	Leu	Pro	Pro	Glu	Arg	Arg	Arg	Arg	Arg	Arg
		20					25					30			
Arg	Arg	Ser	Asn	Ala	Arg	Trp	Arg	Gly	Asn	Leu	Ser	Thr	Thr	Arg	Ser
		35				40						45			

(2) INFORMATION FOR SEQ ID NO:2759:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1601818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2759:

Met	Ala	Arg	Lys	Pro	Leu	Asp	Tyr	Glu	Leu	Asn	Glu	Asn	Val	Lys
1			5					10					15	
Arg	Val	Gln	Tyr	Ala	Val	Arg	Gly	Glu	Leu	Tyr	Leu	Arg	Ala	Ser
		20					25					30		
Leu	Gln	Lys	Glu	Gly	Lys	Lys	Ile	Ile	Phe	Thr	Asn	Val	Gly	Asn
		35				40					45			
His	Ala	Leu	Gly	Gln	Lys	Pro	Leu	Thr	Phe	Pro	Arg	Gln	Val	Val
	50				55				60					
Leu	Cys	Gln	Ala	Pro	Phe	Leu	Leu	Asp	Asp	Pro	His	Val	Gly	Leu
65				70				75						80
Phe	Pro	Ala	Asp	Ala	Ile	Ala	Arg	Ala	Lys	His	Tyr	Leu	Ala	Met
		85					90						95	

(2) INFORMATION FOR SEQ ID NO:2760:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 492 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..492

(D) OTHER INFORMATION: / Ceres Seq. ID 1601823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2760:

aaacctcatt	ttctctcctt	ttgctcgga	cgacacaca	gcccgggtccc	cgatctccga	60
ttccctcgtc	gatccaagat	gcagatcttc	gtcaagacc	tcactggaaa	gactatcacc	120
ctcgaggtgg	agtcttctga	caccattgac	aacgtcaagg	ccaagaatcc	aggacaagga	180
gggcattccc	cggaccagc	agcggtcat	cttcgctggc	aagcagctcg	aggacgggcg	240
cacacttgcc	gactacaaca	tccagaagga	gagcaccctc	caccttggtc	tccgcctcag	300
gggagggcatg	cagatcttcg	tcaagaccct	cactggaaag	actatcacc	tcgaggtgga	360
gtcttctgac	accatcgaca	acgtcaaggc	caagatctag	gacaaggagg	gcattcctcc	420
ggaccagcag	cggctcattt	ttgctggcaa	gcagctcgag	gacgggcgca	cgcttgcccg	480
actacaacat	tc					

(2) INFORMATION FOR SEQ ID NO:2761:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

```
(2) INFORMATION FOR SEQ ID NO:2763:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 96 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: peptide
      (ix) FEATURE:
            (A) NAME/KEY: peptide
            (B) LOCATION: 1..96
            (D) OTHER INFORMATION: / Ceres Seq. ID 1601826
```

[illegible]

(2) INFORMATION FOR SEQ ID NO:2764:

(A) LENGTH: 531 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..531

(D) OTHER INFORMATION: / Ceres Seq. ID 1601840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2764:

aacagcttgc	gtggctctgtg	gtctcatctc	actcacactc	tctctctctc	tggcgacgt	60
ctacgccgag	tgcccaggca	ttcttcaggc	gcaggctcgt	ggctcgtgc	cgccctacac	120
caggtgccc	ggtcttcttc	cgtcccttcg	ccggcgacga	gcactgccag	gacagtatag	180
cggatggctt	cgtcgggtcg	ggcgccatcg	gggtcgggtga	tgcgcgtggc	atcgtcctct	240
tcctcagcag	ccgcggccgg	gggtgtgcggc	acgggctccc	gtgcgcgcgg	tgcaagttcc	300
tgcgtgcgaa	gtgccagccg	gactgcgtgt	tgcgcacctc	cttcccaccg	gacaacccgc	360
agaagttcct	gcgcgtcgac	cgcgtcttcg	gcgcagcgaa	cgtgaccacg	ctgatgaacg	420
aaatccacct	gttgcagcgc	gagctgcgca	tgaactcgtc	cgctcacgag	gccgacatgc	480
gaattccgca	ccccgtctac	ggttcgctgg	gcgtcatctc	catcctccag	c	

(2) INFORMATION FOR SEQ ID NO:2765:

(A) LENGTH: 176 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1601841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2765:

Gln 1	Leu	Ala	Trp	Ser 5	Val	Val	Ser	Ser	His 10	Ser	His	Ser	Leu	Ser 15	Leu
Ser	Ala	Thr	Ser 20	Thr	Pro	Ser	Ala	Gln 25	Ala	Phe	Phe	Arg 30	Arg	Arg	Ser
Leu	Ala	Arg 35	Cys	Arg	Pro	Thr	Pro 40	Gly	Ala	Pro	Val	Phe 45	Arg	Phe	Pro
Phe	Ala	Gly 50	Asp	Glu	His	Cys 55	Gln	Asp	Ser	Ile	Ala 60	Asp	Gly	Phe	Val
Gly 65	Ala	Gly	Ala	Ile 70	Gly	Val	Gly	Asp	Arg 75	Arg	Gly	Ile	Val	Leu 80	Phe
Leu	Ser	Ser	Arg 85	Gly	Arg	Gly	Val	Arg	His 90	Gly	Leu	Pro	Cys 95	Ala	Ala
Cys	Lys	Phe	Leu	Arg	Arg	Lys	Cys	Gln	Pro	Asp	Cys	Val	Phe	Ala	Pro

(2) INFORMATION FOR SEQ ID NO:2766:

(A) LENGTH: 497 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..497
(D) OTHER INFORMATION: / Ceres Seq. ID 1601858

agagccaccc	ggttgctcct	catttccact	ttccactctg	cctccgctgc	cgatcgccgt	60
ccccgaccgc	agcgcaggtg	aggatccaac	cccaacaaac	ttccaggcga	cggactgagg	120
atgagtgaag	aggataaggc	tgctgcttct	gctgagcagc	ctaagagggc	ccctaagctc	180
aatgaaagga	tcctctcctc	tctgtccagg	aggtccgtag	ctgctcatcc	atggcatgat	240
ctcgagatcg	gtcctggtgc	tcttgctgta	ttcaatggtg	ttgttgagat	cacaaaggga	300
agcaaagtcg	aatacgagct	tgacaagaaa	actggactga	ttaaggttga	tcgagtcctt	360
tactcatcga	ttgtataccc	tcacaattat	ggtttcattc	caaggactct	ttgtgaagac	420
aatgacccaa	tggatgtggt	ggtcctgatg	caggagcctg	ttgttcctgg	ttcgttcctg	480
agagctaagq	caattgg					

(A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..125
(D) OTHER INFORMATION: / Ceres Seq. ID 1601859

Met	Ser	Glu	Glu	Asp	Lys	Ala	Ala	Ala	Ser	Ala	Glu	Gln	Pro	Lys	Arg
1				5					10					15	
Ala	Pro	Lys	Leu	Asn	Glu	Arg	Ile	Leu	Ser	Ser	Leu	Ser	Arg	Arg	Ser
			20					25					30		
Val	Ala	Ala	His	Pro	Trp	His	Asp	Leu	Glu	Ile	Gly	Pro	Gly	Ala	Pro
			35				40					45			
Ala	Val	Phe	Asn	Val	Val	Val	Glu	Ile	Thr	Lys	Gly	Ser	Lys	Val	Lys
	50					55					60				
Tyr	Glu	Leu	Asp	Lys	Lys	Thr	Gly	Leu	Ile	Lys	Val	Asp	Arg	Val	Leu
65					70					75				80	
Tyr	Ser	Ser	Val	Val	Tyr	Pro	His	Asn	Tyr	Gly	Phe	Ile	Pro	Arg	Thr
				85					90				95		
Leu	Cys	Glu	Asp	Asn	Asp	Pro	Met	Asp	Val	Leu	Val	Leu	Met	Gln	Glu
			100					105					110		
Pro	Val	Val	Pro	Gly	Ser	Phe	Leu	Arg	Ala	Arg	Ala	Ile			
			115				120					125			

(2) INFORMATION FOR SEQ ID NO:2768:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 523 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..523
 (D) OTHER INFORMATION: / Ceres Seq. ID 1601860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2768:

acaagtttcg	cttctcgtcg	cgacgactgg	gcgagaccgc	cgccgcgcgc	tgagttctgt	60
agaaatggct	gatggtgagg	acatccagcc	tcttgctcgc	gacaatggca	ctggaatggg	120
caaggctggg	tttgctggcg	acgatgcacc	aagggtgtgt	ttccctagta	ttgttggtcg	180
tcctcgccac	actggtgtta	tggtagggat	gggacagaag	gatgcgtatg	ttggcgacga	240
ggcacagtcc	aagagaggta	ttctcacgct	caagtatccg	atcgagcatg	gtattgtgag	300
caactgggat	gacatggaga	aaatctggca	tcacactttc	tacaacgagc	ttcgtgttgc	360
cccagaggag	caccctgtgt	tgctcactga	ggctcctttg	aacccaaagg	ccaacaggga	420
gaagatgacc	cagattatgt	tcgagacttt	caatgttcct	gccatgtacg	ttgcaattca	480
agcagtgtctg	tcactctatg	ccagtggacg	tactactggg	att		

(2) INFORMATION FOR SEQ ID NO:2769:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..174
 (D) OTHER INFORMATION: / Ceres Seq. ID 1601861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2769:

Gln	Val	Ser	Leu	Leu	Val	Ala	Thr	Thr	Gly	Arg	Asp	Arg	Arg	Arg	Arg	
1				5					10					15		
Leu	Ser	Ser	Val	Glu	Met	Ala	Asp	Gly	Glu	Asp	Ile	Gln	Pro	Leu	Val	
			20					25					30			
Cys	Asp	Asn	Gly	Thr	Gly	Met	Val	Lys	Ala	Gly	Phe	Ala	Gly	Asp	Asp	
		35					40					45				
Ala	Pro	Arg	Ala	Val	Phe	Pro	Ser	Ile	Val	Gly	Arg	Pro	Arg	His	Thr	
		50				55					60					
Gly	Val	Met	Val	Gly	Met	Gly	Gln	Lys	Asp	Ala	Tyr	Val	Gly	Asp	Glu	
65					70					75				80		
Ala	Gln	Ser	Lys	Arg	Gly	Ile	Leu	Thr	Leu	Lys	Tyr	Pro	Ile	Glu	His	
			85						90					95		
Gly	Ile	Val	Ser	Asn	Trp	Asp	Asp	Met	Glu	Lys	Ile	Trp	His	His	Thr	
		100						105					110			
Phe	Tyr	Asn	Glu	Leu	Arg	Val	Ala	Pro	Glu	Glu	His	Pro	Val	Leu	Leu	
		115				120						125				
Thr	Glu	Ala	Pro	Leu	Asn	Pro	Lys	Ala	Asn	Arg	Glu	Lys	Met	Thr	Gln	
	130					135					140					
Ile	Met	Phe	Glu	Thr	Phe	Asn	Val	Pro	Ala	Met	Tyr	Val	Ala	Ile	Gln	
145					150					155				160		
Ala	Val	Leu	Ser	Leu	Tyr	Ala	Ser	Gly	Arg	Thr	Thr	Gly	Ile			
			165						170							

(2) INFORMATION FOR SEQ ID NO:2770:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

00669980 104300

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1601862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2770:

Met Ala Asp Gly Glu Asp Ile Gln Pro Leu Val Cys Asp Asn Gly Thr
1 5 10 15
Gly Met Val Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val
20 25 30
Phe Pro Ser Ile Val Gly Arg Pro Arg His Thr Gly Val Met Val Gly
35 40 45
Met Gly Gln Lys Asp Ala Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg
50 55 60
Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Ser Asn
65 70 75 80
Trp Asp Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu
85 90 95
Arg Val Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu
100 105 110
Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr
115 120 125
Phe Asn Val Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu
130 135 140
Tyr Ala Ser Gly Arg Thr Thr Gly Ile
145 150

(2) INFORMATION FOR SEQ ID NO:2771:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1601863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2771:

Met Val Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe
1 5 10 15
Pro Ser Ile Val Gly Arg Pro Arg His Thr Gly Val Met Val Gly Met
20 25 30
Gly Gln Lys Asp Ala Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly
35 40 45
Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Ser Asn Trp
50 55 60
Asp Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg
65 70 75 80
Val Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn
85 90 95
Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe
100 105 110
Asn Val Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr
115 120 125
Ala Ser Gly Arg Thr Thr Gly Ile
130 135

(2) INFORMATION FOR SEQ ID NO:2772:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 494 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

0958980-101300

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..494

(D) OTHER INFORMATION: / Ceres Seq. ID 1601864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2772:

acctgcatcc	tccctctctc	tctcccgtc	ccgtgctctc	tccctctccc	caggatccga	60
attgccagcg	caccagtcga	gctcgcggga	cctcgccggc	gccggcgatg	gcctcctccc	120
ttttggccgg	acggggaggg	ggccaccacc	acaactgggg	ggagacgcgc	gccccgctcg	180
agcccatacc	ccccaacctt	agtcccagcc	agccccaccc	gcgcgccgac	gggtccaagt	240
ccaagccgcg	ggcggcggcc	ggctacgtga	agttccgccc	ggcgtccctg	ggccaccgcg	300
aggcccgcgc	gctccgggac	cgctcgcgg	tggagctcgg	ccaggtccgc	gcctcctct	360
cccgcatacg	cacctggcag	cagcaggccc	cgcgcgcgcg	cgcggtgctc	cgcggggcga	420
tgcggaagcg	gtgcggccag	atcctcagca	ggctgcgcaa	ggacaagcgc	agcgtgtggt	480
tcaacgcgcc	cgtc					

(2) INFORMATION FOR SEQ ID NO:2773:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1601865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2773:

Thr	Cys	Ile	Leu	Pro	Leu	Ser	Leu	Pro	Leu	Pro	Cys	Ser	Leu	Pro	Leu
1				5					10					15	
Pro	Arg	Ile	Arg	Ile	Ala	Ser	Ala	Pro	Val	Glu	Leu	Ala	Gly	Pro	Arg
			20					25					30		
Arg	Arg	Arg	Arg	Trp	Pro	Pro	Pro	Phe	Trp	Pro	Asp	Gly	Glu	Gly	Ala
			35				40					45			
Thr	Thr	Thr	Thr	Gly	Gly	Arg	Arg	Ala	Pro	Arg	Ser	Ser	Pro	Tyr	Pro
			50				55				60				
Pro	Thr	Leu	Val	Pro	Ala	Ser	Pro	Thr	Arg	Ala	Pro	Thr	Gly	Pro	Ser
65					70				75					80	
Pro	Ser	Arg	Gly	Arg	Arg	Pro	Ala	Thr							
					85										

(2) INFORMATION FOR SEQ ID NO:2774:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1601866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2774:

Leu	His	Pro	Pro	Ser	Leu	Ser	Pro	Ala	Pro	Val	Leu	Ser	Pro	Ser	Pro
1					5					10				15	
Gln	Asp	Pro	Asn	Cys	Gln	Arg	Thr	Ser	Arg	Ala	Arg	Gly	Thr	Ser	Pro
			20					25					30		
Ala	Pro	Ala	Met	Ala	Ser	Ser	Leu	Leu	Ala	Gly	Arg	Gly	Gly	Gly	His
			35				40					45			
His	His	Asn	Trp	Gly	Glu	Thr	Arg	Ala	Pro	Leu	Glu	Pro	Ile	Pro	Pro
			50				55				60				
Asn	Pro	Ser	Pro	Ser	Gln	Pro	His	Pro	Arg	Ala	Asp	Gly	Ser	Lys	Ser
65					70				75					80	

Lys Pro Arg Ala Ala Ala Gly Tyr Val Lys Phe Arg Pro Ala Ser Leu
85 90 95
Gly His Arg Glu Ala Arg Ala Leu Arg Asp Arg Leu Ala Val Glu Leu
100 105 110
Gly Gln Val Arg Ala Leu Leu Ser Arg Ile Asp Thr Trp Gln Gln Gln
115 120 125
Xaa Pro Pro Pro Arg Ala Val Leu Arg Gly Ala Met Arg Lys Arg Cys
130 135 140
Gly Gln Ile Leu Ser Arg Leu Arg Lys Asp Lys Arg Ser Val Trp Phe
145 150 155 160
Asn Ala Pro Val

(2) INFORMATION FOR SEQ ID NO:2775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2775:

Met Ala Ser Ser Leu Leu Ala Gly Arg Gly Gly Gly His His His Asn
1 5 10 15
Trp Gly Glu Thr Arg Ala Pro Leu Glu Pro Ile Pro Pro Asn Pro Ser
20 25 30
Pro Ser Gln Pro His Pro Arg Ala Asp Gly Ser Lys Ser Lys Pro Arg
35 40 45
Ala Ala Ala Gly Tyr Val Lys Phe Arg Pro Ala Ser Leu Gly His Arg
50 55 60
Glu Ala Arg Ala Leu Arg Asp Arg Leu Ala Val Glu Leu Gly Gln Val
65 70 75 80
Arg Ala Leu Leu Ser Arg Ile Asp Thr Trp Gln Gln Gln Xaa Pro Pro
85 90 95
Pro Arg Ala Val Leu Arg Gly Ala Met Arg Lys Arg Cys Gly Gln Ile
100 105 110
Leu Ser Arg Leu Arg Lys Asp Lys Arg Ser Val Trp Phe Asn Ala Pro
115 120 125
Val

(2) INFORMATION FOR SEQ ID NO:2776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..411
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2776:

ataacgcaag caaagcctct gctgctgct ctgctcctct ctctcctcca tttgctgccg 60
cagctctccg agctcgccct cgccgcccgc gcctcagcgc agcacagcac agattcggag 120
agcctgccct tagcacgcag cgccagtga gaggccgag ataattggagg tggagacgat 180
gctggacgac gacgtgttct tcgccgagct cagcaagcgg atatcgctgc tcatcaccga 240
cgacgacgag ggcgcggact tcgccgccgc gcagttcatc ccgcgcgcgc ccgcgcgcgc 300
cgcgcccttc caggggttcg cgtcgccgc ccattgtgcg tcgcaggcgt cgctgctggc 360
gccaccggcc tacgcgctgt accactacca ccacggcgcc agctacggcg g

00000000 00000000

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

- (B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1601869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2777:

(2) INFORMATION FOR SEQ ID NO:2778:

(A) LENGTH: 82 amino acids

- (ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

- (B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1601870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2778:

(2) INFORMATION FOR SEQ ID NO:2779:

(A) LENGTH: 77 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide
(B) LOCATION: 1..77
(D) OTHER INFORMATION: / Ceres Seq. ID 1601871

Met	Leu	Asp	Asp	Asp	Val	Phe	Phe	Ala	Glu	Leu	Ser	Lys	Arg	Ile	Ser
1				5					10					15	
Leu	Leu	Ile	Thr	Asp	Asp	Asp	Glu	Gly	Ala	Asp	Phe	Ala	Ala	Ala	Gln
			20					25					30		
Phe	Ile	Pro	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Pro	Leu	Gln	Gly	Phe	Ala
		35					40					45			
Ser	Arg	Ala	His	Val	Pro	Ser	Gln	Ala	Ser	Leu	Leu	Ala	Pro	Pro	Ala
	50					55					60				
Tyr	Ala	Leu	Tyr	His	Tyr	His	His	Gly	Ala	Ser	Tyr	Gly			
65					70					75					

(A) LENGTH: 364 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY: -
(B) LOCATION: 1..364
(D) OTHER INFORMATION: / Ceres Seq. ID 1601872

cattcctcct	ctccctctcc	acggcccacg	cccaccgccc	catccacccc	gaaaccctag	60
cggatcgteg	ccatggccgc	ggcgcgcgtc	cttcgcgcga	tccccgcgc	gcgggccccc	120
gccacggcct	tcatggcggc	gcaccgggtc	tccgattcca	cggcggcgct	caccatcgag	180
acatctgtcc	ctttcacctc	ccacctcgtc	gacccgcctt	cgcgcgatgt	caccaccacc	240
cccgcgcgagc	tgttcacctt	cttcgcgcac	atgtccctca	tgcgcgcgat	ggagatcgct	300
gcgcgactcc	tctataaggc	caagctcatc	cgcgggttct	gccacctcta	cgaaggccag	360
gagg						

(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(A) NAME/KEY: peptide
(B) LOCATION: 1..121
(D) OTHER INFORMATION: / Ceres Seq. ID 1601873

Ile	Pro	Pro	Leu	Pro	Leu	His	Gly	Pro	Arg	Pro	Pro	Pro	His	Pro	Pro
1				5					10					15	
Arg	Asn	Pro	Ser	Gly	Ser	Ser	Pro	Trp	Pro	Arg	Pro	Arg	Ser	Phe	Ala
			20					25					30		
Ala	Ser	Pro	Pro	Arg	Gly	Pro	Arg	Pro	Arg	Pro	Ser	Trp	Arg	Arg	Thr
			35				40					45			
Arg	Ser	Pro	Ile	Pro	Arg	Arg	Arg	Ser	Pro	Ser	Arg	His	Leu	Ser	Leu
			50			55					60				
Ser	Pro	Pro	Thr	Ser	Ser	Thr	Arg	Pro	Arg	Ala	Met	Ser	Pro	Pro	Pro
65					70					75				80	
Pro	Pro	Ser	Ser	Ser	Pro	Ser	Ser	Ala	Thr	Cys	Pro	Ser	Cys	Ala	Ala
				85					90					95	
Trp	Arg	Ser	Leu	Pro	Thr	Pro	Ser	Ile	Arg	Pro	Ser	Ser	Ser	Ala	Gly
			100					105					110		
Ser	Ala	Thr	Ser	Thr	Thr	Ala	Arg	Arg							

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(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
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	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2433	2434	2435	2436	2437	2438	2439	2440	2441	2442	2
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```

      (A) NAME/KEY: -
      (B) LOCATION: 1..174
      (D) OTHER INFORMATION: / Ceres Seq. ID 1601883
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2784:
aaggcctcca ctcattcctg cccccgacac tcccactgcc accagtcctc tcaccgccag      60
gcgccagcca cagcggcaca atgcagccgc ctactaccct tctcccgcta ggcgccgtcg      120
tggtcgccat cctcctgctc gccaccgcc cgagccccgc cgtctcccg t aacc
(2) INFORMATION FOR SEQ ID NO:2785:
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 36 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: peptide
  (ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..36
      (D) OTHER INFORMATION: / Ceres Seq. ID 1601884
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2785:
Lys Ala Ser Thr His Ser Cys Pro Arg His Ser His Cys His Gln Ser
1          5          10          15
Ser His Arg Gln Ala Pro Ala Thr Ala Ala Gln Cys Ser Arg Leu Leu
          20          25          30
Pro Phe Ser Arg
          35
(2) INFORMATION FOR SEQ ID NO:2786:
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 56 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: peptide
  (ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..56
      (D) OTHER INFORMATION: / Ceres Seq. ID 1601885
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2786:
Arg Pro Pro Leu Ile Pro Ala Pro Asp Thr Pro Thr Ala Thr Ser Pro
1          5          10          15
Leu Thr Ala Arg Arg Gln Pro Gln Arg His Asn Ala Ala Ala Tyr Tyr
          20          25          30
Pro Ser Pro Ala Arg Arg Arg Arg Gly Arg His Pro Pro Ala Arg His
          35          40          45
Arg Pro Glu Pro Arg Arg Leu Pro
          50          55
(2) INFORMATION FOR SEQ ID NO:2787:
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 57 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: peptide
  (ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..57
      (D) OTHER INFORMATION: / Ceres Seq. ID 1601886
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2787:
Gly Leu His Ser Phe Leu Pro Pro Thr Leu Pro Leu Pro Pro Val Leu
1          5          10          15
Ser Pro Pro Gly Ala Ser His Ser Gly Thr Met Gln Pro Pro Thr Thr
          20          25          30

```

Leu Leu Pro Leu Gly Ala Val Val Val Ala Ile Leu Leu Leu Ala Thr
35 40 45
Ala Pro Ser Pro Ala Val Ser Arg Asn
50 55

(2) INFORMATION FOR SEQ ID NO:2788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..241
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2788:

aggacaggtt	gcatttgcat	ctgagttcct	gatcggttga	ttccagtttc	ttccgtgagt	60
tttgtgggat	cgcgaggaag	aaggatgtcg	tgcygcggar	gcaactgcgg	gtgcggcgcc	120
ggctgcaagt	gcggcagcgg	ctgcggaggg	tgccgcaccc	gcatttccat	cctgtcgtgg	180
gatcccagcc	accgccgcta	gaagaagagc	tcggcgattc	ccaggtcccg	cgagaatatg	240

C

(2) INFORMATION FOR SEQ ID NO:2789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..38
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2789:

Met	Ser	Cys	Xaa	Gly	Xaa	Asn	Cys	Gly	Cys	Gly	Ala	Gly	Cys	Lys	Cys
1				5				10					15		
Gly	Ser	Gly	Cys	Gly	Gly	Cys	Arg	Thr	Arg	Ile	Ser	Ile	Leu	Ser	Trp
		20					25						30		

Asp Pro Ser His Arg Arg
35

(2) INFORMATION FOR SEQ ID NO:2790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..437
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601892

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2790:

acctctcctt	ccctccaccc	gcgcgctcgc	ctgcctatc	cgatctgcca	cctcctcccg	60
tctcgacagt	tccttcccaa	ctcgcgagcg	tagcctctcc	gcggcgcgat	ccagatccag	120
gtttttcagc	atgggccttg	tgaaggaagg	catcgacatg	gaggagggaa	cccttgagat	180
cggcatggag	tacaggactg	tatctggtgt	tgctgggcct	ctggtcatat	tggataaagt	240
aaagggccca	aagtaccaag	aaattgtaaa	catccgactt	ggagatggca	ccaatcgccg	300
tggtaagtc	ctggaagtgt	atggcgaaaa	agctgtttgt	caggtctttg	aaggaacttc	360
tggaatagac	racaaataca	caaccgtgca	gtttacaggc	gaggttttga	aaactcctgt	420

ctcacttgat atgcttg

(2) INFORMATION FOR SEQ ID NO:2791:

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:2793:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:

[illegible]

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..93
 (D) OTHER INFORMATION: / Ceres Seq. ID 1601895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2793:

```
Met Glu Glu Gly Thr Leu Glu Ile Gly Met Glu Tyr Arg Thr Val Ser
1          5          10          15
Gly Val Ala Gly Pro Leu Val Ile Leu Asp Lys Val Lys Gly Pro Lys
          20          25          30
Tyr Gln Glu Ile Val Asn Ile Arg Leu Gly Asp Gly Thr Asn Arg Arg
          35          40          45
Gly Gln Val Leu Glu Val Asp Gly Glu Lys Ala Val Val Gln Val Phe
          50          55          60
Glu Gly Thr Ser Gly Ile Asp Xaa Lys Tyr Thr Thr Val Gln Phe Thr
65          70          75          80
Gly Glu Val Leu Lys Thr Pro Val Ser Leu Asp Met Leu
          85          90
```

(2) INFORMATION FOR SEQ ID NO:2794:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 341 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..341
 (D) OTHER INFORMATION: / Ceres Seq. ID 1601900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2794:

```
gaaaagaaaa gcacgggaga cgggacggga ccgctgggcg cgccggggccg cgccgagccg      60
agcgagtctgt ccactctcca ctccgccgcg cagcccacg ccccgctctc gcttcgctct      120
cccacaatcc aaggacaccg agcagcaggc ggcggaagca acccgctgtg ggggcggcgt      180
ggagtccagt ttgctcggc tcgtcgctgg gatccgccg ccggcgaagc ggggaaggga      240
agaggagcgg agattggaga gtacaagcag gggaagatgt cagacgcgct gatcaacggc      300
ctcgccggcg ccggcggcgg gatcatcgcc cagctcctta c
```

(2) INFORMATION FOR SEQ ID NO:2795:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..113
 (D) OTHER INFORMATION: / Ceres Seq. ID 1601901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2795:

```
Glu Lys Lys Ser Thr Gly Asp Gly Thr Gly Pro Leu Gly Ala Pro Gly
1          5          10          15
Arg Ala Glu Pro Ser Glu Ser Ser Thr Leu His Ser Ala Arg His Ala
          20          25          30
His Ala Pro Ser Ser Leu Pro Ser Pro Thr Ile Gln Gly His Arg Ala
          35          40          45
Ala Gly Gly Gly Ser Asn Pro Leu Trp Gly Arg Arg Gly Val Gln Phe
          50          55          60
Cys Ser Ala Arg Arg Trp Asp Pro Pro Ala Gly Glu Ala Gly Lys Gly
65          70          75          80
Arg Gly Ala Glu Ile Gly Glu Tyr Lys Gln Gly Lys Met Ser Asp Ala
          85          90          95
```

00000000 101300

Leu Ile Asn Gly Leu Ala Gly Ala Gly Gly Gly Ile Ile Ala Gln Leu
100 105 110
Leu

(2) INFORMATION FOR SEQ ID NO:2796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2796:

Lys Arg Lys Ala Arg Glu Thr Gly Arg Asp Arg Trp Ala Arg Arg Ala
1 5 10 15
Ala Pro Ser Arg Ala Ser Arg Pro Leu Ser Thr Pro Pro Ala Thr Pro
20 25 30
Thr Pro Arg Pro Arg Phe Arg Leu Pro Gln Ser Lys Asp Thr Glu Gln
35 40 45
Gln Ala Ala Glu Ala Thr Arg Cys Gly Gly Gly Val Glu Ser Ser Phe
50 55 60
Ala Arg Leu Val Ala Gly Ile Arg Arg Pro Ala Lys Arg Gly Arg Glu
65 70 75 80
Glu Glu Arg Arg Leu Glu Ser Thr Ser Arg Gly Arg Cys Gln Thr Arg
85 90 95

(2) INFORMATION FOR SEQ ID NO:2797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2797:

Lys Glu Lys His Gly Arg Arg Asp Gly Thr Ala Gly Arg Ala Gly Pro
1 5 10 15
Arg Arg Ala Glu Arg Val Val His Ser Pro Leu Arg Pro Pro Arg Pro
20 25 30
Arg Pro Val Leu Ala Ser Val Ser His Asn Pro Arg Thr Pro Ser Ser
35 40 45
Arg Arg Arg Lys Gln Pro Ala Val Gly Ala Ala Trp Ser Pro Val Leu
50 55 60
Leu Gly Ser Ser Leu Gly Ser Ala Gly Arg Arg Ser Gly Glu Gly Lys
65 70 75 80
Arg Ser Gly Asp Trp Arg Val Gln Ala Gly Glu Asp Val Arg Arg Ala
85 90 95
Asp Gln Arg Pro Arg Arg Arg Arg Arg Asp His Arg Pro Ala Pro
100 105 110
Tyr

(2) INFORMATION FOR SEQ ID NO:2798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs

00669980 101000

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..311
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601904
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2798:

agaggctcca caacggcgga gcaactagcag ctaggccacg agacgatggc ggccccggcg	60
cctcacgtcg cggtggctcg cgccggctct gctcctctc ccgtccctcc tcgtgtcgt	120
cgcgcagacg cccaagggcg ccaaggcttt ctgcattagc cagttcgcca tcgccagcca	180
ggcctgctcc atcctgccgc cgagcccacc cgacgagcac caccacgacg atgacgagga	240
tgatgacgac aacgacgacg agcaccatga ccgcgaccgt cgcagccacc acgcggcgcg	300
catgagcttc t	

(2) INFORMATION FOR SEQ ID NO:2799:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..100
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601905
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2799:

Arg	Leu	His	Asn	Gly	Gly	Ala	Leu	Ala	Ala	Arg	Pro	Arg	Asp	Asp	Gly
1			5						10					15	
Gly	Pro	Gly	Ala	Ser	Arg	Arg	Gly	Gly	Arg	Arg	Arg	Ser	Cys	Ser	Ser
			20				25						30		
Ser	Arg	Pro	Ser	Ser	Leu	Ser	Ser	Arg	Arg	Arg	Pro	Arg	Ala	Pro	Arg
			35				40					45			
Leu	Ser	Ala	Leu	Ala	Ser	Ser	Pro	Ser	Pro	Ala	Arg	Pro	Ala	Pro	Ser
			50				55				60				
Cys	Arg	Arg	Ala	His	Pro	Thr	Ser	Thr	Thr	Thr	Met	Thr	Arg	Met	
65					70				75					80	
Met	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Met	Thr	Ala	Thr	Val	Ala	Ala	Thr
			85					90						95	
Thr	Arg	Arg	Pro												
			100												

(2) INFORMATION FOR SEQ ID NO:2800:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..494
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601909
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2800:

agtccgagaa gaaaaaggaa actgaagaag agacctcgct gtctcgtgca gccgcaagca	60
cgaggctgtg agcgagacag ccaaggtgct catcgactcc agccagccgc ccaaaaagcc	120
aggcgcaaat cacaacctcg cctcctgtcc cctccccggc tcctcgttcc cctctcgccg	180
ctcgctccc cgccgagatc gaggaggcgc caatagcgag agggtttctt cttccctcca	240
cggctccaac gagcccccg cccctccgcc tcaaattcca cgcgccccgt tggccgcccgc	300
ccccgccatg gatgtggatc tgtggatctc caaggtcaag gaaggccagc acctcgccga	360
gcacgagctt cagtctctct gcgaatacgt aaaggagatc ctcatcgaag agtcgaacgt	420
tcaaccgggtg aattagccct gtgacggttt gcggtgacat ccatgggcag ttcatgacct	480

00000000 00000000

gatgaagctc ttcg

(2) INFORMATION FOR SEQ ID NO:2801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2801:

Ser Pro Arg Arg Lys Arg Lys Leu Lys Lys Arg Pro Arg Arg Leu Val
1 5 10 15
Gln Pro Gln Ala Arg Gly Cys Glu Arg Asp Ser Gln Gly Ala His Arg
20 25 30
Leu Gln Pro Ala Ala Gln Lys Ala Arg Arg Lys Ser Gln Pro Arg Leu
35 40 45
Leu Ser Pro Pro Arg Leu Leu Val Pro Leu Ser Pro Leu Ala Ser Pro
50 55 60
Pro Arg Ser Arg Arg Arg Gln
65 70

(2) INFORMATION FOR SEQ ID NO:2802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2802:

Met Asp Val Asp Leu Trp Ile Ser Lys Val Lys Glu Gly Gln His Leu
1 5 10 15
Ala Glu His Glu Leu Gln Ser Leu Cys Glu Tyr Val Lys Glu Ile Leu
20 25 30
Ile Glu Glu Ser Asn Val Gln Pro Val Asn
35 40

(2) INFORMATION FOR SEQ ID NO:2803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..476
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601916

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2803:

aacccctttc tttttcttaa ttctcatcc actcgccgca cgacgaagag agcggtccc 60
attccccacc acctactcg accggagcag caggttctcg aaccgaccgg tgaacattc 120
tcgcgccaat tgtgggggcc atggcgcca acggacacc gccggcgagc accgtcgcg 180
agaacggatc ccactctggc ggaggcggag gagggggagg gggagtgaac cctagcaacg 240
gcggcacggg ggcggtctct cggcacgacc ctggtctggc gcgggagtgg tcgacggagg 300
agcagaccat cctcgacgag ctgctgttca agtatgcatc cgatttacc gtcgttcgct 360
atgcaaaagt tgcaatgaag ttgccagaga aaacagttcg ggatgtagcc ttgcgctgca 420
gatggatgaa taaaaaggag agcgccaaaa gaaagaaaga ggatcacaac togtct

00000000 00000000

Asn Gly Gly Thr Gly Ala Ala Leu Arg His Asp Pro Gly Leu Ala Arg

(2) INFORMATION FOR SEO ID NO:2807:

(A) LENGTH: 472 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..472

(D) OTHER INFORMATION: / Ceres Seq. ID 1601928

gacgcacgcc	tagctgggcc	acaggtgggt	ggaaatcatg	taggctcaaa	ggttgtagta	60
cagcactcca	gtcctagacc	gagctgcagg	agagaagaga	agcaccgcaa	ccctagggttg	120
ccgcctcttt	tctctccac	tctccgcgc	gacgcgacgc	gacgcgacga	caaccggagg	180
gtttttctgcg	gggatttggt	tgtcgccgac	tcgccagcag	ccaagatgag	gccggctcttc	240
gtggggaacc	tggacatatga	caccgcccac	tcggagctcg	accgcctctt	ctaccgctac	300
ggcagggctcg	agcgcactga	catgaagtca	ggctatgctt	ttgtctactt	tgaggatgaa	360
cgtagtgcca	atgatcccat	acaggtcttt	gatggttatc	catttgccc	tggcagacgc	420
aggctttcag	tagagtggtc	acgggggtga	kcaagctggt	agacgtgatg	gc	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..37

(D) OTHER INFORMATION: / Ceres Seq. ID 1601929

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1601930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2809:

Sensitivity analysis	
1. Age	0.00
2. Sex	0.00
3. Education	0.00
4. Income	0.00
5. Health status	0.00
6. Employment	0.00
7. Social network	0.00
8. Health insurance	0.00
9. Health status	0.00
10. Employment	0.00
11. Social network	0.00
12. Health insurance	0.00
13. Health status	0.00
14. Employment	0.00
15. Social network	0.00
16. Health insurance	0.00
17. Health status	0.00
18. Employment	0.00
19. Social network	0.00
20. Health insurance	0.00
21. Health status	0.00
22. Employment	0.00
23. Social network	0.00
24. Health insurance	0.00
25. Health status	0.00
26. Employment	0.00
27. Social network	0.00
28. Health insurance	0.00
29. Health status	0.00
30. Employment	0.00
31. Social network	0.00
32. Health insurance	0.00
33. Health status	0.00
34. Employment	0.00
35. Social network	0.00
36. Health insurance	0.00
37. Health status	0.00
38. Employment	0.00
39. Social network	0.00
40. Health insurance	0.00
41. Health status	0.00
42. Employment	0.00
43. Social network	0.00
44. Health insurance	0.00
45. Health status	0.00
46. Employment	0.00
47. Social network	0.00
48. Health insurance	0.00
49. Health status	0.00
50. Employment	0.00
51. Social network	0.00
52. Health insurance	0.00
53. Health status	0.00
54. Employment	0.00
55. Social network	0.00
56. Health insurance	0.00
57. Health status	0.00
58. Employment	0.00
59. Social network	0.00
60. Health insurance	0.00
61. Health status	0.00
62. Employment	0.00
63. Social network	0.00
64. Health insurance	0.00
65. Health status	0.00
66. Employment	0.00
67. Social network	0.00
68. Health insurance	0.00
69. Health status	0.00
70. Employment	0.00
71. Social network	0.00
72. Health insurance	0.00
73. Health status	0.00
74. Employment	0.00
75. Social network	0.00
76. Health insurance	0.00
77. Health status	0.00
78. Employment	0.00
79. Social network	0.00
80. Health insurance	0.00
81. Health status	0.00
82. Employment	0.00
83. Social network	0.00
84. Health insurance	0.00
85. Health status	0.00
86. Employment	0.00
87. Social network	0.00
88. Health insurance	0.00
89. Health status	0.00
90. Employment	0.00
91. Social network	0.00
92. Health insurance	0.00
93. Health status	0.00
94. Employment	0.00
95. Social network	0.00
96. Health insurance	0.00
97. Health status	0.00
98. Employment	0.00
99. Social network	0.00
100. Health insurance	0.00

Met Arg Pro Val Phe Val Gly Asn Leu Asp Tyr Asp Thr Arg His Ser
1 5 10 15
Glu Leu Asp Arg Leu Phe Tyr Arg Tyr Gly Arg Val Glu Arg Ile Asp
20 25 30
Met Lys Ser Gly Tyr Ala Phe Val Tyr Phe Glu Asp Glu Arg Asp Gly
35 40 45
Asn Asp Ala Ile Gln Ala Leu Asp Gly Tyr Pro Phe Gly Pro Gly Arg
50 55 60
Arg Arg Leu Ser Val Glu Trp Ser Arg Gly
65 70

(2) INFORMATION FOR SEQ ID NO:2810:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..42

(D) OTHER INFORMATION: / Ceres Seq. ID 1601931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2810:

Met Lys Ser Gly Tyr Ala Phe Val Tyr Phe Glu Asp Glu Arg Asp Gly
1 5 10 15
Asn Asp Ala Ile Gln Ala Leu Asp Gly Tyr Pro Phe Gly Pro Gly Arg
20 25 30
Arg Arg Leu Ser Val Glu Trp Ser Arg Gly
35 40

(2) INFORMATION FOR SEQ ID NO:2811:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 412 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..412

(D) OTHER INFORMATION: / Ceres Seq. ID 1601940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2811:

gttcgcgttg	cccgcgactc	tctccgtcct	cctactctca	cacgcttgge	gcgcgcgtgc	60
ttccacacgt	ccgtcgcttc	gcctggctga	ttggtttggg	acctggctcc	agcaatggcg	120
gtgcaggcgc	attatcacca	ccaccaccac	caccaccaac	gcgagtcccc	tttctctgtc	180
agcggcggcg	cgccggaggg	cagccggttg	gcggcggcga	tggagctgca	tcaggcgag	240
aaggaggcta	ctacggcgca	gcagcacgct	ccgcccgaact	tctcgcatgg	aggttgcggc	300
ggcgggaaga	agcggcagcg	cgaggcggac	cccgtgtccc	ggcagctctt	gtcgtttgcag	360
cagcagcaac	cacaggcgca	ggggcccaag	ttcatcaacc	tggcgcaact	gc	

(2) INFORMATION FOR SEQ ID NO:2812:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1601941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2812:

Phe Ala Leu Pro Ala Thr Leu Ser Val Leu Leu Leu Ser His Ala Trp
1 5 10 15

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Arg Ala Arg Ala Ser Thr Arg Pro Ser Pro Arg Leu Ala Asp Trp Phe
20 25 30
Gly Thr Trp Leu Gln Gln Trp Arg Cys Arg Arg Ile Ile Thr Thr Thr
35 40 45
Thr Thr Thr Thr Thr Ala Ser Pro Leu Ser Ser Ser Ala Ala Ala Arg
50 55 60
Arg Arg Ala Ala Gly Trp Arg Arg Arg Trp Ser Cys Ile Arg Arg Arg
65 70 75 80
Arg Arg Leu Leu Arg Arg Ser Ser Thr Leu Arg Pro Thr Ser Arg Met
85 90 95
Glu Val Ala Ala Ala Gly Arg Ser Gly Ser Ala Arg Arg Thr Pro Cys
100 105 110
Pro Gly Ser Ser Cys Arg Cys Ser Ser Asn His Arg Arg Arg Gly
115 120 125
Pro Ser Ser Ser Thr Trp Arg Asn Cys
130 135

(2) INFORMATION FOR SEQ ID NO:2813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1601942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2813:

Ser Arg Cys Pro Arg Leu Ser Pro Ser Ser Tyr Ser His Thr Leu Gly
1 5 10 15
Ala Arg Val Leu Pro His Val Arg Arg Leu Ala Trp Leu Ile Gly Leu
20 25 30
Gly Pro Gly Ser Ser Asn Gly Gly Ala Gly Ala Leu Ser Pro Pro Pro
35 40 45
Pro Pro Pro Pro Pro Arg Val Pro Phe Pro Arg Gln Arg Arg Arg Ala
50 55 60
Gly Gly Gln Pro Val Gly Gly Gly Asp Gly Ala Ala Ser Gly Ala Glu
65 70 75 80
Gly Gly Tyr Tyr Gly Ala Ala Ala Arg Ser Ala Arg Leu Leu Ala Trp
85 90 95
Arg Leu Arg Arg Arg Glu Glu Ala Ala Ala Arg Gly Gly Pro Arg Val
100 105 110
Pro Ala Ala Leu Val Val Ala Ala Ala Ala Thr Thr Gly Ala Gly Ala
115 120 125
Gln Val His Gln Pro Gly Ala Thr
130 135

(2) INFORMATION FOR SEQ ID NO:2814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1601943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2814:

Met Ala Val Gln Ala His Tyr His His His His His His His Arg
1 5 10 15
Glu Ser Pro Phe Leu Val Ser Gly Gly Ala Pro Glu Gly Ser Arg Leu

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(2) INFORMATION FOR SEO ID NO:2815:

(A) LENGTH: 462 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..462

(xi) SEQUENCE DESCRIPTION: SEO ID NO:2815:

(2) INFORMATION FOR SEQ ID NO:2816:

(A) LENGTH: 110 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2816:															
Met	Ala	Ser	Lys	Arg	Ile	Leu	Lys	Glu	Leu	Lys	Asp	Leu	Gln	Lys	Asp
1				5				10						15	
Pro	Pro	Thr	Ser	Cys	Ser	Ala	Gly	Pro	Ala	Gly	Glu	Asp	Met	Phe	His
			20					25					30		
Trp	Gln	Ala	Thr	Ile	Met	Gly	Pro	Pro	Asp	Ser	Pro	Tyr	Ala	Gly	Gly
		35					40					45			
Val	Phe	Leu	Val	Asn	Ile	His	Phe	Pro	Pro	Asp	Tyr	Pro	Phe	Lys	Pro
	50					55					60				
Pro	Lys	Val	Ser	Phe	Lys	Thr	Lys	Val	Phe	His	Pro	Asn	Ile	Asn	Ser
65				70						75				80	
Asn	Gly	Ser	Ile	Cys	Leu	Asp	Ile	Leu	Lys	Glu	Gln	Trp	Ser	Pro	Ala
				85					90					95	
Leu	Thr	Ile	Ser	Lys	Val	Leu	Leu	Ser	Ile	Cys	Ser	Leu	Leu		
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:2817:

(A) LENGTH: 81 amino acids
(B) TYPE: amino acid

(B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..81
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601949
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2817:

Met Phe His Trp Gln Ala Thr Ile Met Gly Pro Pro Asp Ser Pro Tyr
1 5 10 15
Ala Gly Gly Val Phe Leu Val Asn Ile His Phe Pro Pro Asp Tyr Pro
20 25 30
Phe Lys Pro Pro Lys Val Ser Phe Lys Thr Lys Val Phe His Pro Asn
35 40 45
Ile Asn Ser Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp
50 55 60
Ser Pro Ala Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu
65 70 75 80
Leu

- (2) INFORMATION FOR SEQ ID NO:2818:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..73
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601950
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2818:

Met Gly Pro Pro Asp Ser Pro Tyr Ala Gly Gly Val Phe Leu Val Asn
1 5 10 15
Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro Pro Lys Val Ser Phe
20 25 30
Lys Thr Lys Val Phe His Pro Asn Ile Asn Ser Asn Gly Ser Ile Cys
35 40 45
Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala Leu Thr Ile Ser Lys
50 55 60
Val Leu Leu Ser Ile Cys Ser Leu Leu
65 70

- (2) INFORMATION FOR SEQ ID NO:2819:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 445 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:

- (A) NAME/KEY: -
 - (B) LOCATION: 1..445
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601957

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2819:

gaaaagtcaa	aagaacccgc	agcaggggag	actgggagat	agagagagga	gagggagggt	60
ttcctcaaag	agaacccgaa	accaaaccga	agcagagaac	actagcgttc	cctcaccagg	120
gcgtccatcc	cagcagccat	ggcgatggcg	tacaagatgg	cgacggaggg	gatgaacgtg	180
aaggaggagt	gccagcgctg	gttcatggag	atgaagtggg	agaaggtgca	ccgcttcgtg	240
gtgtacaaga	tcgacgagcg	gtcgcgcgcc	gtgctggtgg	acaaggtggg	cgccccggg	300
gaagggtagc	aggagctcgt	ggccgcgctg	cccgccgacg	actgccgcta	cgccgtcttc	360
gacttcgact	tcgtcaccgt	cgacaactgc	cagaagagca	agatcttctt	catcgccctg	420

(2) INFORMATION FOR SEQ ID NO:2820:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1601958

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2820:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2821:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1601959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2821:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2822:

(i) SEQUENCE CHARACTERISTICS:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2823:

(A) LENGTH: 407 base pairs

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(D) OTHER INFORMATION: / Ceres Seq. ID 1601976

gcgggtccaga	tcgatcggtt	tttgcagatt	ggtgcgtcca	cacgagagtt	tacggcggcc	60
caaaccccc	aaatccagtt	ccatcccaat	cgccgagaag	gggaagccaa	atcgatggcg	120
gcgcgcgcgcg	ccggcggcga	gaacagcggc	gcgggcgcgcg	gcgcgcgcga	gggcgagttc	180
tacctgcggt	actacgtggg	gcacaaagggc	aagttcgggc	acgagttcct	cgagttcgag	240
ttccgccccg	acggcaagct	ccgctacgcc	aacaactcca	actacaagaa	cgacaccatg	300
atccgcgaag	aggctctcgt	ctccccctcc	gtcctccgcg	aggccaggag	gatcatccaa	360
ggagtcogag	atcatgaagg	aggacgacag	caactggcct	gagcccg		

(2) INFORMATION FOR SEQ ID NO:2824:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1601977

Ala	Val	Gln	Ile	Asp	Arg	Tyr	Leu	Gln	Ile	Gly	Ala	Ser	Thr	Arg	Glu
1				5					10					15	
Phe	Thr	Ala	Ala	Gln	Thr	Pro	Gln	Ile	Gln	Phe	His	Pro	Asn	Arg	Arg
		20					25					30			
Glu	Gly	Glu	Ala	Lys	Ser	Met	Ala	Ala	Ala	Ala	Gly	Gly	Glu	Asn	
		35					40				45				

Ser Gly Ala Gly Ala Gly Ala Gly Glu Gly Glu Phe Tyr Leu Arg Tyr
50 55 60
Tyr Val Gly His Lys Gly Lys Phe Gly His Glu Phe Leu Glu Phe Glu
65 70 75 80
Phe Arg Pro Asp Gly Lys Leu Arg Tyr Ala Asn Asn Ser Asn Tyr Lys
85 90 95
Asn Asp Thr Met Ile Arg Lys Glu Val Phe Val Ser Pro Ser Val Leu
100 105 110
Arg Glu Ala Arg Arg Ile Ile Gln Gly Val Arg Tyr His Glu Gly Gly
115 120 125
Arg Gln Gln Leu Ala
130

(2) INFORMATION FOR SEQ ID NO:2825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1601978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2825:

Arg Ser Arg Ser Ile Gly Ile Cys Arg Leu Val Arg Pro His Glu Ser
1 5 10 15
Leu Arg Arg Pro Lys Pro Pro Lys Ser Ser Ser Ile Pro Ile Ala Glu
20 25 30
Lys Gly Lys Pro Asn Arg Trp Arg Arg Arg Pro Ala Ala Arg Thr
35 40 45
Ala Ala Arg Ala Arg Ala Arg Ala Arg Ala Ser Ser Thr Cys Gly Thr
50 55 60
Thr Trp Gly Thr Arg Ala Ser Ser Gly Thr Ser Ser Ser Ser Ser Ser
65 70 75 80
Ser Ala Pro Thr Ala Ser Ser Ala Thr Pro Thr Thr Pro Thr Thr Arg
85 90 95
Thr Thr Pro

(2) INFORMATION FOR SEQ ID NO:2826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1601979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2826:

Gly Pro Asp Arg Ser Val Phe Ala Asp Trp Cys Val His Thr Arg Val
1 5 10 15
Tyr Gly Gly Pro Asn Pro Pro Asn Pro Val Pro Ser Gln Ser Pro Arg
20 25 30
Arg Gly Ser Gln Ile Asp Gly Gly Gly Gly Arg Arg Arg Glu Gln
35 40 45
Arg Arg Gly Arg Gly Arg Gly Arg Gly Arg Val Leu Pro Ala Val Leu
50 55 60
Arg Gly Ala Gln Gly Gln Val Arg Ala Arg Val Pro Arg Val Arg Val
65 70 75 80
Pro Pro Arg Arg Gln Ala Pro Leu Arg Gln Gln Leu Gln Leu Gln Glu

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85 90 95
Arg His His Asp Pro Gln Gly Gly Leu Arg Leu Pro Leu Arg Pro Pro
100 105 110
Arg Gly Gln Glu Asp His Pro Arg Ser Pro Ile Ser
115 120

(2) INFORMATION FOR SEQ ID NO:2827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..474
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2827:

atcagacggg ggagagcaac accagctcaa aaccctagcg tccaaactcat atacctgctg 60
ctcgccccga cgcgcatcaa ctcccgccgc cgcccttcc tctccgtcgc tcgcctcgcg 120
cctacgccac cacctctgcc atggcccga agaaggataa ggccccgcgc ccgtcgtcca 180
agccggccaa gtccggaggc gggaagcaga agaagaagaa gtggagcaag ggtaagcaaa 240
aggagaaggt caacaacgct gtgctcttcg accaggccac ctatgacaag ttgctctccg 300
agggtgccaa gtacaagcag atcaccccat ccgtcctctc cgagcgtctc aggattaatg 360
gatcattykg cacggagggc aatcaaggat ctgatggcaa ggggattcat aaggatgatc 420
tctgttcatt ccagccagca gatatacacc agkcaacca acacatgagg gctg

(2) INFORMATION FOR SEQ ID NO:2828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1601981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2828:

Ile Arg Arg Trp Arg Ala Thr Pro Ala Gln Asn Pro Ser Val Gln Leu
1 5 10 15
Ile Tyr Leu Leu Leu Ala Pro Thr Arg Ile Asn Ser Arg Arg Arg Pro
20 25 30
Phe Leu Ser Val Ala Arg Leu Ala Pro Thr Pro Pro Pro Leu Pro Trp
35 40 45
Pro Arg Arg Arg Ile Arg Pro Arg Arg Arg Arg Pro Ser Arg Pro Ser
50 55 60
Pro Glu Ala Gly Ser Arg Arg Arg Ser Gly Ala Arg Val Ser Lys
65 70 75 80
Arg Arg Arg Ser Thr Thr Leu Cys Ser Ser Thr Arg Pro Pro Met Thr
85 90 95
Ser Cys Ser Pro Arg Cys Pro Ser Thr Ser Arg Ser Pro His Pro Ser
100 105 110
Ser Pro Ser Val Ser Gly Leu Met Asp His Xaa Ala Arg Arg Ala Ile
115 120 125
Lys Asp Leu Met Ala Arg Gly Phe Ile Arg Met Ile Ser Val His Ser
130 135 140
Ser Gln Gln Ile Tyr Thr Arg Xaa Thr Asn Thr
145 150 155

(2) INFORMATION FOR SEQ ID NO:2829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid

00500103660360

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..111
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601982
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2829:

Met Ala Pro Lys Lys Asp Lys Ala Pro Pro Pro Ser Ser Lys Pro Ala
1 5 10 15
Lys Ser Gly Gly Lys Gln Lys Lys Lys Trp Ser Lys Gly Lys
20 25 30
Gln Lys Glu Lys Val Asn Asn Ala Val Leu Phe Asp Gln Ala Thr Tyr
35 40 45
Asp Lys Leu Leu Ser Glu Val Pro Lys Tyr Lys Gln Ile Thr Pro Ser
50 55 60
Val Leu Ser Glu Arg Leu Arg Ile Asn Gly Ser Xaa Xaa Thr Glu Gly
65 70 75 80
Asn Gln Gly Ser Asp Gly Lys Gly Ile His Lys Asp Asp Leu Cys Ser
85 90 95
Phe Gln Pro Ala Asp Ile His Gln Xaa Asn Gln His Met Arg Ala
100 105 110

(2) INFORMATION FOR SEQ ID NO:2830:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..390
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601994
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2830:

aaagagaaga taaaggacct gtttgacaaa catggagagg tcacaaaaat cgttctgcct 60
cctgcccaagg ctggtcataa gagagacttt ggctttgttc actttgcaga aagatcaagt 120
gcattgaagg cagttaaagg aagtgaaaaa tatgaaatcg atggatcaagt actggaagtg 180
tccatggcca aaccattggc agataagaaa cctgatcatt cacacaggcc tggaggaggc 240
cctaattatc cccttcctcc ctatggtggt ggtggctaca tgggagatcc atatggtgct 300
tatggtggtg gcggtcctgc atacaaccag ccaatgatat atggcagagg accagcaccg 360
gcaggaatga ggtatggtgcc gatggtgctt

(2) INFORMATION FOR SEQ ID NO:2831:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..130
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1601995
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2831:

Lys Glu Lys Ile Lys Asp Leu Phe Asp Lys His Gly Glu Val Thr Lys
1 5 10 15
Ile Val Leu Pro Pro Ala Lys Ala Gly His Lys Arg Asp Phe Gly Phe
20 25 30
Val His Phe Ala Glu Arg Ser Ser Ala Leu Lys Ala Val Lys Gly Ser
35 40 45
Glu Lys Tyr Glu Ile Asp Gly Gln Val Leu Glu Val Ser Met Ala Lys
50 55 60

00559980-10100

(D) OTHER INFORMATION: / Ceres Seq. ID 1601998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2834:

Thr Gly Ala Asp Gly Glu Asn Phe Glu Thr Arg Ala Arg Pro Pro Pro
1 5 10 15
Pro Arg Gln Ile Glu Pro Ser Arg Phe His Ser Thr Ala Gly Ser Gln
20 25 30
Ile Arg Ala Ser Ile Ile Leu Pro Gly Ile Leu Ser Ser Pro Lys Thr
35 40 45
Arg Thr Ala Pro Arg Glu Ile Lys Ser Cys Lys Ser Leu Ala Ala Thr
50 55 60
Ser Arg Gly Ser Ala Thr Ala Met Thr Ala Ser Phe Ser Ser Val Ala
65 70 75 80
Glu Val Ala Val Pro Ala Ala Ala Ala Val Met Ala Ser Ala Leu Pro
85 90 95
Gln Glu Gln Gln Gln Ala Arg Pro Arg Pro Arg Pro Met His Ala Gly
100 105 110
Gly Gly Gly Gly Gly Gly Gly Gly Ala Asn Gly Arg His His Ala Tyr
115 120 125
Ser Arg
130

(2) INFORMATION FOR SEQ ID NO:2835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..459

(D) OTHER INFORMATION: / Ceres Seq. ID 1602005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2835:

atctcgggttt tattcaaagt ctcaacacgc ttgtttcccg caggagcgtg gtcagatcct 60
ccacaggttc gcggacctga tcgacgagca cgtggaggag ctggcgggcg tggacacggt 120
ggacgccggc aagctgttcg ccgtgggcaa ggcgcgggac atcccgggcg ccgcgcacct 180
gctgcgctac tacgccggcg ccgccgacaa ggtgcacggc gcgacgctca agatggcgca 240
gcggtatcac gggtacacgc tcaaggagcc cgtgggcgtg gtgggccaca tcgtgccctg 300
gaactacccc accaccatgt tcttcttcaa ggtagggccg gcgctcgccg caggctgcgc 360
cgctcgtcgtc aagcccgccg agcagacgcc gctgtccgcg ctcttctaag cgcacctcgc 420
cagggaggcc ggcgtcccg cggcgtgctc aacgtcgtg

(2) INFORMATION FOR SEQ ID NO:2836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1602006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2836:

Ile Ser Val Leu Phe Lys Cys Ser Thr Arg Leu Phe Pro Ala Gly Ala
1 5 10 15
Trp Ser Asp Pro Pro Gln Val Arg Gly Pro Asp Arg Arg Ala Arg Gly
20 25 30
Gly Ala Gly Gly Ala Gly His Gly Gly Arg Arg Gln Ala Val Arg Arg
35 40 45
Gly Gln Gly Ala Gly His Pro Gly Arg Arg Ala Pro Ala Ala Leu Leu
50 55 60
Arg Arg Arg Arg Arg Gln Gly Ala Arg Arg Asp Ala Gln Asp Gly Ala

09689980-101300

65 70 75 80
Ala Asp Ala Arg Val His Ala Gln Gly Ala Arg Gly Arg Gly Gly Pro
85 90 95
His Arg Ala Leu Glu Leu Pro His His His Val Leu Leu Gln Gly Arg
100 105 110
Ala Arg Ala Arg Arg Arg Leu Arg Arg Arg Arg Gln Ala Arg Arg Ala
115 120 125
Asp Ala Ala Val Arg Ala Leu Leu Arg Ala Pro Arg Gln Gly Gly Arg
130 135 140
Arg Pro Ala Gly Val Leu Asn Val Val
145 150

(2) INFORMATION FOR SEQ ID NO:2837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1602007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2837:

Ser Arg Phe Tyr Ser Asn Ala Gln His Ala Cys Phe Pro Gln Glu Arg
1 5 10 15
Gly Gln Ile Leu His Arg Phe Ala Asp Leu Ile Asp Glu His Val Glu
20 25 30
Glu Leu Ala Ala Leu Asp Thr Val Asp Ala Gly Lys Leu Phe Ala Val
35 40 45
Gly Lys Ala Arg Asp Ile Pro Gly Ala Ala His Leu Leu Arg Tyr Tyr
50 55 60
Ala Gly Ala Ala Asp Lys Val His Gly Ala Thr Leu Lys Met Ala Gln
65 70 75 80
Arg Met His Gly Tyr Thr Leu Lys Glu Pro Val Gly Val Val Gly His
85 90 95
Ile Val Pro Trp Asn Tyr Pro Thr Thr Met Phe Phe Phe Lys Val Gly
100 105 110
Pro Ala Leu Ala Ala Gly Cys Ala Val Val Val Lys Pro Ala Glu Gln
115 120 125
Thr Pro Leu Ser Ala Leu Phe Tyr Ala His Leu Ala Arg Glu Ala Gly
130 135 140
Val Pro Pro Ala Cys Ser Thr Ser
145 150

(2) INFORMATION FOR SEQ ID NO:2838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..465

(D) OTHER INFORMATION: / Ceres Seq. ID 1602032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2838:

actctctagc ttcccactcc gctcggccac cagctttgac cgctccctcc cccctccgct 60
cctgttcttc catacccccac tccccgcgag gagcggcgcg gcggcggaag aggcaaaggc 120
aagatgttcg ggcgcgcgcc gaagaagagc gacaacacca agtactacga gatcctcggg 180
gtgcccagtg cggcggtccc ggacgacctc aagaaggcct accgcaaggc cgctatcaag 240
aaccaccccg acaagggcgg tgaccccgag aagttcaagg agctcgaca agcctatgag 300
gttttgagtg atccagagaa acgtgagatt tatgatcagt atggtgaaga tgcccttaag 360

09669980 10100

50 55 60
Arg Asp Ser Lys Gly Gln Arg Leu Gly Val Lys Ile Tyr Gly Asp Gln
65 70 75 80
Leu Ala Lys Pro Gly Ala Ile Ile Ile Arg Gln Arg Gly Thr Arg Val
85 90 95
Tyr Pro Gly Asn Asn Val Gly Met Gly Lys Asp His Thr Leu Phe Ser
100 105 110
Leu Ile Asp Gly Leu Val Lys Phe Glu Lys Tyr Gly Pro Asp Lys Lys
115 120 125
Lys Xaa Ser Val Tyr Pro Tyr Glu Lys Glu Pro Glu Asn Pro Asn Ser
130 135 140
Tyr Arg Ala Arg Lys Arg Glu Tyr
145 150

(2) INFORMATION FOR SEQ ID NO:2846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..466
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2846:

aaaagccctt cccctcctt ttcccccggt cgagttgctc gagctccgac caaatctcgc 60
agcggttagca atccccgagc ccgaagcggg atcagtggag gacgacaccc tcgattctga 120
cctgcggtcg gcgcgactta cagacaaccg gagatgcagc agggcgacag cacggaggcg 180
caggtgacgt gggaggacca gcagaacatc aaccgcttcg gtcgcctcaa caaccgcctc 240
cacgagctcc aggacgagat caaactcgcg aaggaaacga acgagaacct tgacgatgct 300
gggaacgaac tcattcctgtc ggacgaagat gtcgtgcgct tccagatcgg ggaggtgttt 360
gctcacatgc cgagggactg acgtcgagac taggctggag cagatgaaag aggatgcggc 420
taagaagctg gagaggctag aggaggagaa ggaatccgtc ctcgcc

(2) INFORMATION FOR SEQ ID NO:2847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2847:

Lys Ala Leu Pro Pro Phe Pro Pro Phe Glu Leu Leu Glu Leu Arg
1 5 10 15
Pro Asn Leu Ala Ala Val Ala Ile Pro Glu Pro Glu Ala Gly Ser Val
20 25 30
Glu Asp Asp Thr Leu Asp Ser Asp Leu Arg Ser Ala Arg Leu Thr Asp
35 40 45
Asn Arg Arg Cys Ser Arg Ala Thr Ala Arg Arg Arg Arg
50 55 60

(2) INFORMATION FOR SEQ ID NO:2848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

09659900 101300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2848:

(2) INFORMATION FOR SEQ ID NO:2849:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1602056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2849:

(2) INFORMATION FOR SEQ ID NO:2850:

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..488

(D) OTHER INFORMATION: / Ceres Seq. ID 1602060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2850:

(2) INFORMATION FOR SEQ ID NO:2851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..162
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1602061
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2851:

Ala Pro Pro Ser Arg Ile Pro Lys Arg Gln Asn Leu Val Val Thr Pro
1 5 10 15
Thr His Arg Ile Val Arg Phe Leu Ser Ser Thr Pro Leu Leu Phe Ser
20 25 30
Ala Ser Pro Pro Leu Arg Arg Arg Arg Phe Thr Arg Gln Pro Ala
35 40 45
Met Asp Glu Glu Tyr Asp Val Ile Val Leu Gly Thr Gly Leu Lys Glu
50 55 60
Cys Ile Leu Ser Gly Leu Leu Ser Val Asp Gly Leu Lys Val Leu His
65 70 75 80
Met Asp Arg Asn Asp Tyr Tyr Gly Gly Asp Ser Thr Ser Leu Asn Leu
85 90 95
Asn Gln Leu Trp Lys Arg Phe Arg Gly Glu Asp Lys Pro Pro Ala His
100 105 110
Leu Gly Ala Ser Arg Asp Tyr Asn Val Asp Met Val Pro Lys Phe Met
115 120 125
Met Ala Asn Gly Thr Leu Val Arg Thr Leu Ile His Thr Asp Val Thr
130 135 140
Lys Tyr Leu Ser Phe Lys Ala Val Asp Gly Ser Tyr Val Phe Ser Lys
145 150 155 160
Gly Lys

(2) INFORMATION FOR SEQ ID NO:2852:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..114
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1602062
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2852:

Met Asp Glu Glu Tyr Asp Val Ile Val Leu Gly Thr Gly Leu Lys Glu
1 5 10 15
Cys Ile Leu Ser Gly Leu Leu Ser Val Asp Gly Leu Lys Val Leu His
20 25 30
Met Asp Arg Asn Asp Tyr Tyr Gly Gly Asp Ser Thr Ser Leu Asn Leu
35 40 45
Asn Gln Leu Trp Lys Arg Phe Arg Gly Glu Asp Lys Pro Pro Ala His
50 55 60
Leu Gly Ala Ser Arg Asp Tyr Asn Val Asp Met Val Pro Lys Phe Met
65 70 75 80
Met Ala Asn Gly Thr Leu Val Arg Thr Leu Ile His Thr Asp Val Thr
85 90 95
Lys Tyr Leu Ser Phe Lys Ala Val Asp Gly Ser Tyr Val Phe Ser Lys
100 105 110
Gly Lys

(2) INFORMATION FOR SEQ ID NO:2853:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

00669920 10300

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..82
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1602063
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2853:

```
Met Asp Arg Asn Asp Tyr Tyr Gly Gly Asp Ser Thr Ser Leu Asn Leu
1          5          10          15
Asn Gln Leu Trp Lys Arg Phe Arg Gly Glu Asp Lys Pro Pro Ala His
          20          25          30
Leu Gly Ala Ser Arg Asp Tyr Asn Val Asp Met Val Pro Lys Phe Met
          35          40          45
Met Ala Asn Gly Thr Leu Val Arg Thr Leu Ile His Thr Asp Val Thr
          50          55          60
Lys Tyr Leu Ser Phe Lys Ala Val Asp Gly Ser Tyr Val Phe Ser Lys
65          70          75          80
Gly Lys
```

(2) INFORMATION FOR SEQ ID NO:2854:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..513
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1602076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2854:

```
actcttcycc ttttctcct cctctccttt cctctcctct aggtctctagt cctctcgcat      60
ccgcagcttc ccagccagc tagggtttgc agatgacgac cgcggcgcgc ccncctggg      120
cgccggccaa ggcggcaac gagcaggggg gcaccgcgat cttcggtccc tcccagaagt      180
tctctcccg cgacctgcc gcgcacacct cctcaagcc aagaaaagac ggtcaacaga      240
cccaagagga gttacagaag aggaatctca gggaggaact tgaggaacgt gagcgcaagc      300
actactcttc caaggataag tcctatgccg aagaaagaga ccggcggaaa agctctagcc      360
atctactctt agaaggttca aagagagaga cagaggataa gatagttcca cgagaaatcg      420
atgctgatga ctccgatgtg gagcctaaaa gcgatgacga gagcgatgaa gatgatgat      480
acgacgacac tgaagctcta atggcagagc ttg
```

(2) INFORMATION FOR SEQ ID NO:2855:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 140 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..140
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1602077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2855:

```
Met Thr Thr Ala Ala Arg Pro Xaa Trp Ala Pro Ala Lys Gly Gly Asn
1          5          10          15
Glu Gln Gly Gly Thr Arg Ile Phe Gly Pro Ser Gln Lys Phe Ser Ser
          20          25          30
Arg Asp Leu Ala Ala His Thr Ser Leu Lys Pro Arg Lys Asp Gly Gln
          35          40          45
Gln Thr Gln Glu Glu Leu Gln Lys Arg Asn Leu Arg Glu Glu Leu Glu
          50          55          60
Glu Arg Glu Arg Lys His Tyr Ser Ser Lys Asp Lys Ser Tyr Ala Glu
```

00000000 00000000

(X1) SEQUENCE DESCRIPTION: SEQ ID: 1																
Ile	Leu	Val	Ser	Leu	Ile	Ser	Val	Arg	Arg	Arg	Arg	Arg	Arg	Pro	Ile	
1				5				10						15		
Ser	Pro	Phe	Leu	Phe	Ala	Phe	Ser	Pro	Ala	His	His	Pro	Ala	Thr	Thr	
			20					25					30			
Leu	Ser	Leu	Leu	Cys	Leu	Leu	Ala	Ala	Ala	Val	Leu	Pro	Pro	Pro	Arg	
			35				40					45				
Pro	Ala	Ala	Gly	Ser	Ser	His	Ala	Arg	Glu	Pro	Arg	Leu	Gln	Gly	Arg	
			50			55					60					
His	Leu	Leu	Arg	Arg	Thr	Leu	His	Gly	Gln	Arg	His	Ser	Ser	Met	Leu	
65					70					75					80	
Arg	Arg	Asp	Met	Tyr	His	Pro	Ala	Arg	His	Gly	Gln	Gly	Gln	Ala	Pro	
				85					90					95		
Ala	Ala	Glu	Glu	Arg	Arg	Arg	Arg	Arg	Ala	Ser	Gly	Asp	Ala	Ala	Pro	
			100					105					110			
Ala	Leu	Pro	Lys	Tyr	Arg	Gly	Leu	Leu	Gly	Thr	Ala	Ala	Thr	Ile	Ala	
			115				120					125				
Arg	Glu	Glu	Gly	Ala	Ala	Ala	Leu	Trp	Lys	Gly	Ile	Val	Pro	Gly	Xaa	
			130			135					140					
Pro	Pro	Thr	Val	His	Leu	Arg	Gly	Gly	Tyr	Ala	Leu	Ala	Ser	Thr	Ser	

(2) INFORMATION FOR SEQ ID NO:2858:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1602080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2858:

(2) INFORMATION FOR SEQ ID NO:2859:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1602081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2859:

(2) INFORMATION FOR SEQ ID NO:2860:

(A) LENGTH: 464 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..464

(D) OTHER INFORMATION: / Ceres Seq. ID 1602089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2860:

atatattcat	gtcccagaaa	cttgctcaggc	tctcttcctc	cctcgccgcg	gaacacgcgc	60
cccgctcctcg	cccgcccggtg	ttcatctctc	cattccatac	cttgccagtgc	aggtgcgggtg	120
gtagccgagc	gctccggcca	tggcggttctt	ccgggggcctc	accgcggtct	cgaggctgcg	180
atcccgcatg	gcgccaggagg	ccaccacgct	gggtgggtgtg	agatggctgc	agatgcagag	240
cgcgctccgat	ctcgatctta	agtcccagtt	gcagggaattg	attccggaac	agcaggatcg	300
cctaaagaag	cttaaatacag	agcatgggaa	ggttcagctt	ggaaacataa	ctgtggatat	360
ggtccttggt	ggamtgagag	ggatgattgg	aatgcttttg	gaaacatccc	tacttgaccy	420
agaggagggt	attcgtttta	ggggctctctc	gattccagag	tgcc		

(2) INFORMATION FOR SEQ ID NO:2861:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1602090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2861:

Ile	Tyr	Ser	Cys	Pro	Glu	Asn	Leu	Ser	Gly	Ser	Leu	Pro	Pro	Ser	Pro
1				5				10						15	
Arg	Asn	Thr	Arg	Pro	Val	Leu	Ala	Arg	Pro	Cys	Ser	Ser	Leu	His	Ser
			20					25					30		
Ile	Pro	Cys	Ser	Ala	Gly	Ala	Val	Val	Ala	Glu	Arg	Ser	Gly	His	Gly
		35				40						45			
Val	Leu	Pro	Gly	Pro	His	Arg	Gly	Leu	Glu	Ala	Ala	Ile	Pro	His	Gly
	50					55				60					
Ala	Gly	Gly	His	His	Ala	Gly	Trp	Cys	Glu	Met	Ala	Ala	Asp	Ala	Glu
65					70				75						80
Arg	Val	Arg	Ser	Arg	Ser										
				85											

(2) INFORMATION FOR SEQ ID NO:2862:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1602091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2862:

Met	Ala	Phe	Phe	Arg	Gly	Leu	Thr	Ala	Val	Ser	Arg	Leu	Arg	Ser	Arg
1				5				10						15	
Met	Ala	Gln	Glu	Ala	Thr	Thr	Leu	Gly	Gly	Val	Arg	Trp	Leu	Gln	Met
		20						25					30		
Gln	Ser	Ala	Ser	Asp	Leu	Asp	Leu	Lys	Ser	Gln	Leu	Gln	Glu	Leu	Ile
		35					40					45			
Pro	Glu	Gln	Gln	Asp	Arg	Leu	Lys	Lys	Leu	Lys	Ser	Glu	His	Gly	Lys
	50					55				60					
Val	Gln	Leu	Gly	Asn	Ile	Thr	Val	Asp	Met	Val	Leu	Gly	Gly	Xaa	Arg
65					70				75					80	
Gly	Met	Ile	Gly	Met	Leu	Trp	Glu	Thr	Ser	Leu	Leu	Asp	Xaa	Glu	Glu

(2) INFORMATION FOR SEQ ID NO:2863:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1602092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2863:

Met	Ala	Gln	Glu	Ala	Thr	Thr	Leu	Gly	Gly	Val	Arg	Trp	Leu	Gln	Met
1				5					10					15	
Gln	Ser	Ala	Ser	Asp	Leu	Asp	Leu	Lys	Ser	Gln	Leu	Gln	Glu	Leu	Ile
			20					25					30		
Pro	Glu	Gln	Gln	Asp	Arg	Leu	Lys	Lys	Leu	Lys	Ser	Glu	His	Gly	Lys
			35				40					45			
Val	Gln	Leu	Gly	Asn	Ile	Thr	Val	Asp	Met	Val	Leu	Gly	Gly	Xaa	Arg
	50					55					60				
Gly	Met	Ile	Gly	Met	Leu	Trp	Glu	Thr	Ser	Leu	Leu	Asp	Xaa	Glu	Glu
65				70						75				80	
Gly	Ile	Arg	Phe	Arg	Gly	Leu	Ser	Ile	Pro	Glu	Cys				
				85					90						

(2) INFORMATION FOR SEQ ID NO:2864:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 546 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..546

(D) OTHER INFORMATION: / Ceres Seq. ID 1602093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2864:

(X1) SEQUENCE ALIGNMENT: SEQ ID NO: 1								
accggaacga	aacgctgagg	cagcatcttc	ccgcgcgtcc	tccgcgcgct	cccattttca			60
ccttggtcgc	agcctgcaac	acaatcctac	gcttcgcact	tcaacgcgcg	cccctcccat			120
tttcacctag	ccctactcct	ttgtacataa	aggaagatgg	gagcatatgc	aacgactggg			180
atgcagatga	tagcaacacg	cccttccatc	ccggcctaca	ggcaaatact	tgggtcgaca			240
tcagcactat	ctgcatttgg	aagggtcaatc	tggtccagaa	ctggctttgc	catctcttct			300
aaagccaacat	cagcaggacc	actggtttct	tgaattgca	agagggttgt	tgtgagggca			360
atgtcgcaga	gaggtgccca	aggacttccc	attgatctca	caggtaaaaag	agcattttata			420
gctggagttg	ctgatgataa	tggttatggg	tgggcaattg	ctaaggctct	tgctgctgct			480
ggtgctgaga	ttcttgttgg	tacatgggtg	cctgcgttga	acataattga	gacaaaccttg			540
agacgt								

(2) INFORMATION FOR SEQ ID NO:2865:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1602094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2865:

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000

Met	Ile	Ala	Thr	Arg	Pro	Ser	Ile	Pro	Ala	Tyr	Arg	Gln	Ile	Leu	Gly
1				5				10						15	
Ser	Thr	Ser	Ala	Leu	Ser	Ala	Phe	Gly	Arg	Ser	Ile	Cys	Ser	Arg	Thr

Descriptive statistics	
Mean	1.78
SD	0.92
Min	0.00
Max	4.00
Frequency	100
Frequency Percent	
0	10.00
1	20.00
2	30.00
3	20.00
4	20.00
Cumulative Percent	
0	10.00
1	30.00
2	60.00
3	80.00
4	100.00
Chi-Square	
Chi-Square	1.10
df	3
Asymptotic Sig.	.582
Exact Sig.	
Exact Sig. (2x2)	.582
Exact Sig. (2x3)	.582
Exact Sig. (2x4)	.582
Exact Sig. (2x5)	.582
Exact Sig. (2x6)	.582
Exact Sig. (2x7)	.582
Exact Sig. (2x8)	.582
Exact Sig. (2x9)	.582
Exact Sig. (2x10)	.582
Exact Sig. (2x11)	.582
Exact Sig. (2x12)	.582
Exact Sig. (2x13)	.582
Exact Sig. (2x14)	.582
Exact Sig. (2x15)	.582
Exact Sig. (2x16)	.582
Exact Sig. (2x17)	.582
Exact Sig. (2x18)	.582
Exact Sig. (2x19)	.582
Exact Sig. (2x20)	.582
Exact Sig. (2x21)	.582
Exact Sig. (2x22)	.582
Exact Sig. (2x23)	.582
Exact Sig. (2x24)	.582
Exact Sig. (2x25)	.582
Exact Sig. (2x26)	.582
Exact Sig. (2x27)	.582
Exact Sig. (2x28)	.582
Exact Sig. (2x29)	.582
Exact Sig. (2x30)	.582
Exact Sig. (2x31)	.582
Exact Sig. (2x32)	.582
Exact Sig. (2x33)	.582
Exact Sig. (2x34)	.582
Exact Sig. (2x35)	.582
Exact Sig. (2x36)	.582
Exact Sig. (2x37)	.582
Exact Sig. (2x38)	.582
Exact Sig. (2x39)	.582
Exact Sig. (2x40)	.582
Exact Sig. (2x41)	.582
Exact Sig. (2x42)	.582
Exact Sig. (2x43)	.582
Exact Sig. (2x44)	.582
Exact Sig. (2x45)	.582
Exact Sig. (2x46)	.582
Exact Sig. (2x47)	.582
Exact Sig. (2x48)	.582
Exact Sig. (2x49)	.582
Exact Sig. (2x50)	.582
Exact Sig. (2x51)	.582
Exact Sig. (2x52)	.582
Exact Sig. (2x53)	.582
Exact Sig. (2x54)	.582
Exact Sig. (2x55)	.582
Exact Sig. (2x56)	.582
Exact Sig. (2x57)	.582
Exact Sig. (2x58)	.582
Exact Sig. (2x59)	.582
Exact Sig. (2x60)	.582
Exact Sig. (2x61)	.582
Exact Sig. (2x62)	.582
Exact Sig. (2x63)	.582
Exact Sig. (2x64)	.582
Exact Sig. (2x65)	.582
Exact Sig. (2x66)	.582
Exact Sig. (2x67)	.582
Exact Sig. (2x68)	.582
Exact Sig. (2x69)	.582
Exact Sig. (2x70)	.582
Exact Sig. (2x71)	.582
Exact Sig. (2x72)	.582
Exact Sig. (2x73)	.582
Exact Sig. (2x74)	.582
Exact Sig. (2x75)	.582
Exact Sig. (2x76)	.582
Exact Sig. (2x77)	.582
Exact Sig. (2x78)	.582
Exact Sig. (2x79)	.582
Exact Sig. (2x80)	.582
Exact Sig. (2x81)	.582
Exact Sig. (2x82)	.582
Exact Sig. (2x83)	.582
Exact Sig. (2x84)	.582
Exact Sig. (2x85)	.582
Exact Sig. (2x86)	.582
Exact Sig. (2x87)	.582
Exact Sig. (2x88)	.582
Exact Sig. (2x89)	.582
Exact Sig. (2x90)	.582
Exact Sig. (2x91)	.582
Exact Sig. (2x92)	.582
Exact Sig. (2x93)	.582
Exact Sig. (2x94)	.582
Exact Sig. (2x95)	.582
Exact Sig. (2x96)	.582
Exact Sig. (2x97)	.582
Exact Sig. (2x98)	.582
Exact Sig. (2x99)	.582
Exact Sig. (2x100)	.582

20 25 30
Gly Phe Ala Ile Ser Ser Lys Ala Thr Ser Ala Gly Pro Leu Val Ser
35 40 45
Ser Asn Cys Lys Arg Val Val Val Arg Ala Met Ser Gln Arg Gly Ala
50 55 60
Gln Gly Leu Pro Ile Asp Leu Thr Gly Lys Arg Ala Phe Ile Ala Gly
65 70 75 80
Val Ala Asp Asp Asn Gly Tyr Gly Trp Ala Ile Ala Lys Ala Leu Ala
85 90 95
Ala Ala Gly Ala Glu Ile Leu Val Gly Thr Trp Val Pro Ala Leu Asn
100 105 110
Ile Phe Glu Thr Ser Leu Arg Arg
115 120

(2) INFORMATION FOR SEQ ID NO:2868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..553
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2868:

agaccaattc aagcacccca cgggagcgcg tccatcccct tccgccgacg gagccagggc	60
ccaggccgag caacctggtg ctccgcccct cgccgttaca gcggcgccct gccctccggt	120
tccacagcgt ctgcctgcct ggcgagccct gtgaccgtga ggcgacacga cgccgagaga	180
tcacccgccc cccgcctcgt gtccgccccg cttgggattg tgaggtaaag cgtgatggca	240
gcgcgcgcgg cgagggctcg agccgactac gactacctaa tcaaactgct cctcatcgga	300
gacagcggcg ttggaaaaag ttgcctcctg ttacggtttt cagatggatc attcaccact	360
agcttcatta ccactattgg cattgacttc aagataagaa ctgtttgagtt ggatggcaaa	420
aggattaagt tgcagatctg ggatactgca ggccaagaac gtttccgcac aattaccact	480
gcctactaca ggggagcaat ggggcatctt acttgtgtta tgatgtcmcm gacgagtcac	540
ctttcaataa cct	

(2) INFORMATION FOR SEQ ID NO:2869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2869:

Arg Pro Ile Gln Ala Pro His Gly Ser Ala Ser Ile Pro Phe Arg Arg
1 5 10 15
Ser Ser Gln Gly Pro Gly Arg Ala Thr Trp Cys Ser Ala Pro Arg Arg
20 25 30
Tyr Ser Gly Ala Ser Ala Ser Gly Ser Thr Ala Ser Ala Cys Leu Arg
35 40 45
Ser Pro Val Thr Val Arg Arg His Asp Ala Glu Arg Ser Pro Ala Pro
50 55 60
Arg Ile Val Ser Ala Pro Leu Gly Ile Val Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:2870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid

DOCKET# 08663560

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..119
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1602106
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2870:

Thr Asn Ser Ser Thr Pro Arg Glu Arg Val His Pro Leu Pro Pro Ile
1 5 10 15
Glu Pro Gly Pro Arg Pro Ser Asn Leu Val Leu Arg Pro Ser Pro Leu
20 25 30
Gln Arg Arg Leu Gly Leu Arg Phe His Ser Val Cys Leu Pro Ala Gln
35 40 45
Pro Cys Asp Arg Glu Ala Thr Arg Arg Arg Glu Ile Thr Arg Pro Pro
50 55 60
His Arg Val Arg Pro Ala Trp Asp Cys Glu Val Lys Arg Asp Gly Ser
65 70 75 80
Ala Ala Gly Glu Gly Ser Ser Arg Leu Arg Leu Pro Asn Gln Thr Ala
85 90 95
Pro His Arg Arg Gln Arg Arg Trp Lys Lys Leu Pro Pro Val Thr Val
100 105 110
Phe Arg Trp Ile Ile His His
115

(2) INFORMATION FOR SEQ ID NO:2871:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..106
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1602107
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2871:

Met Ala Ala Pro Pro Ala Arg Ala Arg Ala Asp Tyr Asp Tyr Leu Ile
1 5 10 15
Lys Leu Leu Leu Ile Gly Asp Ser Gly Val Gly Lys Ser Cys Leu Leu
20 25 30
Leu Arg Phe Ser Asp Gly Ser Phe Thr Thr Ser Phe Ile Thr Thr Ile
35 40 45
Gly Ile Asp Phe Lys Ile Arg Thr Val Glu Leu Asp Gly Lys Arg Ile
50 55 60
Lys Leu Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Ile
65 70 75 80
Thr Thr Ala Tyr Tyr Arg Gly Ala Met Gly His Leu Thr Cys Val Met
85 90 95
Met Xaa Xaa Thr Ser His Leu Ser Ile Thr
100 105

(2) INFORMATION FOR SEQ ID NO:2872:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..492
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1602114

00689900 "101300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2872:
cgccactac cctctccggc tctccgctaa caaatctag aacctctga accctccaca 60
ttcctccaga tcgaataata acctagctct gcacaccgcc cagccaccag tggcagcagg 120
agcaggggtc ggaacaagat ggtggtgacg gcggccggca gcgcggagga ggctgtgcgg 180
cggtgggtgg acgcccggc aggacgcctc gtcctcgacg gcgggctggc cacggagctc 240
gaggccaacg gcgcggacct caacgaccgc ctctggagcg ctaagtgcct cctctcctcc 300
ccgcacctca tccgcaaggt ccacatggac tatctggaag ctggcgcaaa cattataatc 360
acagcatcgt atcaggccac tattcaaggg tttgaatcaa agggtttttc aaaagaacag 420
agtgaact tactaacaaa gagtgtcgag attgcactgg aagctcgtga gatgttcttg 480
aaggaacatc tg

(2) INFORMATION FOR SEQ ID NO:2873:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1602115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2873:

Met Val Val Thr Ala Ala Gly Ser Ala Glu Glu Ala Val Arg Arg Trp
1 5 10 15
Val Asp Ala Ala Gly Gly Arg Leu Val Leu Asp Gly Gly Leu Ala Thr
20 25 30
Glu Leu Glu Ala Asn Gly Ala Asp Leu Asn Asp Pro Leu Trp Ser Ala
35 40 45
Lys Cys Leu Leu Ser Ser Pro His Leu Ile Arg Lys Val His Met Asp
50 55 60
Tyr Leu Glu Ala Gly Ala Asn Ile Ile Ile Thr Ala Ser Tyr Gln Ala
65 70 75 80
Thr Ile Gln Gly Phe Glu Ser Lys Gly Phe Ser Lys Glu Gln Ser Glu
85 90 95
Asn Leu Leu Thr Lys Ser Val Glu Ile Ala Leu Glu Ala Arg Glu Met
100 105 110
Phe Leu Lys Glu His Leu
115

(2) INFORMATION FOR SEQ ID NO:2874:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 441 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..441

(D) OTHER INFORMATION: / Ceres Seq. ID 1602137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2874:

aaccatgatt tgctctaaag ccattctcatt cctctccac ctcccagacct tccgccgcct 60
cacccccacc tcttccctcc gcgcgcgcgc gccatgtcc tctctctcgt ccgcggtcgc 120
cgccccgacg gagcatttcg tgctcttcaa ggcccgcgcg gaggcgggtg cctcgggcgc 180
cgcggcggcg atgggtctct cgtgcaggc gctggccacg ctcttcccgg gcttgcccta 240
catccacgca ggaccgggtc tccgcctccg atccccggcc gcggaggcgc tgggccccac 300
gcacctctc cacaccgcgt acgccaccaa ggaggacctg gcgtcctacg cggcgacccc 360
gggcacgtg gccgcgcgtg caggggcacg tcttcccaaa cgcgctcgac atcaccgcgc 420
gtcgactggg tcaacgcgcg g

(2) INFORMATION FOR SEQ ID NO:2875:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

DOCKET "09553960"

[illegible][illegible]

(2) INFORMATION FOR SEQ ID NO:2877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2877:

Met Ile Cys Leu Lys Ala Ile Ser Ser Pro Leu His Leu Pro Thr Phe
1 5 10 15
Arg Arg Leu Thr Pro Thr Ser Ser Leu Arg Ala Ala Ala Ala Met Ser
20 25 30
Ser Ser Ser Ser Ala Val Ala Ala Pro Ile Glu His Phe Val Leu Phe
35 40 45
Lys Ala Arg Pro Glu Ala Val Ala Ser Gly Ala Ala Ala Met Val
50 55 60
Ser Ser Leu Gln Ala Leu Ala Thr Leu Val Pro Gly Leu Ala Tyr Ile
65 70 75 80
His Ala Gly Pro Val Leu Arg Leu Arg Ser Pro Ala Ala Glu Ala Leu
85 90 95
Gly Pro Thr His Leu Leu His Thr Arg Tyr Ala Thr Lys Glu Asp Leu
100 105 110
Ala Ser Tyr Ala Ala His Pro Ala His Val Ala Arg Arg Ala Gly Ala
115 120 125
Arg Pro Pro Gln Arg Ala Arg His His Pro Pro Ser Thr Gly Ser Thr
130 135 140
Pro
145

(2) INFORMATION FOR SEQ ID NO:2878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..449
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2878:

atctcattcg cagatcgcaa ctggttcgac cagaaacaga cctgcacggc tccactccaa 60
ctccctccca agccccaac cacttcctt ttccacatcc acaccgcccc gggtttcctc 120
acgcctccgc cctcccaagt cccacccgct cactcccgct cctatccacc gcgatggcct 180
ccgcctccgc cgtcgccgct gccgtgcgcg cgcccgcgct gtctccttcc ccggtcgcca 240
ccgtcgcccc gccccgcgct gccctccgcc gaggcctccc gccgacgtgg cacgctctcc 300
gcgccctccc tcgatmccgt ggcgcagcgg tcgtgtgcca ggcccarggc ggccaggaca 360
ccgccatcca agttcctgat gtgagcaaat ccacatggca atcacttggtg gtggagagcg 420
agcttcccgt cctcgttcag ttctgggccc

(2) INFORMATION FOR SEQ ID NO:2879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

00669900 "101300"

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1602142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2879:

Ile Ser Phe Ala Asp Arg Asn Ser Phe Asp Gln Lys Gln Thr Cys Thr
1 5 10 15
Ala Pro Leu Gln Leu Pro Pro Lys Pro Pro Thr Thr Phe Leu Phe His
20 25 30
Ile His Thr Ala Pro Gly Phe Leu Thr Pro Pro Pro Ser Gln Val Pro
35 40 45
Pro Ala His Ser Arg Pro Tyr Pro Pro Arg Trp Pro Pro Ala Ser Pro
50 55 60
Ser Pro Ser Pro Ser Pro Arg Pro Arg Arg Leu Leu Pro Arg Ser Pro
65 70 75 80
Pro Ser Pro Arg Pro Ala Ser Pro Ser Ala Glu Ala Ser Arg Arg Arg
85 90 95
Gly Thr Leu Ser Ala Pro Ser Leu Asp Xaa Val Ala Gln Pro Ser Cys
100 105 110
Ala Arg Pro Xaa Ala Ala Arg Thr Pro Pro Ser Lys Phe Leu Met
115 120 125

(2) INFORMATION FOR SEQ ID NO:2880:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1602143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2880:

Ser His Ser Gln Ile Ala Thr Arg Ser Thr Arg Asn Arg Pro Ala Arg
1 5 10 15
Leu His Ser Asn Ser Leu Pro Ser Pro Gln Pro Pro Ser Phe Ser Thr
20 25 30
Ser Thr Pro Pro Arg Val Ser Ser Arg Leu Arg Pro Pro Lys Ser His
35 40 45
Pro Leu Thr Pro Val Pro Ile His Arg Asp Gly Leu Pro Pro Arg Arg
50 55 60
Arg Arg Arg Arg Arg Arg Ala Arg Val Val Ser Phe Pro Gly Arg His
65 70 75 80
Arg Arg Pro Ala Pro Arg Arg Pro Pro Pro Arg Pro Pro Ala Asp Val
85 90 95
Ala Arg Ser Pro Arg Pro Pro Ser Xaa Pro Trp Arg Ser Arg Arg Val
100 105 110
Pro Gly Pro Xaa Arg Pro Gly His Arg His Pro Ser Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:2881:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1602144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2881:

Leu Ile Arg Arg Ser Gln Leu Val Arg Pro Glu Thr Asp Leu His Gly
1 5 10 15

00665980-101300

Ser Thr Pro Thr Pro Ser Gln Ala Pro Asn His Leu Pro Phe Pro His
20 25 30
Pro His Arg Pro Gly Phe Pro His Ala Ser Ala Leu Pro Ser Pro Thr
35 40 45
Arg Ser Leu Pro Ser Leu Ser Thr Ala Met Ala Ser Arg Leu Ala Val
50 55 60
Ala Val Ala Val Ala Ala Pro Ala Ser Ser Pro Ser Pro Val Ala Thr
65 70 75 80
Val Ala Pro Pro Arg Val Ala Leu Arg Arg Gly Leu Pro Pro Thr Trp
85 90 95
His Ala Leu Arg Ala Leu Pro Arg Xaa Arg Gly Ala Ala Val Val Cys
100 105 110
Gln Ala Xaa Gly Gly Gln Asp Thr Ala Ile Gln Val Pro Asp Val Ser
115 120 125
Lys Ser Thr Trp Gln Ser Leu Val Val Glu Ser Glu Leu Pro Val Leu
130 135 140
Val Gln Phe Trp Ala
145

(2) INFORMATION FOR SEQ ID NO:2882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..426
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2882:

aatccccacc	cgcaacaaac	caaaccacac	cgcaactgca	acacagaggc	atctctctcc	60
gcctccacgc	cgcgcgcccc	agaccctcct	sgatccagcg	gtssattcgc	cgggctcccc	120
rrcccgcca	tggatttgct	ggcgctcttg	gccgccgagg	agcgggtggct	gttcccggcg	180
ttccctcgcc	atgtacgccg	ccatctactg	cgccggccag	ctcgctcgtgt	tccggcggtg	240
ggcgccgcgg	cagaggctcg	acggcgccag	ctgcctcatc	tcgctattcc	acggcacccc	300
cgcgcgcgtg	gccgcgcggg	gggccatcct	cgcgcttccc	gcggagtcce	gctccttcgc	360
cgcgccaac	gcgcgcctcc	aggaccacgt	cctcgactac	agcgtcgcct	acttcaccat	420
ggacct						

(2) INFORMATION FOR SEQ ID NO:2883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2883:

Asn Pro His Pro Gln Gln Thr Lys Pro Asn Arg Asn Cys Asn Thr Glu
1 5 10 15
Ala Ser Leu Ser Ala Ser Thr Pro Pro Pro Asp Pro Pro Xaa Ser
20 25 30
Ser Gly Xaa Phe Ala Gly Leu Pro Xaa Pro Ala Met Asp Leu Leu Ala
35 40 45
Ser Leu Ala Ala Glu Glu Arg Trp Leu Phe Pro Ala Phe Pro Arg His
50 55 60
Val Arg Arg His Leu Leu Arg Arg Pro Ala Arg Arg Val Pro Ala Val
65 70 75 80
Gly Ala Ala Ala Glu Ala Arg Arg Arg Gln Leu Pro His Leu Ala Ile

DOCKET "08553360"

(X1) SEQUENCE DESCRIPTION: SEQ ID: 1																
Ser	Pro	Pro	Ala	Thr	Asn	Gln	Thr	Gln	Pro	Gln	Leu	Gln	His	Arg	Gly	
1				5					10					15		
Ile	Ser	Leu	Arg	Leu	His	Ala	Ala	Ala	Pro	Arg	Pro	Ser	Xaa	Ile	Gln	
		20						25					30			
Arg	Xaa	Ile	Arg	Arg	Ala	Pro	Xaa	Pro	Gly	His	Gly	Phe	Ala	Gly	Val	
		35					40					45				
Leu	Gly	Arg	Arg	Gly	Ala	Val	Ala	Val	Pro	Gly	Val	Pro	Ser	Pro	Cys	
	50					55					60					
Thr	Pro	Pro	Ser	Thr	Ala	Pro	Ala	Ser	Ser	Ser	Cys	Ser	Gly	Gly	Gly	
65				70					75					80		
Arg	Arg	Gly	Arg	Gly	Ser	Thr	Ala	Pro	Ala	Ala	Ser	Ser	Arg	Tyr	Ser	
				85					90					95		

(A) LENGTH: 105 amino acids

[illegible]

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..105
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1602158
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2888:

Met Gly Lys Gly Phe Ala Ser Tyr Leu Ala Met Lys Thr Gly Pro Glu
1 5 10 15
Gly Gly Asp Ala Ala Ala Gln Gln Ala Leu Ile Asp Ala Asp Leu
20 25 30
Arg Glu Leu Gly Val Ala Ala Arg Lys Leu Ala Asn His Ala Phe Val
35 40 45
Leu Gly Gly Gly Leu Gly Phe Gly Thr Ser Phe Leu Lys Trp Leu Ala
50 55 60
Phe Leu Ala Ala Val Tyr Leu Leu Ile Leu Asp Arg Thr Asn Trp Lys
65 70 75 80
Thr Asn Met Leu Thr Ala Leu Leu Val Pro Tyr Ile Phe Phe Thr Leu
85 90 95
Pro Asn Val Leu Phe Ser Leu Ile Arg
100 105

(2) INFORMATION FOR SEQ ID NO:2889:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..95
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1602159
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2889:

Met Lys Thr Gly Pro Glu Gly Gly Asp Ala Ala Ala Ala Gln Gln Ala
1 5 10 15
Leu Ile Asp Ala Asp Leu Arg Glu Leu Gly Val Ala Ala Arg Lys Leu
20 25 30
Ala Asn His Ala Phe Val Leu Gly Gly Gly Leu Gly Phe Gly Thr Ser
35 40 45
Phe Leu Lys Trp Leu Ala Phe Leu Ala Ala Val Tyr Leu Leu Ile Leu
50 55 60
Asp Arg Thr Asn Trp Lys Thr Asn Met Leu Thr Ala Leu Leu Val Pro
65 70 75 80
Tyr Ile Phe Phe Thr Leu Pro Asn Val Leu Phe Ser Leu Ile Arg
85 90 95

(2) INFORMATION FOR SEQ ID NO:2890:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 441 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..441
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1602160
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2890:

attcttcttt ctccgtcctt tccatcccag gtgccaccg cgtctccgcc cttccctcct
ccccaccatc ttcagcacga ggcagcacgc gcggacgtcc ctcccgacac ggagaacccc

60
120

005501 08553360

gctccgcgcg ctgcattca tcgcgccgcc acccaggtcc cagccggccg cgcgcccgcg 180
cccccccgcc gccggccgtg ccatgccgcg gccggggcgag acggcgggtg tccccattga 240
cgtggcgctcc gccggcgcg gcgcagggca tgagcggccc aagagagagc gccaccggag 300
ccacggcncc gccgcacag gtccgcaccg gagtcgccg ccgccccygc ccccgccggc 360
gttcgggccg ttccggcggt ggttcccgtt ccttggtgcg ctattcatcg tcgctaaca 420
cgctctcttc gtgctcacca t

(2) INFORMATION FOR SEQ ID NO:2891:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1602161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2891:

Ile Leu Leu Ser Pro Ser Phe Pro Ser Gln Val Ala Thr Ala Ser Pro
1 5 10 15
Pro Phe Pro Pro His His Leu Gln His Glu Ala Ala Arg Ala Asp
20 25 30
Val Pro Pro Asp Thr Glu Asn Pro Ala Pro Arg Ala Arg Ile His Arg
35 40 45
Ala Ala Thr Gln Val Pro Ala Gly Arg Ala Pro Ala Pro Pro Arg Arg
50 55 60
Arg Pro Cys His Ala Ala Ala Gly Arg Asp Gly Gly Gly Pro His
65 70 75

(2) INFORMATION FOR SEQ ID NO:2892:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1602162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2892:

Phe Phe Phe Leu Arg Pro Phe His Pro Arg Ser Pro Pro Arg Leu Arg
1 5 10 15
Pro Ser Leu Leu Pro Thr Ile Phe Ser Thr Arg Gln His Ala Arg Thr
20 25 30
Ser Leu Pro Thr Arg Arg Thr Pro Leu Arg Ala Leu Ala Phe Ile Ala
35 40 45
Pro Pro Pro Arg Ser Gln Pro Ala Ala Arg Pro Arg Pro Pro Ala Ala
50 55 60
Gly Arg Ala Met Pro Arg Arg Gly Glu Thr Ala Val Val Pro Ile Asp
65 70 75 80
Val Ala Ser Ala Gly Gly Gly Arg Gly Asp Glu Arg Pro Lys Arg Glu
85 90 95
Arg His Arg Ser His Gly Xaa Gly Arg His Gly Pro His Arg Ser Arg
100 105 110
Pro Pro Pro Xaa Pro Pro Pro Ala Phe Arg Pro Phe Arg Trp Phe
115 120 125
Pro Phe Leu Val Pro Leu Phe Ile Val Ala Asn Ile Val Leu Phe Val
130 135 140
Leu Thr
145

(2) INFORMATION FOR SEQ ID NO:2893:

00000000 00000000

```
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
      {A} NAME/KEY: peptide
```

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1602173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2895:

```
Met Ala Asp Glu Tyr Gly Arg Ser Gly Tyr Gly Arg Ser Gly Ala Gly
1          5          10          15
Asp Asp Tyr Asp Ser Gly Tyr Asn Ser Lys Ser Gly Thr Asp Asp Tyr
20          25          30
Gly Arg Gly Glu Gly Gly Tyr Asn Lys Ser Gly Gly Asp Asp Asp Tyr
35          40          45
Gly Arg Ser Gly Gly Asp Gly Tyr Gly Arg Ser Gly Gly Asp Asp Tyr
50          55          60
Gly Arg Gly Thr Gly Gly Gly Tyr Asn Lys Ser Gly Gly Gly Asp
65          70          75          80
Asp Tyr Gly Arg Ser Gly Gly Asp Gly Tyr Gly Arg Ser Gly Gly Asp
85          90          95
Asp Tyr Gly Arg Gly Thr Gly Xaa Gly Gly Tyr Asn Lys Ser Gly Asn
100         105         110
Asp Gly Tyr Asp Ser Gly Tyr Asn Arg Ser Gly Thr Thr Asn Asp Asp
115         120         125
Glu Tyr Gly Arg Gly Thr Gly Gly Tyr
130         135
```

(2) INFORMATION FOR SEQ ID NO:2896:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1602174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2896:

```
Met Thr Thr Ala Val Ala Lys Val Ala Thr Thr Ser Arg Ala Ala Met
1          5          10          15
Thr Thr Thr Ala Ala Ala Ala Met Gly Thr Ala Gly Pro Ala Ala
20          25          30
Thr Thr Thr Ala Val Ala Pro Ala Val Val Ala Thr Thr Ser Pro Ala
35          40          45
Ala Ala Thr Thr Thr Ala Ala Ala Ala Ala Met Gly Met Glu Gly Pro
50          55          60
Ala Ala Thr Thr Thr Ala Val Ala Pro Ala Xaa Ala Gly Thr Thr Ser
65          70          75          80
Pro Ala Thr Thr Ala Thr Thr Ala Gly Thr Thr Asp Arg Ala Pro Pro
85          90          95
Thr Thr Thr Asn Thr Ala Val Ala Pro Ala Ala Gly
100         105
```

(2) INFORMATION FOR SEQ ID NO:2897:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1602175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2897:

```
Met Thr Thr Thr Ala Ala Ala Ala Ala Met Gly Thr Ala Gly Pro Ala
1          5          10          15
```

Ala Thr Thr Thr Ala Val Ala Pro Ala Val Val Ala Thr Thr Ser Pro
20 25 30
Ala Ala Ala Thr Thr Thr Ala Ala Ala Ala Met Gly Met Glu Gly
35 40 45
Pro Ala Ala Thr Thr Thr Ala Val Ala Pro Ala Xaa Ala Gly Thr Thr
50 55 60
Ser Pro Ala Thr Thr Ala Thr Thr Ala Gly Thr Thr Asp Arg Ala Pro
65 70 75 80
Pro Thr Thr Thr Asn Thr Ala Val Ala Pro Ala Ala Gly
85 90

(2) INFORMATION FOR SEQ ID NO:2898:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 427 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..427

(D) OTHER INFORMATION: / Ceres Seq. ID 1602183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2898:

atcggtttct gacttattcc ggggcatttt ttttttcttg tttcgagcct gtgagtctga	60
ttccattttg acccatggcg gggcgggcgg cggcggttca tgagccggag gtgatccgcg	120
acaaggcggc gatgcgcgcg tggtcgcgcc gccgcgcgc ggagggaaag gccgtcgtt	180
tagtccccac gatgggcttc ctccacgagg gacacctctc gtcctatctcc gcggccgtgg	240
cggcctccgc cggccccatc gccgtcgtcg tctccatcta cgtcaacccc agccagttcg	300
ccccaccga ggacctgcgc acctaccct ccgacttcgc cggcgacctc cgcaagctgg	360
ccgccaccgg ggtcgtgcgc gcagtatttt gtccccaga cctctacgtc cgcggcagcg	420
ctgatcg	

(2) INFORMATION FOR SEQ ID NO:2899:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1602184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2899:

Met Ala Ala Ala Ala Ala Val His Glu Pro Glu Val Ile Arg Asp	
1 5 10 15	
Lys Ala Ala Met Arg Ala Trp Ser Arg Arg Arg Ala Glu Gly Lys	
20 25 30	
Ala Val Ala Leu Val Pro Thr Met Gly Phe Leu His Glu Gly His Leu	
35 40 45	
Ser Leu Ile Ser Ala Ala Val Ala Ala Ser Ala Gly Pro Ile Ala Val	
50 55 60	
Val Val Ser Ile Tyr Val Asn Pro Ser Gln Phe Ala Pro Thr Glu Asp	
65 70 75 80	
Leu Ala Thr Tyr Pro Ser Asp Phe Ala Gly Asp Leu Arg Lys Leu Ala	
85 90 95	
Ala Thr Gly Val Val Ala Ala Val Phe Cys Pro Pro Asp Leu Tyr Val	
100 105 110	
Arg Gly Ser Ala Asp	
115	

(2) INFORMATION FOR SEQ ID NO:2900:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..98
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1602185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2900:

Met Arg Ala Trp Ser Arg Arg Arg Arg Ala Glu Gly Lys Ala Val Ala
1 5 10 15
Leu Val Pro Thr Met Gly Phe Leu His Glu Gly His Leu Ser Leu Ile
20 25 30
Ser Ala Ala Val Ala Ala Ser Ala Gly Pro Ile Ala Val Val Val Ser
35 40 45
Ile Tyr Val Asn Pro Ser Gln Phe Ala Pro Thr Glu Asp Leu Ala Thr
50 55 60
Tyr Pro Ser Asp Phe Ala Gly Asp Leu Arg Lys Leu Ala Ala Thr Gly
65 70 75 80
Val Val Ala Ala Val Phe Cys Pro Pro Asp Leu Tyr Val Arg Gly Ser
85 90 95
Ala Asp

(2) INFORMATION FOR SEQ ID NO:2901:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..78
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1602186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2901:

Met Gly Phe Leu His Glu Gly His Leu Ser Leu Ile Ser Ala Ala Val
1 5 10 15
Ala Ala Ser Ala Gly Pro Ile Ala Val Val Val Ser Ile Tyr Val Asn
20 25 30
Pro Ser Gln Phe Ala Pro Thr Glu Asp Leu Ala Thr Tyr Pro Ser Asp
35 40 45
Phe Ala Gly Asp Leu Arg Lys Leu Ala Ala Thr Gly Val Val Ala Ala
50 55 60
Val Phe Cys Pro Pro Asp Leu Tyr Val Arg Gly Ser Ala Asp
65 70 75

(2) INFORMATION FOR SEQ ID NO:2902:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..480
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2902:

tcccggtcccg agagtctga atcgaaaccg tcggccacga gagcagtgcg aggcgcccac	60
cgcgatggct cgaaccaagc accaggccgt gaggaagacg gcggagaagc ccaagaagaa	120
gctccagttc gagcgctcag gtggtgcgag tacctcggcg acgccggaaa gggctgctgg	180
gaccggggga agagcggcgt ctggaggtga ctcagttaag aagacgaaac cacgccaccg	240


```
ctggcgggcca gggactgtag cgctgcggga gatcaggaag taccagaagt ccactgaacc 300
gtcatcccc tttgcgcctt tcgtccgtgt ggtgagggag ttaaccaatt tcgtaacaaa 360
cgggaaaagta gagcgctata ccgcagaagc cctccttgcg ctgcaagagg cagcagaatt 420
ccacttgata gaactgtttg aaatggcgaa tctgtgtgcc atccatgcc aagcgtgtcac 480
```

(2) INFORMATION FOR SEQ ID NO:2903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2903:

Pro Val Pro Arg Val Leu Asn Arg Asn Arg Arg Pro Arg Glu Gln Cys
1 5 10 15
Glu Ala Pro Thr Ala Met Ala Arg Thr Lys His Gln Ala Val Arg Lys
20 25 30
Thr Ala Glu Lys Pro Lys Lys Lys Leu Gln Phe Glu Arg Ser Gly Gly
35 40 45
Ala Ser Thr Ser Ala Thr Pro Glu Arg Ala Ala Gly Thr Gly Gly Arg
50 55 60
Ala Ala Ser Gly Gly Asp Ser Val Lys Lys Thr Lys Pro Arg His Arg
65 70 75 80
Trp Arg Pro Gly Thr Val Ala Leu Arg Glu Ile Arg Lys Tyr Gln Lys
85 90 95
Ser Thr Glu Pro Leu Ile Pro Phe Ala Pro Phe Val Arg Val Val Arg
100 105 110
Glu Leu Thr Asn Phe Val Thr Asn Gly Lys Val Glu Arg Tyr Thr Ala
115 120 125
Glu Ala Leu Leu Ala Leu Gln Glu Ala Ala Glu Phe His Leu Ile Glu
130 135 140
Leu Phe Glu Met Ala Asn Leu Cys Ala Ile His Ala Lys Arg Val
145 150 155

(2) INFORMATION FOR SEQ ID NO:2904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2904:

Met Ala Arg Thr Lys His Gln Ala Val Arg Lys Thr Ala Glu Lys Pro
1 5 10 15
Lys Lys Lys Leu Gln Phe Glu Arg Ser Gly Gly Ala Ser Thr Ser Ala
20 25 30
Thr Pro Glu Arg Ala Ala Gly Thr Gly Gly Arg Ala Ala Ser Gly Gly
35 40 45
Asp Ser Val Lys Lys Thr Lys Pro Arg His Arg Trp Arg Pro Gly Thr
50 55 60
Val Ala Leu Arg Glu Ile Arg Lys Tyr Gln Lys Ser Thr Glu Pro Leu
65 70 75 80
Ile Pro Phe Ala Pro Phe Val Arg Val Val Arg Glu Leu Thr Asn Phe
85 90 95

CONFIDENTIAL

Val Thr Asn Gly Lys Val Glu Arg Tyr Thr Ala Glu Ala Leu Leu Ala
100 105 110
Leu Gln Glu Ala Ala Glu Phe His Leu Ile Glu Leu Phe Glu Met Ala
115 120 125
Asn Leu Cys Ala Ile His Ala Lys Arg Val
130 135

(2) INFORMATION FOR SEQ ID NO:2905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..486
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2905:

taatgagaaa atcacaaaag cagtggttac agtcccagca tatttcaatg attcacaaag	60
gacagcaact aaagatgctg gccgcattgc aggactggaa gttctccgta ttattaatga	120
accaactgct gcacgcttgg cctatggttt cgagaagaaa aataatgaaa caattctagt	180
gtttgatttg ggaggcggaa cctttgatgt atctgtattg gaagttgggt atggtgtgtt	240
tgaggtgctt tccacatctg gtgacacaca ccttggtggt gatgacttcg ataagagaat	300
agtagatttg cttgctagca acttcaagaa agatgaacgt attgatcttc tgaaggataa	360
acaagccctt cagaggctta ctgaggcagc agagaaagct aagatggaac tgtcaacgct	420
gacacaggca aatattagcc taccattcat tactgctact gctgatgggc caaaacacat	480
cgaggc	

(2) INFORMATION FOR SEQ ID NO:2906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2906:

Asn Glu Lys Ile Thr Lys Ala Val Val Thr Val Pro Ala Tyr Phe Asn	
1 5 10 15	
Asp Ser Gln Arg Thr Ala Thr Lys Asp Ala Gly Arg Ile Ala Gly Leu	
20 25 30	
Glu Val Leu Arg Ile Ile Asn Glu Pro Thr Ala Ala Ser Leu Ala Tyr	
35 40 45	
Gly Phe Glu Lys Lys Asn Asn Glu Thr Ile Leu Val Phe Asp Leu Gly	
50 55 60	
Gly Gly Thr Phe Asp Val Ser Val Leu Glu Val Gly Asp Gly Val Phe	
65 70 75 80	
Glu Val Leu Ser Thr Ser Gly Asp Thr His Leu Gly Gly Asp Asp Phe	
85 90 95	
Asp Lys Arg Ile Val Asp Trp Leu Ala Ser Asn Phe Lys Lys Asp Glu	
100 105 110	
Arg Ile Asp Leu Leu Lys Asp Lys Gln Ala Leu Gln Arg Leu Thr Glu	
115 120 125	
Ala Ala Glu Lys Ala Lys Met Glu Leu Ser Thr Leu Thr Gln Ala Asn	
130 135 140	
Ile Ser Leu Pro Phe Ile Thr Ala Thr Ala Asp Gly Pro Lys His Ile	
145 150 155 160	
Glu	

gtgttgaagc	cgtctaaact	tccattttat	cgagtgtgtc	gtgtttcata	atgccaat	60
tctctccgca	gccgactcgc	cccgggtggg	ctgactgagc	tccggtccgc	ctcgaccgcg	120
ggcgtacgc	cccgagctc	caccgcgtcg	gccgcgtcgg	agctcgtcgc	cggcgatggc	180
ttccgcggtg	ggcgcttcga	ccgccacgcg	gttcctcccg	cggctcccgg	acccgtggcg	240
gccgcgtcgt	gcgcgcgcgg	cgtcccgcc	gtcacgtgg	cggcctcccg	cggtcacggt	300
ggccgcggcg	tcgccccagc	ctggggaaag	ggaaggtagg	cggcgggaga	ggacgcggag	360
gcggcgcgcg	aggggcgcgc	ggcaagagga	aggcgtctcg	ctaagctctg	aaaaggagac	420
gctaaattct	actccacgtg	ctcaaaccaa	c			

Met	Ala	Ser	Ala	Val	Gly	Ala	Ser	Thr	Ala	Thr	Arg	Phe	Leu	Pro	Arg
1				5					10					15	
Leu	Pro	Asp	Pro	Trp	Arg	Pro	Arg	Arg	Ala	Arg	Ala	Ala	Leu	Pro	Pro
			20					25					30		
Leu	Thr	Trp	Arg	Pro	Pro	Ala	Val	Thr	Val	Ala	Ala	Ala	Ser	Pro	Arg
			35				40					45			
Pro	Gly	Glu	Ala	Glu	Gly	Arg	Arg	Arg	Glu	Arg	Thr	Arg	Arg	Arg	Arg
	50					55					60				
Ala	Arg	Gly	Pro	Gly	Gln	Glu	Glu	Gly	Val	Ser	Leu	Ser	Ser	Glu	Lys
65					70					75					80
Glu	Thr	Leu	Asn	Ser	Thr	Pro	Arg	Ala	Gln	Thr	Asn				
				85					90						

ctccacttgc	agagggttcgc	gactcgcgac	gcttcgcgag	ccccagcccc	agccccacgc	60
cccgcgatcc	aaaccctagc	cccctccacc	gtaccgccac	cgtcattggcc	gaaccatccg	120
ccgcccgcgt	caccgcagct	gagggtcggg	aggagtcgga	tgccgcccgcg	atggaggagg	180
tgcgcggcgg	cgcgaagagg	tggcgggggt	ggcccgggga	cagcgtgttc	cggtcgttgg	240
tgcgaagtct	caaggtcgga	agcataatcg	ggcggaaggg	cgaagtcatc	aagcgccttg	300

tcgaggggac caaggccaga gtccgcatcc tcgagggccc cgtcggcgcc accgagcgta 360
tcgttttgggt ttctggaaaa gaagatccag gcttggagct atctccagcc atggatgctt 420
ctcatgagag tttttaagcg tgtcattggg ataacagatg gagctgc

(2) INFORMATION FOR SEQ ID NO:2910:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2910:

Leu His Leu Gln Arg Phe Ala Thr Arg Asp Ala Ser Ala Ala Pro Ala
1 5 10 15
Pro Ala Pro Arg Pro Ala Ile Gln Thr Leu Ala Pro Ser Thr Val Pro
20 25 30
Pro Pro Ser Trp Pro Asn His Pro Pro Pro Ser Pro Gln Leu Arg
35 40 45
Ser Gly Arg Ser Pro Met Pro Pro Arg Trp Arg Arg Ser Arg Arg Pro
50 55 60
Arg Arg Gly Gly Arg Gly Gly Pro Gly Thr Ala Cys Ser Gly Trp Trp
65 70 75 80
Cys Gln Cys Ser Arg Ser Glu Ala
85

(2) INFORMATION FOR SEQ ID NO:2911:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2911:

Pro Leu Ala Glu Val Arg Asp Ser Arg Arg Leu Arg Ser Pro Ser Pro
1 5 10 15
Ser Pro Thr Pro Arg Asp Pro Asn Pro Ser Pro Leu His Arg Thr Ala
20 25 30
Thr Val Met Ala Glu Pro Ser Ala Ala Ala Val Thr Ala Ala Glu Val
35 40 45
Gly Glu Glu Ser Asp Ala Ala Ala Met Glu Glu Val Ala Ala Ala
50 55 60
Lys Arg Trp Pro Gly Trp Pro Gly Asp Ser Val Phe Arg Leu Val Val
65 70 75 80
Pro Val Leu Lys Val Gly Ser Ile Ile Gly Arg Lys Gly Glu Leu Ile
85 90 95
Lys Arg Leu Val Glu Gly Thr Lys Ala Arg Val Arg Ile Leu Glu Gly
100 105 110
Pro Val Gly Ala Thr Glu Arg Ile Val Leu Val Ser Gly Lys Glu Asp
115 120 125
Pro Gly Leu Glu Leu Ser Pro Ala Met Asp Ala Ser His Glu Ser Phe
130 135 140

(2) INFORMATION FOR SEQ ID NO:2912:

(i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2912:															
Met	Ala	Glu	Pro	Ser	Ala	Ala	Ala	Val	Thr	Ala	Ala	Glu	Val	Gly	Glu
1				5					10					15	
Glu	Ser	Asp	Ala	Ala	Ala	Met	Glu	Glu	Val	Ala	Ala	Ala	Ala	Lys	Arg
			20					25					30		
Trp	Pro	Gly	Trp	Pro	Gly	Asp	Ser	Val	Phe	Arg	Leu	Val	Val	Pro	Val
		35					40					45			
Leu	Lys	Val	Gly	Ser	Ile	Ile	Gly	Arg	Lys	Gly	Glu	Leu	Ile	Lys	Arg
	50					55					60				
Leu	Val	Glu	Gly	Thr	Lys	Ala	Arg	Val	Arg	Ile	Leu	Glu	Gly	Pro	Val
65					70					75				80	
Gly	Ala	Thr	Glu	Arg	Ile	Val	Leu	Val	Ser	Gly	Lys	Glu	Asp	Pro	Gly
				85					90					95	
Leu	Glu	Leu	Ser	Pro	Ala	Met	Asp	Ala	Ser	His	Glu	Ser	Phe		
			100					105					110		

gttcatctttt	cctggcgcac	agccagcccc	cccacaggag	cttctctgag	gaagttgctg	60
cacttaaccg	ctacttkggc	ggcctgacaa	tctggtggtg	atgcatatgt	gattggagat	120
ccagcaagac	ctggacagaa	gtggcacgtc	ttctacgcc	ctgagtacc	agagcaacca	180
atgattaacc	ttgagatgtg	catgactggt	ctggacaaga	agaaaagctt	tgtctttttc	240
aagactaatg	ctgatgggaa	cacaacatgt	gccaaagaaa	tgacaaagct	ctctggcctc	300
tctgyaaatc	atccccgaga	ttgagatctg	cgatttcgac	tttgaaccct	gtggctaccc	360
atgaatgcga	tccatggctc	yttoattctc	c			

Met	Ile	Asn	Leu	Glu	Met	Cys	Met	Thr	Gly	Leu	Asp	Lys	Lys	Lys	Ala
1				5					10					15	
Ser	Val	Phe	Phe	Lys	Thr	Asn	Ala	Asp	Gly	Asn	Thr	Thr	Cys	Ala	Lys
			20					25					30		
Glu	Met	Thr	Lys	Leu	Ser	Gly	Ile	Ser	Xaa	Asn	His	Pro	Arg	Asp	Gly
			35				40					45			

Asp Leu Arg Phe Arg Leu
50

(2) INFORMATION FOR SEQ ID NO:2915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2915:

Met	Cys	Met	Thr	Gly	Leu	Asp	Lys	Lys	Lys	Ala	Ser	Val	Phe	Phe	Lys
1				5					10					15	
Thr	Asn	Ala	Asp	Gly	Asn	Thr	Thr	Cys	Ala	Lys	Glu	Met	Thr	Lys	Leu
		20						25					30		
Ser	Gly	Ile	Ser	Xaa	Asn	His	Pro	Arg	Asp	Gly	Asp	Leu	Arg	Phe	Arg
		35					40					45			
Leu															

(2) INFORMATION FOR SEQ ID NO:2916:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2916:

Met	Thr	Gly	Leu	Asp	Lys	Lys	Lys	Ala	Ser	Val	Phe	Phe	Lys	Thr	Asn
1				5				10					15		
Ala	Asp	Gly	Asn	Thr	Thr	Cys	Ala	Lys	Glu	Met	Thr	Lys	Leu	Ser	Gly
		20					25					30			
Ile	Ser	Xaa	Asn	His	Pro	Arg	Asp	Gly	Asp	Leu	Arg	Phe	Arg	Leu	
		35				40						45			

(2) INFORMATION FOR SEQ ID NO:2917:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..503
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2917:

tgggcagctg	cgagcactgc	catctccatc	cacctgcgtt	ctgagcagta	catccattcc	60
attccgtccc	atcgatcggg	ccactggaac	atggettccc	tcttctgtt	cctgcgagcc	120
attgtcatca	gtgccgatga	cgaggaactc	acgggcgcgg	acgagggacg	ggatgcggcg	180
gcgcgtgaac	ggcgaccgga	gaactgcgcg	ttcgggcccg	cggcggcgcg	cgacacggag	240
gaggaggagg	aggaggagga	gaacccaagc	aactggcctt	ctctgctgcc	ctcggtgtca	300
cgattgggat	ctttccgata	tgtgggacca	ctgttattct	tgggtgctgtt	gttgtagcaa	360
tgttgggaag	tcgttgcaat	gctgttactc	ttatggttct	aaatttggcc	gccactccaa	420
ttgaactaag	cttgatcgtc	cctttcttgc	gtttgggtga	agccgtcact	tggcagcggg	480
cattcccct	tgacagccga	cgc				

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2918:

(2) INFORMATION FOR SEQ ID NO:2919:

(A) LENGTH: 140 amino acids

(C) STRANDEDNESS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1602215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2919:

(2) INFORMATION FOR SEQ ID NO:2920:

(A) LENGTH: 95 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..95
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1602216
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2920:

Met Thr Arg Asn Ser Arg Ala Arg Thr Arg Asp Gly Met Arg Arg Arg
1 5 10 15
Val Asn Gly Asp Arg Arg Thr Ala Arg Ser Gly Arg Arg Arg Ala
20 25 30
Thr Arg Arg Arg Arg Arg Arg Arg Arg Thr Gln Ala Thr Gly Leu
35 40 45
Leu Cys Cys Pro Arg Cys His Asp Trp Asp Leu Ser Asp Met Trp Asp
50 55 60
His Cys Tyr Ser Trp Cys Cys Cys Cys Ser Asn Val Gly Lys Ser Leu
65 70 75 80
Gln Cys Cys Tyr Ser Tyr Gly Ser Lys Phe Gly Arg His Ser Asn
85 90 95

- (2) INFORMATION FOR SEQ ID NO:2921:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..427
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1602221

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2921:

aaacacgctc tccttcttca aggacctggg cgccaacgtg ggcgtcattt cgggcctcat 60
caacgaggtc acgccgccgt gggtggtgct cgccatgggc gccgccatga acctggcggg 120
ctacctcatg atctacctcg ccacgcacgg gcgcaccggc agggcccccg tctggctcat 180
gtgcatctac atctgcgtgg gcgccaactc ccagtccttc gccaacaccg gcgcgctcgt 240
cacctgcgtc aagaacttcc cggagagccg cggcgtcgtg ctgggcctcc tcaagggtt 300
cgtcggcctc agcggcgcca tcttcacgca gctctacctc gccatctacg gcgacgacgc 360
caagtgcgtc gtgctgctca tcgcctgggt ccccgccggc gtctccatcc tcttcgtcca 420
caccgtc

- (2) INFORMATION FOR SEQ ID NO:2922:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602222

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2922:

Lys His Ala Leu Leu Gln Gly Pro Gly Arg Gln Arg Gly Arg His
1 5 10 15
Phe Gly Pro His Gln Arg Gly His Ala Ala Val Gly Gly Ala Arg His
20 25 30
Gly Arg Arg His Glu Pro Gly Gly Leu Pro His Asp Leu Pro Arg His
35 40 45
Arg Arg Ala His Arg Gln Ala Pro Arg Leu Ala His Val His Leu His
50 55 60

Leu Arg Gly Arg Gln Leu Pro Val Leu Arg Gln His Arg Arg Ala Arg
65 70 75 80
His Leu Arg Gln Glu Leu Pro Gly Glu Pro Arg Arg Arg Ala Arg Pro
85 90 95
Pro Gln Gly Leu Arg Arg Pro Gln Arg Arg His Leu His Ala Ala Leu
100 105 110
Pro Arg His Leu Arg Arg Arg Arg Gln Val Ala Arg Ala Ala His Arg
115 120 125
Leu Ala Pro Arg Arg Arg Leu His Pro Leu Arg Pro His Arg
130 135 140

(2) INFORMATION FOR SEQ ID NO:2923:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1602223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2923:

Asn Thr Leu Ser Phe Phe Lys Asp Leu Gly Ala Asn Val Gly Val Ile
1 5 10 15
Ser Gly Leu Ile Asn Glu Val Thr Pro Pro Trp Val Val Leu Ala Met
20 25 30
Gly Ala Ala Met Asn Leu Ala Gly Tyr Leu Met Ile Tyr Leu Ala Ile
35 40 45
Asp Gly Arg Thr Gly Arg Pro Pro Val Trp Leu Met Cys Ile Tyr Ile
50 55 60
Cys Val Gly Ala Asn Ser Gln Ser Phe Ala Asn Thr Gly Ala Leu Val
65 70 75 80
Thr Cys Val Lys Asn Phe Pro Glu Ser Arg Gly Val Val Leu Gly Leu
85 90 95
Leu Lys Gly Phe Val Gly Leu Ser Gly Ala Ile Phe Thr Gln Leu Tyr
100 105 110
Leu Ala Ile Tyr Gly Asp Asp Ala Lys Ser Leu Val Leu Leu Ile Ala
115 120 125
Trp Leu Pro Ala Ala Val Ser Ile Leu Phe Val His Thr Val
130 135 140

(2) INFORMATION FOR SEQ ID NO:2924:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1602224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2924:

Met Gly Ala Ala Met Asn Leu Ala Gly Tyr Leu Met Ile Tyr Leu Ala
1 5 10 15
Ile Asp Gly Arg Thr Gly Arg Pro Pro Val Trp Leu Met Cys Ile Tyr
20 25 30
Ile Cys Val Gly Ala Asn Ser Gln Ser Phe Ala Asn Thr Gly Ala Leu
35 40 45
Val Thr Cys Val Lys Asn Phe Pro Glu Ser Arg Gly Val Val Leu Gly
50 55 60
Leu Leu Lys Gly Phe Val Gly Leu Ser Gly Ala Ile Phe Thr Gln Leu

(2) INFORMATION FOR SEQ ID NO:2925:

(A) LENGTH: 550 base pairs

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..550

(D) OTHER INFORMATION: / Ceres Seq. ID 1602229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2925:

(X1) SEQUENCE	DESCRIPTION	SEQ ID NO	LENGTH			
actgttccac	tccagtcggt	cgaggagtag	ggttctagcg	cctatctggt	ttctccctgc	60
cgccgcgcgc	ccgcgcgtgga	caaccggagc	gtagtgggag	gggatgatgg	agggaggtag	120
ccgcgcgggat	gggcggaatc	cgaaccagct	ccggccggtc	acctgcaccg	ggaacccgct	180
ccaccgcgcc	cacggctcgc	cgcgggtggc	gcagggcgac	accgtcgtgc	tggccgctgt	240
gtacggggcc	aagtcgggaa	cccgggaagg	cgagaacccc	gagaaggcct	ccatcgaggt	300
cgtgtggaag	cccaagaccg	gccagatcgg	aaggcaagag	aggggaatat	agatgacact	360
caagaggacg	ttgcagagca	tctgcttgct	cacagttcat	cctaacacca	ccacctctgt	420
cgtgcttcag	gttggtgggtg	atgatggttc	tcttatgtca	tgtgcaatta	atgcttcttg	480
tgtgctctct	gmatttgctg	gaatccctat	ggaaacatct	cgctggtcgc	gattagctgt	540
ggagtcatcg						

(2) INFORMATION FOR SEQ ID NO:2926:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1602230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2926:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2927:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..146
(D) OTHER INFORMATION: / Ceres Seq. ID 1602231
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2927:
Met Glu Gly Gly Ser Arg Ala Asp Gly Arg Asn Pro Asn Gln Leu Arg
1 5 10 15
Pro Phe Thr Cys Thr Gly Asn Pro Leu His Arg Ala His Gly Ser Ala
20 25 30
Arg Trp Ala Gln Gly Asp Thr Val Val Leu Ala Ala Val Tyr Gly Pro
35 40 45
Lys Ser Gly Thr Arg Lys Gly Glu Asn Pro Glu Lys Ala Ser Ile Glu
50 55 60
Val Val Trp Lys Pro Lys Thr Gly Gln Ile Gly Arg Gln Glu Arg Glu
65 70 75 80
Tyr Glu Met Thr Leu Lys Arg Thr Leu Gln Ser Ile Cys Leu Leu Thr
85 90 95
Val His Pro Asn Thr Thr Thr Ser Val Val Leu Gln Val Val Gly Asp
100 105 110
Asp Gly Ser Leu Met Ser Cys Ala Ile Asn Ala Ser Cys Ala Ala Leu
115 120 125
Xaa Phe Ala Gly Ile Pro Met Glu Thr Ser Arg Trp Ser Arg Leu Ala
130 135 140
Val Glu
145

(2) INFORMATION FOR SEQ ID NO:2928:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1602232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2928:

Met Gly Gly Ile Arg Thr Ser Ser Gly Arg Ser Pro Ala Pro Gly Thr
1 5 10 15
Arg Ser Thr Ala Pro Thr Ala Pro Arg Gly Gly Arg Arg Ala Thr Pro
20 25 30
Ser Cys Trp Pro Leu Cys Thr Gly Pro Ser Arg Glu Pro Gly Arg Ala
35 40 45
Arg Thr Pro Arg Arg Pro Pro Ser Arg Ser Cys Gly Ser Pro Arg Pro
50 55 60
Ala Arg Ser Glu Gly Lys Arg Gly Asn Met Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:2929:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..377

(D) OTHER INFORMATION: / Ceres Seq. ID 1602233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2929:

acatccta	at	cgaaaa	accc	atcgcc	acca	ccaatc	aatc	catcac	gtta	gctgc	ac	ctg	60
cgctct	ct	tgagg	tgcg	cagcc	agcaa	tggc	gtg	ctc	caaag	cgg	tg	ctgc	120
cgctc	ctag	cgtcg	cagga	gcgct	ctct	ccgct	gcgg	gtggg	agg	ac	tac	gacc	180
acatgt	acca	cagg	tgtac	aggtc	ctgca	tgagg	aagt	cgacg	acgac	gatg	ccg	atg	240
atgcatt	gaa	gaatag	catc	agcccc	ggtt	ccacct	ccgt	gtcgg	atgat	catg	acc	acg	300
accatg	acga	ccacc	acgat	gatcac	gacc	acgacc	acga	ccaca	ac	cat	gacc	acc	360
acaatg	atca	tgacc	ac										

(2) INFORMATION FOR SEQ ID NO:2930:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1602234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2930:

Ile	Leu	Ile	Glu	Lys	Pro	Ile	Ala	Thr	Thr	Asn	Gln	Ser	Ile	Thr	Leu	
1				5					10					15		
Ala	Ala	Pro	Ala	Pro	Leu	Leu	Glu	Val	Ala	Gln	Pro	Ala	Met	Ala	Cys	
				20				25					30			
Ser	Lys	Ala	Val	Leu	Leu	Ala	Ala	Leu	Leu	Ala	Val	Ala	Gly	Ala	Leu	
				35			40						45			
Ser	Ser	Ala	Ala	Val	Trp	Glu	Asp	Tyr	Asp	His	His	Met	Tyr	His	Arg	
				50			55				60					
Cys	Tyr	Arg	Ser	Cys	Met	Arg	Lys	Cys	Asp	Asp	Asp	Asp	Ala	Asp	Asp	
65				70					75					80		
Ala	Leu	Lys	Asn	Ser	Ile	Ser	Pro	Val	Ala	Thr	Ser	Val	Ser	Asp	Asp	
				85				90						95		
His	Asp	His	Asp	His	Asp	Asp	His	His	Asp	Asp	His	Asp	His	Asp	His	
				100			105						110			
Asp	His	Asn	His	Asp	Asp	His	His	Asn	Asp	His	Asp	His				
				115			120						125			

(2) INFORMATION FOR SEQ ID NO:2931:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1602235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2931:

Met	Ala	Cys	Ser	Lys	Ala	Val	Leu	Leu	Ala	Ala	Leu	Leu	Ala	Val	Ala	
1				5					10					15		
Gly	Ala	Leu	Ser	Ser	Ala	Ala	Val	Trp	Glu	Asp	Tyr	Asp	His	His	Met	
				20				25					30			
Tyr	His	Arg	Cys	Tyr	Arg	Ser	Cys	Met	Arg	Lys	Cys	Asp	Asp	Asp	Asp	
				35			40					45				
Ala	Asp	Asp	Ala	Leu	Lys	Asn	Ser	Ile	Ser	Pro	Val	Ala	Thr	Ser	Val	
				50			55				60					
Ser	Asp	Asp	His	Asp	His	Asp	His	Asp	Asp	His	His	Asp	Asp	His	Asp	
65				70					75					80		
His	Asp	His	Asp	His	Asn	His	Asp	Asp	His	His	Asn	Asp	His	Asp	His	

85

90

95

(2) INFORMATION FOR SEQ ID NO:2932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2932:

```
Met Tyr His Arg Cys Tyr Arg Ser Cys Met Arg Lys Cys Asp Asp Asp
1           5           10           15
Asp Ala Asp Asp Ala Leu Lys Asn Ser Ile Ser Pro Val Ala Thr Ser
20           25           30
Val Ser Asp Asp His Asp His Asp His Asp Asp His His Asp Asp His
35           40           45
Asp His Asp His Asp His Asn His Asp Asp His His Asn Asp His Asp
50           55           60
His
65
```

(2) INFORMATION FOR SEQ ID NO:2933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..475
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2933:

```
aaatgtttga caaacacaaa gaatctaggc ggcggcatct ggctatccat actccaataa      60
ttattcctgt ttggtctcag gttcggatgg ttgaggatga tttaatgtat agcacttttc      120
ttgaggtgta tgaaattaat tgtgcacggc ataatagaga agctgactcg cctattacaa      180
ttttcaaaga gcagcttaat caagccgttt cagggcagct ctctcctgaa gcaattgtgg      240
agctacgtct gcaagcatac aatgagatta caaaaaatat tgtaaatgat aatattttct      300
cccaatatat gcacaagatt ctgccaaactg gcaactacct gtggaccttc aagaaacaat      360
ttgcaatoca agtggctctc tctgtcttca tgtcgtatat gctgcagatt ggcggcaggg      420
ctcctaacaa aattctatct gctaaaaata ctgggaagat cttccagact gactt
```

(2) INFORMATION FOR SEQ ID NO:2934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2934:

```
Met Phe Asp Lys His Lys Glu Ser Arg Arg Arg His Leu Ala Ile His
1           5           10           15
Thr Pro Ile Ile Ile Pro Val Trp Ser Gln Val Arg Met Val Glu Asp
20           25           30
```

Asp Leu Met Tyr Ser Thr Phe Leu Glu Val Tyr Glu Ile Asn Cys Ala
35 40 45
Arg His Asn Arg Glu Ala Asp Ser Pro Ile Thr Ile Phe Lys Glu Gln
50 55 60
Leu Asn Gln Ala Val Ser Gly Gln Leu Ser Pro Glu Ala Ile Val Glu
65 70 75 80
Leu Arg Leu Gln Ala Tyr Asn Glu Ile Thr Lys Asn Ile Val Asn Asp
85 90 95
Asn Ile Phe Ser Gln Tyr Met His Lys Ile Leu Pro Thr Gly Asn Tyr
100 105 110
Leu Trp Thr Phe Lys Lys Gln Phe Ala Ile Gln Val Ala Leu Ser Cys
115 120 125
Phe Met Ser Tyr Met Leu Gln Ile Gly Gly Arg Ala Pro Asn Lys Ile
130 135 140
Leu Phe Ala Lys Asn Thr Gly Lys Ile Phe Gln Thr Asp
145 150 155

(2) INFORMATION FOR SEQ ID NO:2935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1602242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2935:

Met Val Glu Asp Asp Leu Met Tyr Ser Thr Phe Leu Glu Val Tyr Glu
1 5 10 15
Ile Asn Cys Ala Arg His Asn Arg Glu Ala Asp Ser Pro Ile Thr Ile
20 25 30
Phe Lys Glu Gln Leu Asn Gln Ala Val Ser Gly Gln Leu Ser Pro Glu
35 40 45
Ala Ile Val Glu Leu Arg Leu Gln Ala Tyr Asn Glu Ile Thr Lys Asn
50 55 60
Ile Val Asn Asp Asn Ile Phe Ser Gln Tyr Met His Lys Ile Leu Pro
65 70 75 80
Thr Gly Asn Tyr Leu Trp Thr Phe Lys Lys Gln Phe Ala Ile Gln Val
85 90 95
Ala Leu Ser Cys Phe Met Ser Tyr Met Leu Gln Ile Gly Gly Arg Ala
100 105 110
Pro Asn Lys Ile Leu Phe Ala Lys Asn Thr Gly Lys Ile Phe Gln Thr
115 120 125
Asp

(2) INFORMATION FOR SEQ ID NO:2936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..406

(D) OTHER INFORMATION: / Ceres Seq. ID 1602253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2936:

acggcccaac	cccatccact	cctttcctcc	caccgcgcag	ccgtcacccg	cgcggtgcagc	60
cagcttccct	gctacccccg	cgcgccgcca	gccgagcgga	cgccggccct	gccccgcacg	120
ccggcacgcg	gcacgcgcag	ccagctgccc	cacacgacgc	cggccgcct	cgactcccc	180

```
accgcgctac ccggcagccc cgcgctaccc ggtcctcgct cggcgtcctt gattcccacc 240
gcacggcggc ccttctcttg ccaccgcaca ccgcgcagga gcactgccct tcgccccttg 300
tttagctgca gcaggagcgc cgcccagccg gccaccacca ccgcagcttg agagttgaga 360
cctgcagttg acgaccagag gccagagggc gttgctngcg ctgctt
```

(2) INFORMATION FOR SEQ ID NO:2937:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2937:

```
Thr Ala Gln Pro His Pro Leu Leu Ser Ser His Pro Pro Ala Val Thr
1          5          10          15
Arg Ala Cys Ser Gln Leu Pro Cys Tyr Pro Arg Ala Pro Pro Ala Glu
          20          25          30
Arg Thr Pro Ala Leu Pro Arg Thr Pro Ala Arg Gly Thr Arg Ser Gln
          35          40          45
Leu Pro His Thr Thr Pro Ala Ala Leu Ala Leu Pro Thr Ala Leu Pro
          50          55          60
Gly Ser Pro Ala Leu Pro Gly Pro Arg Ser Ala Ser Leu Ile Pro Thr
65          70          75          80
Ala Arg Arg Pro Phe Phe Cys His Arg Thr Pro Arg Arg Ser Thr Ala
          85          90          95
Leu Arg Pro Leu Phe Ser Cys Ser Arg Ser Ala Ala Gln Pro Ala Thr
          100          105          110
Thr Thr Ala Ala
          115
```

(2) INFORMATION FOR SEQ ID NO:2938:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2938:

```
Arg Pro Asn Pro Ile His Ser Phe Pro Pro Thr Arg Gln Pro Ser Pro
1          5          10          15
Ala Arg Ala Ala Ser Phe Pro Ala Thr Pro Ala Arg Arg Gln Pro Ser
          20          25          30
Gly Arg Arg Pro Cys Pro Ala Arg Arg His Ala Ala Arg Ala Ala Ser
          35          40          45
Cys Pro Thr Arg Arg Arg Pro Pro Ser His Ser Pro Pro Arg Tyr Pro
          50          55          60
Ala Ala Pro Arg Tyr Pro Val Leu Ala Arg Arg Pro
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:2939:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2939:

Gly Pro Thr Pro Ser Thr Pro Phe Leu Pro Pro Ala Ser Arg His Pro
1 5 10 15
Arg Val Gln Pro Ala Ser Leu Leu Pro Pro Arg Ala Ala Ser Arg Ala
20 25 30
Asp Ala Gly Pro Ala Pro His Ala Gly Thr Arg His Ala Gln Pro Ala
35 40 45
Ala Pro His Asp Ala Gly Arg Pro Arg Thr Pro His Arg Ala Thr Arg
50 55 60
Gln Pro Arg Ala Thr Arg Ser Ser Leu Gly Val Leu Asp Ser His Arg
65 70 75 80
Thr Ala Ala Leu Leu Leu Pro Pro His Thr Ala Gln Glu His Cys Pro
85 90 95
Ser Pro Leu Val
100

(2) INFORMATION FOR SEQ ID NO:2940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..357
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2940:

aaaaaactgc atcgaacacc aatggcattc ttgcattgaa ggaaccttcc ctccacctcc 60
accgcccagag agcgagcggc cggacggggt tttggttggg catggctgcc ccggcgatgc 120
tccaagtggg gatcctcgcc gcggtcctcc ttctccggt cctcagcgtg ccgggcgcgcg 180
aggcacagac caagaagttc tgcctcacgc agttcgccat cgctagccag gcctgcgcca 240
tcctgccacc caccagtcct gagcaccacc accatcatca cgatgacgag gacaatgacg 300
aggacaacga cgaagatgag gacgaagacg aggacaacga tgaagatgaa gacgagg

(2) INFORMATION FOR SEQ ID NO:2941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2941:

Lys Thr Ala Ser Asn Thr Asn Gly Ile Leu Ala Leu Lys Glu Pro Ser
1 5 10 15
Leu His Leu His Arg Pro Arg Ala Ser Gly Arg Thr Gly Phe Trp Leu
20 25 30
Gly Met Ala Ala Pro Ala Met Leu Gln Val Val Ile Leu Ala Ala Val
35 40 45
Leu Leu Leu Pro Phe Leu Ser Val Pro Gly Ala Glu Ala Gln Thr Lys
50 55 60
Lys Phe Cys Leu Thr Gln Phe Ala Ile Ala Ser Gln Ala Cys Ala Ile
65 70 75 80
Leu Pro Pro Thr Ser Pro Glu His His His His His His Asp Asp Glu
85 90 95

Asp Asn Asp Glu Asp Asn Asp Glu Asp Glu Asp Glu Asp Asn
100 105 110
Asp Glu Asp Glu Asp Glu
115

(2) INFORMATION FOR SEQ ID NO:2942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1602266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2942:

Met Ala Ala Pro Ala Met Leu Gln Val Val Ile Leu Ala Ala Val Leu
1 5 10 15
Leu Leu Pro Phe Leu Ser Val Pro Gly Ala Glu Ala Gln Thr Lys Lys
20 25 30
Phe Cys Leu Thr Gln Phe Ala Ile Ala Ser Gln Ala Cys Ala Ile Leu
35 40 45
Pro Pro Thr Ser Pro Glu His His His His His Asp Asp Glu Asp
50 55 60
Asn Asp Glu Asp Asn Asp Glu Asp Glu Asp Glu Asp Glu Asp Asn Asp
65 70 75 80
Glu Asp Glu Asp Glu
85

(2) INFORMATION FOR SEQ ID NO:2943:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1602267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2943:

Met Leu Gln Val Val Ile Leu Ala Ala Val Leu Leu Leu Pro Phe Leu
1 5 10 15
Ser Val Pro Gly Ala Glu Ala Gln Thr Lys Lys Phe Cys Leu Thr Gln
20 25 30
Phe Ala Ile Ala Ser Gln Ala Cys Ala Ile Leu Pro Pro Thr Ser Pro
35 40 45
Glu His His His His His His Asp Asp Glu Asp Asn Asp Glu Asp Asn
50 55 60
Asp Glu Asp Glu Asp Glu Asp Glu Asp Asn Asp Glu Asp Glu Asp Glu
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:2944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..466

(D) OTHER INFORMATION: / Ceres Seq. ID 1602284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2944:

acacactcct	tcgcctcgcg	cgggcgctcg	tgcctccct	ccaccgaacg	atccctcctc	60
ctcctcctcc	tcctcctcct	cgcataccac	csgsrcccca	ccttctcctt	aaagctacct	120
gmcatacccg	gcggttgccg	cgcgcgcaat	cgatcgaccg	gaagagaaag	agcagctagc	180
tagctagcag	atcgagcac	ggcaacaagg	cgatggggcg	cggcaaggta	cagctgaagc	240
ggatagagaa	caagataaac	cggcaggtga	ccttctccaa	gcgccggaac	ggcctgctca	300
agaaggcgca	cgagatctcc	gtcctctgcg	atgcgaggt	cgccgtcatc	gtcttctycc	360
ccaagggcaa	gctctacgag	tacgccaccg	actccgcat	ggacaaaatt	cttgaacgct	420
atgagcgata	ttcctatgct	gaaaaggctc	ttatttcagc	tgaatc		

(2) INFORMATION FOR SEQ ID NO:2945:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..60

(D) OTHER INFORMATION: / Ceres Seq. ID 1602285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2945:

Thr	His	Ser	Phe	Ala	Ser	Arg	Arg	Pro	Ser	Ser	Pro	Pro	Ser	Thr	Glu
1				5					10					15	
Arg	Ser	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Ser	His	Xaa	Xaa
				20					25					30	
Pro	Thr	Phe	Ser	Leu	Lys	Leu	Pro	Xaa	Ile	Pro	Gly	Gly	Cys	Arg	Arg
				35				40					45		
Arg	Asn	Arg	Ser	Thr	Gly	Arg	Glu	Arg	Ala	Ala	Ser				
				50			55				60				

(2) INFORMATION FOR SEQ ID NO:2946:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1602286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2946:

Thr	Leu	Leu	Arg	Leu	Ala	Pro	Ala	Val	Val	Ala	Ser	Leu	His	Arg	Thr
1				5					10					15	
Ile	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Arg	Ile	Pro	Xaa	Xaa	Pro	
				20					25					30	
His	Leu	Leu	Leu	Lys	Ala	Thr	Xaa	His	Thr	Arg	Arg	Leu	Pro	Pro	Pro
				35				40					45		
Gln	Ser	Ile	Asp	Arg	Lys	Arg	Lys	Ser	Ser						
				50			55								

(2) INFORMATION FOR SEQ ID NO:2947:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

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(D) OTHER INFORMATION: / Ceres Seq. ID 1602287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2947:

```
Met Gly Arg Gly Lys Val Gln Leu Lys Arg Ile Glu Asn Lys Ile Asn
1          5          10          15
Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala
          20          25          30
His Glu Ile Ser Val Leu Cys Asp Ala Glu Val Ala Val Ile Val Phe
          35          40          45
Xaa Pro Lys Gly Lys Leu Tyr Glu Tyr Ala Thr Asp Ser Arg Met Asp
          50          55          60
Lys Ile Leu Glu Arg Tyr Glu Arg Tyr Ser Tyr Ala Glu Lys Ala Leu
65          70          75          80
Ile Ser Ala Glu
```

(2) INFORMATION FOR SEQ ID NO:2948:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..445
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2948:

```
gttcccaacc cattacattt gcaagccctt ttacattgca gaggcctcgct cgctctcgga      60
acagagctag gcagtaaca gacgaagaag aagcaagcca agcagcaagc gaagcgagag      120
agaggcgagg acgtggcgac gacggcagcc gcgatggcga caacgacgga cctgggggttc      180
gaggcgacgg agctccgcct gggcctgccc ggcggcagcg gcgggggagg gggaggggag      240
ctggcgctgg gcggcgaggg gaggagctcg tctccgctc ccggcaagag gggcttcgcc      300
gagaccatcg acctgaagct gaagctggag ccagcggccg tcgtggaggc ggaggaggag      360
gaggaggacc acggcgttgc tgttgccctt gagaaggagg aggaggccgg gaagatgaag      420
cgggtccccga gccagagcag cgctcg
```

(2) INFORMATION FOR SEQ ID NO:2949:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2949:

```
Ser Gln Pro Ile Thr Phe Ala Ser Pro Phe Thr Leu Gln Ser Leu Ala
1          5          10          15
Arg Ser Arg Asn Arg Ala Arg Gln Leu Thr Asp Glu Glu Glu Ala Ser
          20          25          30
Gln Ala Ala Ser Glu Ala Arg Glu Arg Arg Gly Arg Gly Asp Asp Gly
          35          40          45
Ser Arg Asp Gly Asp Asn Asp Gly Pro Gly Val Arg Gly Asp Gly Ala
          50          55          60
Pro Pro Gly Pro Ala Arg Arg Gln Arg Arg Gly Arg Gly Arg Gly Ala
65          70          75          80
Gly Ala Gly Arg Arg Gly Glu Glu Leu Val Leu Arg Leu Arg Gln Glu
          85          90          95
Gly Leu Arg Arg Asp His Arg Pro Glu Ala Glu Ala Gly Ala Ser Gly
          100          105          110
Arg Arg Gly Gly Gly Gly Gly Gly Gly Gly Pro Arg Arg Cys Cys Cys
```

115 120 125
Pro

(2) INFORMATION FOR SEQ ID NO:2950:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2950:

Met Ala Thr Thr Thr Asp Leu Gly Phe Glu Ala Thr Glu Leu Arg Leu
1 5 10 15
Gly Leu Pro Gly Gly Ser Gly Gly Gly Gly Gly Glu Leu Ala Leu
20 25 30
Gly Gly Glu Gly Arg Ser Ser Ser Ala Ser Gly Lys Arg Gly Phe
35 40 45
Ala Glu Thr Ile Asp Leu Lys Leu Lys Leu Glu Pro Ala Ala Val Val
50 55 60
Glu Ala Glu Glu Glu Glu Asp His Gly Val Ala Val Ala Leu Glu
65 70 75 80
Lys Glu Glu Glu Ala Gly Lys Met Lys Arg Ser Pro Ser Gln Ser Ser
85 90 95
Val

(2) INFORMATION FOR SEQ ID NO:2951:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..472
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2951:

ggggttctcg accaatcact ccagtatcca gtctctctct cggctctcct ctccccgatt 60
tcttcccca cccgctgtca gtctcactcc ccgcgcgcgc gctctctctt tctcgccctt 120
cgccgcgcgc gacgagcttg agctcgagct ggttcctcgt atagaagacg acggccgcgcg 180
tatggagccc atgaacgtag acaacggcgg cagcgggtggc cttgacgcgc agatcgaaca 240
gctgatgcag tgccgcccgc tcgccgagca agaggttaag gcaactgtgc agaaggccaa 300
ggagatattg atbgaggaaa gcaacgttca gcctgtcaag agtccagtga caatatgtgg 360
tgatatacat ggacaattcc acgatcttgt agagcttttc cgaattggcg ggaagtgtcc 420
agacacaatt acttatttat gggagattat gtagatcgtg gctactattc tg

(2) INFORMATION FOR SEQ ID NO:2952:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2952:

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Gly Phe Ser Thr Asn His Ser Ser Ile Gln Ser Leu Ser Arg Leu Ser
1 5 10 15
Ser Pro Arg Phe Pro Ser Pro Pro Ala Val Ser Leu Thr Pro Arg Ala
20 25 30
Arg Ala Leu Ser Phe Leu Ala Phe Ala Ala Gly Asp Glu Leu Glu Leu
35 40 45
Glu Leu Val Pro Arg Ile Glu Asp Asp Gly Arg Gly Met Glu Pro Met
50 55 60
Asn Val Asp Asn Gly Gly Ser Gly Gly Leu Asp Ala Gln Ile Glu Gln
65 70 75 80
Leu Met Gln Cys Arg Pro Leu Ala Glu Gln Glu Val Lys Ala Leu Cys
85 90 95
Glu Lys Ala Lys Glu Ile Leu Xaa Glu Glu Ser Asn Val Gln Pro Val
100 105 110
Lys Ser Pro Val Thr Ile Cys Gly Asp Ile His Gly Gln Phe His Asp
115 120 125
Leu Val Glu Leu Phe Arg Ile Gly Gly Lys Cys Pro Asp Thr Ile Thr
130 135 140
Tyr Leu Trp Glu Ile Met
145 150

(2) INFORMATION FOR SEQ ID NO:2953:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2953:

Met Glu Pro Met Asn Val Asp Asn Gly Gly Ser Gly Gly Leu Asp Ala
1 5 10 15
Gln Ile Glu Gln Leu Met Gln Cys Arg Pro Leu Ala Glu Gln Glu Val
20 25 30
Lys Ala Leu Cys Glu Lys Ala Lys Glu Ile Leu Xaa Glu Glu Ser Asn
35 40 45
Val Gln Pro Val Lys Ser Pro Val Thr Ile Cys Gly Asp Ile His Gly
50 55 60
Gln Phe His Asp Leu Val Glu Leu Phe Arg Ile Gly Gly Lys Cys Pro
65 70 75 80
Asp Thr Ile Thr Tyr Leu Trp Glu Ile Met
85 90

(2) INFORMATION FOR SEQ ID NO:2954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2954:

Met Asn Val Asp Asn Gly Gly Ser Gly Gly Leu Asp Ala Gln Ile Glu
1 5 10 15
Gln Leu Met Gln Cys Arg Pro Leu Ala Glu Gln Glu Val Lys Ala Leu
20 25 30
Cys Glu Lys Ala Lys Glu Ile Leu Xaa Glu Glu Ser Asn Val Gln Pro

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(i) SEQUENCE CHARACTERISTICS:

Phe Ser Phe Thr Thr Pro Cys Ser Arg Ser Cys Cys Asp Gly Arg Phe
1 5 10 15
Ala Cys Thr Ser Asp His Pro Ser Ala Pro Phe Ser Pro Ile Ala Ser
20 25 30

Asn Leu Glu Ile Gln Pro Arg Ser Ser His Glu Gly Asp Ser Pro His
35 40 45
Pro Gly Trp Thr Val Arg Gln Pro Asp Arg Phe Gln Val Leu Gly Gly
50 55 60
Arg Leu Arg Arg Ala Trp Tyr Arg Pro His Arg Thr Leu Cys Arg His
65 70 75 80
Leu Arg Pro Pro Ala Arg Ala Arg Gln Cys Leu Leu Gln Arg Gly Leu
85 90 95
Met Arg Pro Leu Arg Ala Ala Arg Arg Ala His Gly Pro Arg Ala Arg
100 105 110
His His Gly Gln Arg Pro His Arg Ala Val Arg Pro Asp Leu Pro Pro
115 120 125
Arg Gln Leu Arg Leu Arg Pro Val Trp Arg Gly Xaa Thr Thr Gly Pro
130 135 140
Arg Ala Thr Thr Gln Arg Ala Leu Ser Ser Ser Thr Leu Cys Leu Thr
145 150 155 160
Ser

(2) INFORMATION FOR SEQ ID NO:2960:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1602322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2960:

Met Arg Glu Ile Leu His Ile Gln Gly Gly Gln Cys Gly Asn Gln Ile
1 5 10 15
Gly Ser Lys Phe Trp Glu Val Val Cys Asp Glu His Gly Ile Asp Pro
20 25 30
Thr Gly Arg Tyr Val Gly Thr Ser Asp Leu Gln Leu Glu Arg Val Asn
35 40 45
Val Tyr Tyr Asn Glu Ala Ser Cys Gly Arg Phe Val Pro Arg Ala Val
50 55 60
Leu Met Asp Leu Glu Pro Gly Thr Met Asp Ser Val Arg Thr Gly Pro
65 70 75 80
Tyr Gly Gln Ile Phe Arg Pro Asp Asn Phe Val Phe Gly Gln Ser Gly
85 90 95
Ala Gly Xaa Gln Leu Gly Gln Gly Pro Leu His Arg Gly Arg
100 105 110

(2) INFORMATION FOR SEQ ID NO:2961:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1602323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2961:

Met Val Ser Thr Pro Pro Asp Ala Met Ser Ala Pro Pro Thr Ser Ser
1 5 10 15
Ser Ser Ala Ser Met Ser Thr Thr Thr Arg Pro His Ala Ala Ala Ser
20 25 30
Cys Arg Ala Pro Cys Ser Trp Thr Ser Ser Pro Ala Pro Trp Thr Ala

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```

          35              40              45
Ser Ala Pro Gly Arg Thr Ala Arg Ser Ser Ala Pro Thr Thr Ser Ser
  50              55              60
Ser Ala Ser Leu Ala Arg Xaa Asn Asn Trp Ala Lys Gly His Tyr Thr
  65              70              75              80
Glu Gly Ala Glu Leu Ile Asp Ser Val Leu Asp Val Val Arg
          85              90
```

(2) INFORMATION FOR SEQ ID NO:2962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..486
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2962:

```

aagaatagcg aacaaacatc gactacagtc ggctaggtaa tctggtggta cgacgactga      60
cgacgacatg gcggccacca gcagcaagtc gtcgtcgtcc tcgagctcgg cgcagcgggc      120
agcagctgcc gccctgctcg tggcgggtgc cgtcctgggtg gtgggcgcgg cggcgggtgtg      180
cgacatgagc aactagcagt tcatgtcgtg ccagcccgcg gcggccaaga cgacggaccc      240
gccggccgcg ccgtcgcagg cgtgctgcga cgcgctggcg ggggcggacc tcaagtgcct      300
gtgcggttac aagaactcgc cgtggatggg cgtctacaac atcgacccca agcgcgccat      360
ggagcttccg gccaaagtgc gcctcgccac gccgcccgac tgctagcagt gtgctagcca      420
agccaagcca agcaggaagg cccccgggca ttgctagctg tacgtgtctg tgtgtgcate      480
tgcagc
```

(2) INFORMATION FOR SEQ ID NO:2963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2963:

```

Met Ala Ala Thr Ser Ser Lys Ser Ser Ser Ser Ser Ser Ala Gln
  1              5              10              15
Arg Ala Ala Ala Ala Ala Leu Leu Val Ala Val Ser Val Leu Val Val
          20              25              30
Gly Ala Ala Ala Val Cys Asp Met Ser Asn
          35              40
```

(2) INFORMATION FOR SEQ ID NO:2964:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2964:

```

Met Ser Cys Gln Pro Ala Ala Ala Lys Thr Thr Asp Pro Pro Ala Ala
  1              5              10              15
Pro Ser Gln Ala Cys Cys Asp Ala Leu Ala Gly Ala Asp Leu Lys Cys
```

20 25 30
Leu Cys Gly Tyr Lys Asn Ser Pro Trp Met Gly Val Tyr Asn Ile Asp
35 40 45
Pro Lys Arg Ala Met Glu Leu Pro Ala Lys Cys Gly Leu Ala Thr Pro
50 55 60
Pro Asp Cys
65

(2) INFORMATION FOR SEQ ID NO:2965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2965:

caagcttaaaa ccacaacgca aacaaccacc aaagcaatcg aaaagcaacc ctgcaagtgc 60
aggcaaagag agggcgcgac caaacagatc caatccaatg gcgatggcac cgtccgcagc 120
atgcgtcgtc togttccccg cccgccggc ggcgtccacg gccgggcccc gcgcgcgcgc 180
ggcgccggg gcgggtccacg ctttcgcggg gtcggcggag ggcgccaagt ggtgggcgcc 240
gctgctgggg tggtcgggga aggcgcacta cctggaggcc ccggcccccg cgccggcggg 300
ggcgcaggac gaggcgccgc ggaggcagtt cgtgggggtg atgacggagg agaaggcccg 360
ggagctgcgg gcgcggatgg cgcagacgga gtccttcac gacgccatgt accactccgc 420
catcgctcg cgcctgcac gtcctccta gggttgggtg gcgcgcggcc agctcgcc

(2) INFORMATION FOR SEQ ID NO:2966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2966:

Lys Leu Lys Pro Gln Arg Lys Gln Pro Pro Lys Gln Ser Lys Ser Asn
1 5 10 15
Pro Ala Ser Ala Gly Lys Glu Arg Ala Arg Pro Asn Arg Ser Asn Pro
20 25 30
Met Ala Met Ala Pro Ser Ala Ala Cys Val Val Ser Phe Pro Ala Arg
35 40 45
Pro Ala Ala Ser Thr Ala Gly Pro Arg Ala Ala Gly Ala Gly Ala
50 55 60
Val His Ala Phe Ala Gly Ser Ala Glu Gly Ala Lys Trp Trp Ala Pro
65 70 75 80
Leu Leu Gly Trp Ser Gly Lys Ala Asp Tyr Leu Glu Ala Pro Ala Pro
85 90 95
Ala Pro Ala Gly Ala Gln Asp Glu Ala Pro Arg Arg Gln Phe Val Gly
100 105 110
Val Met Thr Glu Glu Lys Ala Arg Glu Leu Arg Ala Arg Met Ala Gln
115 120 125
Thr Glu Ser Phe His Asp Ala Met Tyr His Ser Ala Ile Ala Ser Arg
130 135 140
Leu Ala Arg Ser Ser
145

(2) INFORMATION FOR SEQ ID NO:2967:

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..404

(D) OTHER INFORMATION: / Ceres Seq. ID 1602334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2969:

agaaccgaaa ccaagcaacc caatccaaac cagacaagca aggaatcccc cgatgggtca	60
tcgcgtttctc ctccctctct ctctcgcgtc ggccgcgcgc gttgcgcgcg gtcgacgcgg	120
aggaccgcgt gatccggcag gtggttcccg gtggagatga caacgatctg gagctgaacg	180
cggagtccca ctctctgagc ttctgtcagc ggttcggcaa gtcctacaag gacgccgacg	240
agcacgcgta ccggctgtcc gttttcaagg ccaacctgcg ccgcgcgcgc cggcaccagc	300
tgctggaccc gtcggcggag caccgcgtca ctaagttctc cgacctcacg ccggcagagt	360
tccgccggac ctacctcggc ctccgcaagt cccggcgcgc tctc	

(2) INFORMATION FOR SEQ ID NO:2970:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1602335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2970:

Asn Arg Asn Gln Ala Thr Gln Ser Lys Pro Asp Lys Gln Gly Ile Pro	
1 5 10 15	
Arg Trp Leu Ile Ala Phe Ser Ser Ser Ser Leu Ser Arg Arg Pro Pro	
20 25 30	
Arg Leu Arg Arg Val Asp Ala Glu Asp Pro Leu Ile Arg Gln Val Val	
35 40 45	
Pro Gly Gly Asp Asp Asn Asp Leu Glu Leu Asn Ala Glu Ser His Phe	
50 55 60	
Leu Ser Phe Val Gln Arg Phe Gly Lys Ser Tyr Lys Asp Ala Asp Glu	
65 70 75 80	
His Ala Tyr Arg Leu Ser Val Phe Lys Ala Asn Leu Arg Arg Ala Arg	
85 90 95	
Arg His Gln Leu Leu Asp Pro Ser Ala Glu His Gly Val Thr Lys Phe	
100 105 110	
Ser Asp Leu Thr Pro Ala Glu Phe Arg Arg Thr Tyr Leu Gly Leu Arg	
115 120 125	
Lys Ser Arg Arg Ala Leu	
130	

(2) INFORMATION FOR SEQ ID NO:2971:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 483 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..483

(D) OTHER INFORMATION: / Ceres Seq. ID 1602346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2971:

actcctgccc ttcttccaac tctctcgttc cccgttccct cctctaccac tggccccggc	60
accgcgggag cgcgcaccgc ctgctcgtct cgcgcgcagc cgtccctgag ccggaaccct	120
agcggccgcc attgccacg cgcgcgcgcg ccgatggacg gcgggggctc cgggccggcg	180
cccaacgccg cgcacaccgc ggaagaggtc ttccgcgact acaaagcccg ccgcgccggc	240
atgatcaagg cactcaccac cgatgtggag aggttcttca agctctgtga ccccgaaaag	300
gagaacttgt gcctctatgg ctatcccgat gagacatggg aggttacctt gccagctgag	360
gaagtgcccc cagagatccc tgaaccagca ttaggaatca actttgctag ggatggcatg	420

aatgagaagg actggctggc gctagttgca gtccacagtg attccctggt tactatctgt 480
cgc

(2) INFORMATION FOR SEQ ID NO:2972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1602347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2972:

Thr	Pro	Ala	Leu	Arg	Pro	Thr	Pro	Pro	Phe	Pro	Val	Pro	Ser	Ser	Thr
1				5					10					15	
Thr	Gly	Pro	Gly	Thr	Ala	Gly	Ala	Pro	Thr	Ala	Cys	Ser	Ser	Arg	Arg
			20					25						30	
Ser	Pro	Ser	Leu	Ser	Arg	Asn	Pro	Ser	Gly	Arg	His	Cys	Pro	Arg	Ala
			35				40					45			
Ala	Arg	Pro	Met	Asp	Gly	Gly	Gly	Ser	Gly	Pro	Ala	Pro	Asn	Ala	Ala
			50			55					60				
His	Thr	Ala	Glu	Glu	Val	Phe	Arg	Asp	Tyr	Lys	Ala	Arg	Arg	Ala	Gly
					70					75				80	
Met	Ile	Lys	Ala	Leu	Thr	Thr	Asp	Val	Glu	Arg	Phe	Phe	Lys	Leu	Cys
				85					90					95	
Asp	Pro	Glu	Lys	Glu	Asn	Leu	Cys	Leu	Tyr	Gly	Tyr	Pro	Asp	Glu	Thr
			100					105					110		
Trp	Glu	Val	Thr	Leu	Pro	Ala	Glu	Glu	Val	Pro	Pro	Glu	Ile	Pro	Glu
			115				120						125		
Pro	Ala	Leu	Gly	Ile	Asn	Phe	Ala	Arg	Asp	Gly	Met	Asn	Glu	Lys	Asp
			130			135					140				
Trp	Leu	Ala	Leu	Val	Ala	Val	His	Ser	Asp	Ser	Leu	Val	Thr	Ile	Cys
					150					155					160
Arg															

(2) INFORMATION FOR SEQ ID NO:2973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1602348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2973:

Met	Asp	Gly	Gly	Ser	Gly	Pro	Ala	Pro	Asn	Ala	Ala	His	Thr	Ala
1				5					10				15	
Glu	Glu	Val	Phe	Arg	Asp	Tyr	Lys	Ala	Arg	Arg	Ala	Gly	Met	Ile
			20					25					30	
Ala	Leu	Thr	Thr	Asp	Val	Glu	Arg	Phe	Phe	Lys	Leu	Cys	Asp	Pro
			35				40					45		
Lys	Glu	Asn	Leu	Cys	Leu	Tyr	Gly	Tyr	Pro	Asp	Glu	Thr	Trp	Glu
			50			55				60				65
Thr	Leu	Pro	Ala	Glu	Glu	Val	Pro	Pro	Glu	Ile	Pro	Glu	Pro	Ala
					70					75				80
Gly	Ile	Asn	Phe	Ala	Arg	Asp	Gly	Met	Asn	Glu	Lys	Asp	Trp	Leu
				85					90					95
Leu	Val	Ala	Val	His	Ser	Asp	Ser	Leu	Val	Thr	Ile	Cys	Arg	

100 105 110

(2) INFORMATION FOR SEQ ID NO:2974:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..81

(D) OTHER INFORMATION: / Ceres Seq. ID 1602349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2974:

Met	Ile	Lys	Ala	Leu	Thr	Thr	Asp	Val	Glu	Arg	Phe	Phe	Lys	Leu	Cys
1				5					10					15	
Asp	Pro	Glu	Lys	Glu	Asn	Leu	Cys	Leu	Tyr	Gly	Tyr	Pro	Asp	Glu	Thr
		20						25					30		
Trp	Glu	Val	Thr	Leu	Pro	Ala	Glu	Glu	Val	Pro	Pro	Glu	Ile	Pro	Glu
		35					40					45			
Pro	Ala	Leu	Gly	Ile	Asn	Phe	Ala	Arg	Asp	Gly	Met	Asn	Glu	Lys	Asp
	50				55				60						
Trp	Leu	Ala	Leu	Val	Ala	Val	His	Ser	Asp	Ser	Leu	Val	Thr	Ile	Cys
65				70				75						80	
Arg															

(2) INFORMATION FOR SEQ ID NO:2975:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 484 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..484

(D) OTHER INFORMATION: / Ceres Seq. ID 1602360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2975:

acctcgaaac	cctagcgccg	gcgccctccac	ttcgttttcc	tcactctctc	ctccagctca	60
gggtccggcg	gcgaagggaa	ggcaagatgt	acaccgcgag	gaagaagatc	cagaaggaga	120
agggctcttga	gccctccgag	ttcgaggact	ccgttgccca	ggctttcttt	gatctggaga	180
acgggaacca	ggagctcaag	agcgacctca	aggacctgta	catcaacaat	gctatccaga	240
tggatgttac	cgggagtagg	aaggctgttg	tcattcacgt	cccataccgc	ctgcgcaagg	300
ccttcaggaa	gatccatgtc	agactcgta	gggagctgga	gaagaaattc	agcggcaagg	360
atgtggtaat	tggtgctaca	cggaggattg	tgaggccacc	caagaagggt	tcagctgttc	420
tgcgccctcg	caccaggact	ctgactgctg	ttcacgatgg	catcttgtag	gatgttgtct	480
accc						

(2) INFORMATION FOR SEQ ID NO:2976:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1602361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2976:

Leu	Glu	Thr	Leu	Ala	Pro	Ala	Pro	Pro	Leu	Arg	Phe	Pro	His	Ser	Leu
1				5					10					15	
Leu	Gln	Leu	Arg	Val	Arg	Arg	Arg	Arg	Glu	Gly	Lys	Met	Tyr	Thr	Ala

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2978:

Met Asp Val Thr Gly Ser Arg Lys Ala Val Val Ile His Val Pro Tyr
1 5 10 15
Arg Leu Arg Lys Ala Phe Arg Lys Ile His Val Arg Leu Val Arg Glu
20 25 30
Leu Glu Lys Lys Phe Ser Gly Lys Asp Val Val Ile Val Ala Thr Arg
35 40 45
Arg Ile Val Arg Pro Pro Lys Lys Gly Ser Ala Val Leu Arg Pro Arg
50 55 60
Thr Arg Thr Leu Thr Ala Val His Asp Gly Ile Leu Glu Asp Val Val
65 70 75 80
Tyr

(2) INFORMATION FOR SEQ ID NO:2979:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..498
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2979:

atcgagccag tgcaaacctg gccgacctct tctcctcgcg ccgcccgcgc tgcccgcgtc	60
gtcatgtcga agcgcgggag gggagggacg gcggggaaca agttccgcat gtcgctgggt	120
ctccccgtcg cagcgaccgt gaactgtgcg gacaacacag gcgccaagaa cctctacatc	180
atctccgtca agggcatcaa gggtaggctc aaccgcctgc cgtccgcctg cgtcggcgac	240
atgggtcatgg ccaccgtcaa gaagggttaag cccgacctca ggaagaaggc catgcccgcc	300
gtcatgctcc gccagcgcaa gctgtggcgc cgcaaggacg gactctacat gtacttcgaa	360
gataatgctg gagtcattgt gaaccccaag ggcgagatga aaggatctgc tatcactgga	420
cctattggca aggagtgcgc tgacctttgg cctaggattg ctagtgcagc aaatgctatt	480
gtctgatact actggttg	

(2) INFORMATION FOR SEQ ID NO:2980:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2980:

Met Ser Lys Arg Gly Arg Gly Gly Thr Ala Gly Asn Lys Phe Arg Met
1 5 10 15
Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn Thr
20 25 30
Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly Arg
35 40 45
Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala Thr
50 55 60
Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Met Pro Ala Val
65 70 75 80
Ile Val Arg Gln Arg Lys Leu Trp Arg Arg Lys Asp Gly Val Tyr Met
85 90 95
Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys Gly Glu Met
100 105 110
Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys Ala Asp Leu
115 120 125

(2) INFORMATION FOR SEQ ID NO:2981:

- | (X1) SEQUENCE DESCRIPTION: SEQ INFORMATION | | | | | | | | | | | | | | | |
|--|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Leu | Gly | Leu | Pro | Val | Ala | Ala | Thr | Val | Asn | Cys | Ala | Asp | Asn |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Thr | Gly | Ala | Lys | Asn | Leu | Tyr | Ile | Ile | Ser | Val | Lys | Gly | Ile | Lys | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Arg | Leu | Asn | Arg | Leu | Pro | Ser | Ala | Cys | Val | Gly | Asp | Met | Val | Met | Ala |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Thr | Val | Lys | Lys | Gly | Lys | Pro | Asp | Leu | Arg | Lys | Lys | Val | Met | Pro | Ala |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Val | Ile | Val | Arg | Gln | Arg | Lys | Leu | Trp | Arg | Arg | Lys | Asp | Gly | Val | Tyr |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Met | Tyr | Phe | Glu | Asp | Asn | Ala | Gly | Val | Ile | Val | Asn | Pro | Lys | Gly | Glu |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Met | Lys | Gly | Ser | Ala | Ile | Thr | Gly | Pro | Ile | Gly | Lys | Glu | Cys | Ala | Asp |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Leu | Trp | Pro | Arg | Ile | Ala | Ser | Ala | Ala | Asn | Ala | Ile | Val | | | |
| | | 115 | | | | | 120 | | | | | 125 | | | |

```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 81 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
    (A) NAME/KEY: peptide
    (B) LOCATION: 1..81
    (D) OTHER INFORMATION: / Ceres Seq. ID 1602367
```

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2982:

(2) INFORMATION FOR SEQ ID NO:2983:

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 535 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
```

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..535

(D) OTHER INFORMATION: / Ceres Seq. ID 1602370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2983:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| aattcgaacg | acggagcacg | acgcacgcag | agccgcagag  | atccgtcaca | ctgcaagttt | 60  |
| tgaaaactga | actgtaagat | ggcatcagca | gagctttccc  | gtgaggaaaa | tgtgtacatg | 120 |
| gcgaagctcg | ccgagcaggc | agagaggtac | gaggaaatgg  | ttgagttcat | ggagaaggtg | 180 |
| gcgaaaactg | ttgactcgga | ggagctcact | gtggaggagc  | gcaacctcct | gtctgttgca | 240 |
| tacaagaacg | tcattggagc | ccgccgtgcc | tcattggcgca | tcattctctc | catcgagcag | 300 |
| aaggaggagg | gtcgaggcaa | tgaggaccgt | gtaacactca  | tcaaggacta | ccgtggcaag | 360 |
| attgaaactg | agctcaccaa | gatctgtgat | ggcatcctca  | agcttctcga | atctcacctt | 420 |
| gtgccgttct | ccaccgtccc | cgagtccaag | gtcttctatc  | tcaagatgaa | gggtgactac | 480 |
| tacagatacc | tttgctgagt | tcaagactgg | agctgagaga  | aaggacgctg | ctgag      |     |

(2) INFORMATION FOR SEQ ID NO:2984:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1602371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2984:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Ala | Glu | Leu | Ser | Arg | Glu | Glu | Asn | Val | Tyr | Met | Ala | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Ala | Glu | Gln | Ala | Glu | Arg | Tyr | Glu | Glu | Met | Val | Glu | Phe | Met | Glu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Lys | Val | Ala | Lys | Thr | Val | Asp | Ser | Glu | Glu | Leu | Thr | Val | Glu | Glu | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Leu | Leu | Ser | Val | Ala | Tyr | Lys | Asn | Val | Ile | Gly | Ala | Arg | Arg | Ala |
|     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Ser | Trp | Arg | Ile | Ile | Ser | Ser | Ile | Glu | Gln | Lys | Glu | Glu | Gly | Arg | Gly |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Asn | Glu | Asp | Arg | Val | Thr | Leu | Ile | Lys | Asp | Tyr | Arg | Gly | Lys | Ile | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Thr | Glu | Leu | Thr | Lys | Ile | Cys | Asp | Gly | Ile | Leu | Lys | Leu | Leu | Glu | Ser |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Leu | Val | Pro | Ser | Ser | Thr | Ala | Pro | Glu | Ser | Lys | Val | Phe | Tyr | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Lys | Met | Lys | Gly | Asp | Tyr | Tyr | Arg | Tyr | Leu | Cys |     |     |     |     |     |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2985:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1602372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2985:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Leu | Ala | Glu | Gln | Ala | Glu | Arg | Tyr | Glu | Glu | Met | Val | Glu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Phe | Met | Glu | Lys | Val | Ala | Lys | Thr | Val | Asp | Ser | Glu | Glu | Leu | Thr | Val |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Glu | Arg | Asn | Leu | Leu | Ser | Val | Ala | Tyr | Lys | Asn | Val | Ile | Gly | Ala |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 35  |     | 40  |     | 45  |     |     |     |     |     |     |     |     |     |     |
| Arg | Arg | Ala | Ser | Trp | Arg | Ile | Ile | Ser | Ser | Ile | Glu | Gln | Lys | Glu | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Arg | Gly | Asn | Glu | Asp | Arg | Val | Thr | Leu | Ile | Lys | Asp | Tyr | Arg | Gly |
|     | 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Ile | Glu | Thr | Glu | Leu | Thr | Lys | Ile | Cys | Asp | Gly | Ile | Leu | Lys | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Glu | Ser | His | Leu | Val | Pro | Ser | Ser | Thr | Ala | Pro | Glu | Ser | Lys | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Tyr | Leu | Lys | Met | Lys | Gly | Asp | Tyr | Tyr | Arg | Tyr | Leu | Cys |     |     |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2986:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1602373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2986:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Glu | Phe | Met | Glu | Lys | Val | Ala | Lys | Thr | Val | Asp | Ser | Glu | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Thr | Val | Glu | Glu | Arg | Asn | Leu | Leu | Ser | Val | Ala | Tyr | Lys | Asn | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Gly | Ala | Arg | Arg | Ala | Ser | Trp | Arg | Ile | Ile | Ser | Ser | Ile | Glu | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Glu | Glu | Gly | Arg | Gly | Asn | Glu | Asp | Arg | Val | Thr | Leu | Ile | Lys | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Arg | Gly | Lys | Ile | Glu | Thr | Glu | Leu | Thr | Lys | Ile | Cys | Asp | Gly | Ile |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Lys | Leu | Leu | Glu | Ser | His | Leu | Val | Pro | Ser | Ser | Thr | Ala | Pro | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Lys | Val | Phe | Tyr | Leu | Lys | Met | Lys | Gly | Asp | Tyr | Tyr | Arg | Tyr | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..396

(D) OTHER INFORMATION: / Ceres Seq. ID 1602389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2987:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ttgttcttga | ctctggtgat | ggtgtgagcc | acactgtgcc | catttacgga | aggatatgcc | 60  |
| cttcctcatg | ccattcttcg | tttgatctt  | gctggctggg | acctcacaga | ctccctcatg | 120 |
| aaaatcctga | ctgagagggg | ttactccttc | acaacctctg | ccgagcgaga | aattgtaagg | 180 |
| gacatcaagg | agaagctggs | atatatagcc | cttgactatg | agcaagagtt | ggaaactgcc | 240 |
| aagaacagct | cctcagttga | aaagagctat | gagctacctg | atggccaagt | aatcaccatt | 300 |
| ggtgcagaga | gattcagatg | ccctgaggtc | ctcttcacgc | catccatgat | tggtatggag | 360 |
| gctgccggaa | tccatgagac | aacatacaat | tcaatc     |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..93
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602390
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2988:

Met Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Ser Ala Glu  
1 5 10 15  
Arg Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Xaa Tyr Ile Ala Leu  
20 25 30  
Asp Tyr Glu Gln Glu Leu Glu Thr Ala Lys Asn Ser Ser Ser Val Glu  
35 40 45  
Lys Ser Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Ala Glu  
50 55 60  
Arg Phe Arg Cys Pro Glu Val Leu Phe Gln Pro Ser Met Ile Gly Met  
65 70 75 80  
Glu Ala Ala Gly Ile His Glu Thr Thr Tyr Asn Ser Ile  
85 90

(2) INFORMATION FOR SEQ ID NO:2989:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 459 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..459
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2989:

agaatctccg ctctctgcga ggcaaccgga gccaatgtct ctgaggtggc ttacgccgtg 60  
ggcaaggaca cgagaattgg cccaagtgc ctgaacgcca gtgttggtt cgtgggtca 120  
tgcttccaga aggacatcct gaacctggtg tacatctgcg agtgcaacgg cctgcccag 180  
gtggccaact actggaagca ggtgatcaag atcaacgact accagaagag ccggttcgtg 240  
aaccgcgtcg tggcctccat gttcaacacc gtcgccggca agaagatcgc cgtcctcggc 300  
ttcgcttca agaaagacac cggtgacacc agggagaccc cggccattga cgtctgcaag 360  
ggcctgctgg gcgacaaggc ccagatcagc atctacgacc cccaggtgac ggaggaccag 420  
atccagcggg acctggccat gaacaagttc gactgggac

(2) INFORMATION FOR SEQ ID NO:2990:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 153 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2990:

Arg Ile Ser Ala Leu Cys Glu Ala Thr Gly Ala Asn Val Ser Glu Val  
1 5 10 15  
Ala Tyr Ala Val Gly Lys Asp Thr Arg Ile Gly Pro Lys Phe Leu Asn  
20 25 30  
Ala Ser Val Gly Phe Gly Gly Ser Cys Phe Gln Lys Asp Ile Leu Asn  
35 40 45  
Leu Val Tyr Ile Cys Glu Cys Asn Gly Leu Pro Glu Val Ala Asn Tyr  
50 55 60

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Trp Lys Gln Val Ile Lys Ile Asn Asp Tyr Gln Lys Ser Arg Phe Val  
65 70 75 80  
Asn Arg Val Val Ala Ser Met Phe Asn Thr Val Ala Gly Lys Lys Ile  
85 90 95  
Ala Val Leu Gly Phe Ala Phe Lys Lys Asp Thr Gly Asp Thr Arg Glu  
100 105 110  
Thr Pro Ala Ile Asp Val Cys Lys Gly Leu Leu Gly Asp Lys Ala Gln  
115 120 125  
Ile Ser Ile Tyr Asp Pro Gln Val Thr Glu Asp Gln Ile Gln Arg Asp  
130 135 140  
Leu Ala Met Asn Lys Phe Asp Trp Asp  
145 150

(2) INFORMATION FOR SEQ ID NO:2991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..475
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2991:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| agcctccgcc ccaccaaccc ttgcctcccc acacctcagc atcaaccact cgtctctttt | 60  |
| tctccgcccc gcccgagcc gagggaggaga ggggagcagc gagatcgtgc gcgcctccga | 120 |
| gatctccacg aagtgtgtgt aacatggggc tcaccttcac gaagctcttc agccggctct | 180 |
| tctccaagaa agagatgagg atccttatgg ttggtctoga tgcagctggt aagaccacca | 240 |
| tcctctacaa gctcaagctc ggagaaatcg tgaccacatc cctacaatcg ggtttaatgt | 300 |
| ggagactgtt gaatacaaga acattagctt cactgtctgg gatgttgag gtcaggacaa  | 360 |
| gacaggcca ttgtggaggc actatttcca gaacacccaa ggccttatct ttgtgttga   | 420 |
| tagcaatgac agagatcgtg tcgttgaagc aaaggatgag ctccacagga tgctg      |     |

(2) INFORMATION FOR SEQ ID NO:2992:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2992:

Pro Pro Pro His Gln Pro Leu Pro Pro His Thr Ser Ala Ser Thr Thr  
1 5 10 15  
Arg Leu Phe Phe Ser Ala Pro Pro Glu Ala Glu Glu Glu Arg Gly Ala  
20 25 30  
Ala Arg Ser Cys Ala Pro Pro Arg Ser Pro Arg Ser Cys Gly Asn Met  
35 40 45  
Gly Leu Thr Phe Thr Lys Leu Phe Ser Arg Leu Phe Ser Lys Lys Glu  
50 55 60  
Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr Ile  
65 70 75 80  
Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ser Leu Gln Ser  
85 90 95  
Gly Leu Met Trp Arg Leu Leu Asn Thr Arg Thr Leu Ala Ser Leu Ser  
100 105 110  
Gly Met Leu Glu Val Arg Thr Arg Ser Gly His Cys Gly Gly Thr Ile  
115 120 125  
Ser Arg Thr Pro Lys Ala Leu Ser Leu Leu Leu Ile Ala Met Thr Glu

130 135 140  
Ile Val Ser Leu Lys Gln Arg Met Ser Ser Thr Gly Cys  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2993:

Met Gly Leu Thr Phe Thr Lys Leu Phe Ser Arg Leu Phe Ser Lys Lys  
1 5 10 15  
Glu Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr  
20 25 30  
Ile Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ser Leu Gln  
35 40 45  
Ser Gly Leu Met Trp Arg Leu Leu Asn Thr Arg Thr Leu Ala Ser Leu  
50 55 60  
Ser Gly Met Leu Glu Val Arg Thr Arg Ser Gly His Cys Gly Gly Thr  
65 70 75 80  
Ile Ser Arg Thr Pro Lys Ala Leu Ser Leu Leu Leu Ile Ala Met Thr  
85 90 95  
Glu Ile Val Ser Leu Lys Gln Arg Met Ser Ser Thr Gly Cys  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2994:

Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr Ile  
1 5 10 15  
Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ser Leu Gln Ser  
20 25 30  
Gly Leu Met Trp Arg Leu Leu Asn Thr Arg Thr Leu Ala Ser Leu Ser  
35 40 45  
Gly Met Leu Glu Val Arg Thr Arg Ser Gly His Cys Gly Gly Thr Ile  
50 55 60  
Ser Arg Thr Pro Lys Ala Leu Ser Leu Leu Leu Ile Ala Met Thr Glu  
65 70 75 80  
Ile Val Ser Leu Lys Gln Arg Met Ser Ser Thr Gly Cys  
85 90

(2) INFORMATION FOR SEQ ID NO:2995:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..448  
(D) OTHER INFORMATION: / Ceres Seq. ID 1602398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2995:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| atctcccata | acggagagag  | acgaagagag | cagaagcgaa | gagcagcggc | gcaaaggaaa | 60  |
| gggagccatg | ctcgccctgc  | cggcgctcgc | cggcgcccac | tccttcgcgg | cgcccggtga | 120 |
| tggaaacatc | ctcgtcccct  | cgccctccgt | ccccgcgcgc | gcacgtcgcg | cggcgctgtc | 180 |
| cgctcgtgcc | aaggtcaagg  | tggccacgcc | ccaggacgac | cgcatcgccc | gccacgtccg | 240 |
| cctgcgcaag | aaggtcaagt  | gcaccactga | gaggccgagg | ttgagtgttt | tccgctcaaa | 300 |
| caaacatctg | tacgctcaag  | tcacgcagca | cacaaagcaa | tgtactctgg | cttcagcttc | 360 |
| aacctgcac  | aaatctctct  | ccaaggaatt | tgaatactcg | gctggggcaa | cgatcgaaat | 420 |
| agcacaaaag | atcgggtgagg | tgattgcc   |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2996:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 89 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..89  
(D) OTHER INFORMATION: / Ceres Seq. ID 1602399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2996:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Ser | His | Asn | Gly | Glu | Arg | Arg | Arg | Glu | Gln | Lys | Arg | Arg | Ala | Ala |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Ala | Gln | Arg | Lys | Gly | Ser | His | Ala | Arg | Leu | Ala | Gly | Ala | Arg | Arg | Arg |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Pro | Leu | Leu | Arg | Gly | Val | Arg | Val | Trp | Lys | His | Pro | Arg | Pro | Leu | Ala |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Ser | Arg | Pro | Arg | Ala | Gly | Thr | Ser | Arg | Gly | Ala | Val | Arg | Arg | Arg | Gln |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Gly | Gln | Gly | Gly | His | Ala | Pro | Gly | Arg | Pro | His | Arg | Pro | Pro | Arg | Pro |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Pro | Ala | Gln | Glu | Gly | Lys | Trp | His | His |     |     |     |     |     |     |     |  |
|     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2997:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 149 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..149  
(D) OTHER INFORMATION: / Ceres Seq. ID 1602400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2997:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Pro | Ile | Thr | Glu | Arg | Asp | Glu | Glu | Ser | Arg | Ser | Glu | Glu | Gln | Arg |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Arg | Lys | Gly | Lys | Gly | Ala | Met | Leu | Ala | Ser | Pro | Ala | Leu | Ala | Gly | Ala |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| His | Ser | Phe | Ala | Ala | Ser | Val | Tyr | Gly | Asn | Ile | Leu | Val | Pro | Ser | Pro |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Pro | Val | Pro | Ala | Pro | Ala | Arg | Arg | Ala | Ala | Leu | Ser | Val | Val | Ala | Lys |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Val | Lys | Val | Ala | Thr | Pro | Gln | Asp | Asp | Arg | Ile | Ala | Arg | His | Val | Arg |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Leu | Arg | Lys | Lys | Val | Ser | Gly | Thr | Thr | Glu | Arg | Pro | Arg | Leu | Ser | Val |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Phe | Arg | Ser | Asn | Lys | His | Leu | Tyr | Ala | Gln | Val | Ile | Asp | Asp | Thr | Lys |  |

100 105 110  
Gln Cys Thr Leu Ala Ser Ala Ser Thr Met His Lys Ser Leu Ser Lys  
115 120 125  
Glu Phe Glu Tyr Ser Ala Gly Pro Thr Ile Glu Ile Ala Gln Lys Ile  
130 135 140  
Gly Glu Val Ile Ala  
145

(2) INFORMATION FOR SEQ ID NO:2998:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1602401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2998:

Met Leu Ala Ser Pro Ala Leu Ala Gly Ala His Ser Phe Ala Ala Ser  
1 5 10 15  
Val Tyr Gly Asn Ile Leu Val Pro Ser Pro Pro Val Pro Ala Pro Ala  
20 25 30  
Arg Arg Ala Ala Leu Ser Val Val Ala Lys Val Lys Val Ala Thr Pro  
35 40 45  
Gln Asp Asp Arg Ile Ala Arg His Val Arg Leu Arg Lys Lys Val Ser  
50 55 60  
Gly Thr Thr Glu Arg Pro Arg Leu Ser Val Phe Arg Ser Asn Lys His  
65 70 75 80  
Leu Tyr Ala Gln Val Ile Asp Asp Thr Lys Gln Cys Thr Leu Ala Ser  
85 90 95  
Ala Ser Thr Met His Lys Ser Leu Ser Lys Glu Phe Glu Tyr Ser Ala  
100 105 110  
Gly Pro Thr Ile Glu Ile Ala Gln Lys Ile Gly Glu Val Ile Ala  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..437

(D) OTHER INFORMATION: / Ceres Seq. ID 1602402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2999:

agaaggaaca gattcatcga gacctcttct cctcgcgccg ccgcgctgcg ccgtcgtcac 60  
gtcgaagcgc gggaggggag ggacggcggg gaacaagtgc cgcattgtgc tgggtctccc 120  
cgctgcagcg accgtgaact gtgcggacaa cacaggcgcc aagaacctct acatcatctc 180  
cgtcaagggc atcaagggtg ggctcaaccg cctgccgtcc gcctgcgtcg gcgacatggt 240  
catggccacc gtcaagaagg gtaagcccga cctcaggaag aaggatcatgc ccgccgtcat 300  
cgctccgccag cgcaagctgt ggccgcccga ggacggagtc tacatgtact tcgaagataa 360  
tgctggagtc attgtgaacc ccaagggcga gatgaaagga tctgctatca ctggacctat 420  
tggcaaggag tgcgctg

(2) INFORMATION FOR SEQ ID NO:3000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear



- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..145
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602403
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3000:

Glu Gly Thr Asp Ser Ser Arg Pro Leu Leu Leu Ala Pro Pro Arg Cys  
1 5 10 15  
Ala Val Val Met Ser Lys Arg Gly Arg Gly Gly Thr Ala Gly Asn Lys  
20 25 30  
Phe Arg Met Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala  
35 40 45  
Asp Asn Thr Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile  
50 55 60  
Lys Gly Arg Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val  
65 70 75 80  
Met Ala Thr Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Met  
85 90 95  
Pro Ala Val Ile Val Arg Gln Arg Lys Leu Trp Arg Arg Lys Asp Gly  
100 105 110  
Val Tyr Met Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys  
115 120 125  
Gly Glu Met Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys  
130 135 140  
Ala  
145

(2) INFORMATION FOR SEQ ID NO:3001:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 126 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3001:

Met Ser Lys Arg Gly Gly Gly Thr Ala Gly Asn Lys Phe Arg Met  
1 5 10 15  
Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn Thr  
20 25 30  
Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly Arg  
35 40 45  
Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala Thr  
50 55 60  
Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Met Pro Ala Val  
65 70 75 80  
Ile Val Arg Gln Arg Lys Leu Trp Arg Arg Lys Asp Gly Val Tyr Met  
85 90 95  
Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys Gly Glu Met  
100 105 110  
Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys Ala  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3002:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 111 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3002:

Met Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn  
1 5 10 15  
Thr Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly  
20 25 30  
Arg Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala  
35 40 45  
Thr Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Met Pro Ala  
50 55 60  
Val Ile Val Arg Gln Arg Lys Leu Trp Arg Arg Lys Asp Gly Val Tyr  
65 70 75 80  
Met Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys Gly Glu  
85 90 95  
Met Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys Ala  
100 105 110

(2) INFORMATION FOR SEQ ID NO:3003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..501
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3003:

aacacgagta cacgaccacg agagactggt cggctctgga ctgtctctga ccgctgaccg 60  
cactctcttc tgcttctgtc tttctctctc tccctgtcc cccttccaga tttctccat 120  
tcgcggtttg cctctctgcc ttctgacctg ctccctccc tccgtcagat ccccgctcgg 180  
gttgccatgg cggaccagct caccgacgaa cagatgcgc agttcaagga ggccttcagc 240  
ctcttcgaca aggacggcga cggctgcac accaccaagg aacttggcac tgtgatgcgc 300  
tcattggggc agaaccctac tgaggctgag cttcaggaca tgatcaatga ggttgatgct 360  
gatggcaatg gaaccatcga ctttctgag tttctcaacc tgatggcacg caagatgaag 420  
gacaccgact ctgaggagga gctcaaggag gccttcogtg tgttcgacaa ggaccagaac 480  
ggctcatctc cgctgctgag c

(2) INFORMATION FOR SEQ ID NO:3004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3004:

Thr Arg Val His Asp His Glu Arg Leu Val Gly Leu Arg Leu Ser Leu  
1 5 10 15  
Thr Ala Asp Arg Thr Leu Leu Cys Phe Cys Leu Ser Leu Ser Pro Leu  
20 25 30  
Ser Pro Phe Gln Ile Ser Ser Ile Arg Gly Leu Pro Leu Cys Leu Pro  
35 40 45  
Ala Cys Phe Pro Pro Ser Val Arg Ser Pro Leu Gly Leu Pro Trp Arg  
50 55 60  
Thr Ser Ser Pro Thr Asn Arg Ser Pro Ser Ser Arg Arg Pro Ser Ala

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     | 70  |     | 75  |     | 80  |     |     |     |     |     |     |     |     |     |
| Ser | Ser | Thr | Arg | Thr | Ala | Thr | Ala | Ala | Ser | Pro | Pro | Arg | Asn | Leu | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3005:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asp | Gln | Leu | Thr | Asp | Glu | Gln | Ile | Ala | Glu | Phe | Lys | Glu | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Ser | Leu | Phe | Asp | Lys | Asp | Gly | Asp | Gly | Cys | Ile | Thr | Thr | Lys | Glu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Leu | Gly | Thr | Val | Met | Arg | Ser | Leu | Gly | Gln | Asn | Pro | Thr | Glu | Ala | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Gln | Asp | Met | Ile | Asn | Glu | Val | Asp | Ala | Asp | Gly | Asn | Gly | Thr | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asp | Phe | Pro | Glu | Phe | Leu | Asn | Leu | Met | Ala | Arg | Lys | Met | Lys | Asp | Thr |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Ser | Glu | Glu | Glu | Leu | Lys | Glu | Ala | Phe | Arg | Val | Phe | Asp | Lys | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gln | Asn | Gly | Ser | Ser | Pro | Leu | Leu | Ser |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3006:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ser | Leu | Gly | Gln | Asn | Pro | Thr | Glu | Ala | Glu | Leu | Gln | Asp | Met |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | Asn | Glu | Val | Asp | Ala | Asp | Gly | Asn | Gly | Thr | Ile | Asp | Phe | Pro | Glu |
|     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Phe | Leu | Asn | Leu | Met | Ala | Arg | Lys | Met | Lys | Asp | Thr | Asp | Ser | Glu | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Glu | Leu | Lys | Glu | Ala | Phe | Arg | Val | Phe | Asp | Lys | Asp | Gln | Asn | Gly | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ser | Pro | Leu | Leu | Ser |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..511  
(D) OTHER INFORMATION: / Ceres Seq. ID 1602415

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3007:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| actccgccgc | cgtgctttac | cgcctatctc | gccaagcacc | gccgcatcac  | cgaaggttcg | 60  |
| caaagatggc | ggtgccgctg | ctgacgcaga | agatcgtgaa | gaagaggggtc | aagcagttca | 120 |
| agaggcccca | tcttgaccgc | tacaagtgcc | ttaagccaag | ctggcgcagg  | ccaagggta  | 180 |
| tcgactcccg | cgtgaggcgt | aagttcaagg | gatgcacctt | gatgcccaac  | attggatatg | 240 |
| gctccgacaa | gaagaccagg | cactaccttc | ccaacaagtt | caaaaagttt  | gttggtcaca | 300 |
| atgtctccga | gctggagctg | ctgctgatgc | acaacaggac | ctactgcgct  | gagatcgccc | 360 |
| acaacgtgtc | cacccgcaag | cgcaagtaga | ttgtcgagcg | tgctgcgcaa  | atggacatcg | 420 |
| tggtcaccaa | caagcttgcc | aggctccgca | gccaagagga | cgagtgaat   | gttgagtagt | 480 |
| tttgattgtg | ctctgctggt | gttgaagatg | t          |             |            |     |

(2) INFORMATION FOR SEQ ID NO:3008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..128  
(D) OTHER INFORMATION: / Ceres Seq. ID 1602416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3008:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ala | Ala | Ala | Tyr | Arg | Leu | Ser | Arg | Gln | Ala | Pro | Pro | His | His |     |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Arg | Arg | Phe | Ala | Lys | Met | Ala | Val | Pro | Leu | Leu | Thr | Gln | Lys | Ile | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Lys | Lys | Arg | Val | Lys | Gln | Phe | Lys | Arg | Pro | His | Leu | Asp | Arg | Tyr | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Leu | Lys | Pro | Ser | Trp | Arg | Arg | Pro | Lys | Gly | Ile | Asp | Ser | Arg | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Arg | Lys | Phe | Lys | Gly | Cys | Thr | Leu | Met | Pro | Asn | Ile | Gly | Tyr | Gly |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Asp | Lys | Lys | Thr | Arg | His | Tyr | Leu | Pro | Asn | Lys | Phe | Lys | Lys | Phe |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Val | Val | His | Asn | Val | Ser | Glu | Leu | Glu | Leu | Leu | Leu | Met | His | Asn | Arg |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Thr | Tyr | Cys | Ala | Glu | Ile | Ala | His | Asn | Val | Ser | Thr | Arg | Lys | Arg | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |

(2) INFORMATION FOR SEQ ID NO:3009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..107  
(D) OTHER INFORMATION: / Ceres Seq. ID 1602417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3009:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Val | Pro | Leu | Leu | Thr | Gln | Lys | Ile | Val | Lys | Lys | Arg | Val | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Gln | Phe | Lys | Arg | Pro | His | Leu | Asp | Arg | Tyr | Lys | Cys | Leu | Lys | Pro | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Trp | Arg | Arg | Pro | Lys | Gly | Ile | Asp | Ser | Arg | Val | Arg | Arg | Lys | Phe | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |

Gly Cys Thr Leu Met Pro Asn Ile Gly Tyr Gly Ser Asp Lys Lys Thr  
50 55 60  
Arg His Tyr Leu Pro Asn Lys Phe Lys Lys Phe Val Val His Asn Val  
65 70 75 80  
Ser Glu Leu Glu Leu Leu Leu Met His Asn Arg Thr Tyr Cys Ala Glu  
85 90 95  
Ile Ala His Asn Val Ser Thr Arg Lys Arg Lys  
100 105

(2) INFORMATION FOR SEQ ID NO:3010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..489
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3010:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| aactgcagac ttgtcggcac agccgtcgta atatatccat tcgatcgaag caatcgcgcc   | 60  |
| ttgaacccta gtcctcgccg ccaccccacg cctgcagcca tgccgcccac gctcgaccg    | 120 |
| tcgcaggtgg tggaggtggt cgtccgtgtg accggcgggc aggtaggcgc ggcgtcttcg   | 180 |
| ttggccccca agatcgggtcc gctcgggtctt tctcccaaga agatcggaga ggacattgcc | 240 |
| aaggagacgg ccaaggactg gaagggcctc cgcgtcaccg ttaagctcac tgtccagaac   | 300 |
| cgacaggccm saggtctccg tcgttccttc tgccgcggcg ctcgtcatca aggcgtcaa    | 360 |
| ggagcccagag agggaccgca agaaggtcaa gaacatcaga gcacagcggc aacatcagtc  | 420 |
| tcgacgacgt catcgagatt gccaggacca tgaggcccag gtccatggcc aaggaaatgt   | 480 |
| ccggctgcg                                                           |     |

(2) INFORMATION FOR SEQ ID NO:3011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3011:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Asn Cys Arg Leu Val Gly Thr Ala Val Val Ile Tyr Pro Phe Asp Arg |  |
| 1 5 10 15                                                       |  |
| Ser Asn Arg Ala Leu Asn Pro Ser Ser Arg Arg His Pro Thr Pro Ala |  |
| 20 25 30                                                        |  |
| Ala Met Pro Pro Lys Leu Asp Pro Ser Gln Val Val Glu Val Phe Val |  |
| 35 40 45                                                        |  |
| Arg Val Thr Gly Gly Glu Val Gly Ala Ala Ser Ser Leu Ala Pro Lys |  |
| 50 55 60                                                        |  |
| Ile Gly Pro Leu Gly Leu Ser Pro Lys Lys Ile Gly Glu Asp Ile Ala |  |
| 65 70 75 80                                                     |  |
| Lys Glu Thr Ala Lys Asp Trp Lys Gly Leu Arg Val Thr Val Lys Leu |  |
| 85 90 95                                                        |  |
| Thr Val Gln Asn Arg Gln Ala Xaa Gly Leu Arg Arg Ser Leu Cys Arg |  |
| 100 105 110                                                     |  |
| Gly Ala Arg His Gln Gly Ala Gln Gly Ala Arg Glu Gly Pro Gln Glu |  |
| 115 120 125                                                     |  |
| Gly Gln Glu His Gln Ser Thr Ala Ala Thr Ser Val Ser Thr Thr Ser |  |
| 130 135 140                                                     |  |
| Ser Arg Leu Pro Gly Pro                                         |  |
| 145 150                                                         |  |

(2) INFORMATION FOR SEQ ID NO:3012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..117  
(D) OTHER INFORMATION: / Ceres Seq. ID 1602424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3012:

[illegible]

(2) INFORMATION FOR SEQ ID NO:3013:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..502  
(D) OTHER INFORMATION: / Ceres Seq. ID 1602425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3013:

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| aggatgaatc | ggaagagaga | atcctaccaa | acctagctac  | caactcgatc  | gtcgtggctc | 60  |
| acgagtcgtg | ctggagcgac | ctcgagttct | gcgagaaaac  | caggaaactgg | tactgctacg | 120 |
| gcaaggcggg | ggcggagcag | gcggcggtgg | agacggcccg  | gcggcggggc  | gtggacctgg | 180 |
| tggtggtgaa | ccccgtgctg | gtggtggggc | ccctgctgca  | ggcgacgggtg | aacgccagca | 240 |
| tcgcgcacat | cctcaagtac | ctggacggct | cggcccgcac  | cttcgccaac  | gccgtgcagg | 300 |
| cgtacgtgga | cgtgcgcgac | gtggccgacg | cgcacctccg  | cgtcttcgag  | agcccccgcg | 360 |
| cgtccggccg | ccacctctgc | gccgagcgcg | tcctccaccg  | cgaggacgtc  | gtccgcctcc | 420 |
| tcgcaagact | cttccccgag | taccccgtcc | cagccagggtg | ctccgacgag  | gtgaatccgc | 480 |
| ggaagcagcc | qtacaaqtcc | tc         |             |             |            |     |

(2) INFORMATION FOR SEQ ID NO:3014:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..166  
(D) OTHER INFORMATION: / Ceres Seq. ID 1602426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3014:

Asp Glu Ser Glu Glu Arg Ile Leu Pro Asn Leu Ala Thr Asn Ser Ile  
1 5 10 15  
Val Val Val Asp Glu Ser Cys Trp Ser Asp Leu Glu Phe Cys Glu Lys  
20 25 30  
Thr Arg Asn Trp Tyr Cys Tyr Gly Lys Ala Val Ala Glu Gln Ala Ala  
35 40 45  
Trp Glu Thr Ala Arg Arg Arg Gly Val Asp Leu Val Val Val Asn Pro  
50 55 60  
Val Leu Val Val Gly Pro Leu Leu Gln Ala Thr Val Asn Ala Ser Ile  
65 70 75 80  
Ala His Ile Leu Lys Tyr Leu Asp Gly Ser Ala Arg Thr Phe Ala Asn  
85 90 95  
Ala Val Gln Ala Tyr Val Asp Val Arg Asp Val Ala Asp Ala His Leu  
100 105 110  
Arg Val Phe Glu Ser Pro Arg Ala Ser Gly Arg His Leu Cys Ala Glu  
115 120 125  
Arg Val Leu His Arg Glu Asp Val Val Arg Ile Leu Ala Lys Leu Phe  
130 135 140  
Pro Glu Tyr Pro Val Pro Ala Arg Cys Ser Asp Glu Val Asn Pro Arg  
145 150 155 160  
Lys Gln Pro Tyr Lys Phe  
165

(2) INFORMATION FOR SEQ ID NO:3015:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..466
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3015:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| catcctaatac gaaaacacac accactccac agcagtagca agagggatag agcaaggcca  | 60  |
| cacacacaca cacaccacta ggctaggtta gccttttaat cgtcgtagag aagcaagaag   | 120 |
| ggcgcgacag caagcaggca agcaagaaga gagccgatcg accgagagct agcacgcgat   | 180 |
| ggcgaggtct tccaagatga tgggtggcggc agctctgctg gccttggccc tggcgtgtc   | 240 |
| gaccgccgag gcgaggaaca tcaagaccac gacgacggar aagaaggacg acgcggtggt   | 300 |
| gcagccgcag accttcccgc ccttcgaccg cctcggcggc ggcgcgctccc cggcggttcgg | 360 |
| cggcctcccc ggcggcagca ttcttgacag cagcattccc gggttcagca tgcccggcag   | 420 |
| cggcagcagc ctaccgggt acagcttgcc cggcagcggc agcatg                   |     |

(2) INFORMATION FOR SEQ ID NO:3016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3016:

Met Ala Arg Ser Lys Met Met Val Ala Ala Ala Leu Leu Ala Leu  
1 5 10 15  
Ala Leu Ala Val Ser Thr Ala Glu Ala Arg Asn Ile Lys Thr Thr Thr  
20 25 30  
Thr Xaa Lys Lys Asp Asp Ala Val Val Gln Pro Gln Thr Phe Pro Pro  
35 40 45  
Phe Asp Arg Leu Gly Gly Gly Ala Ser Pro Ala Phe Gly Gly Leu Pro

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| 50                                                              | 55 | 60 |
| Gly Gly Ser Ile Pro Gly Ser Ser Ile Pro Gly Phe Ser Met Pro Gly |    |    |
| 65                                                              | 70 | 75 |
| Ser Gly Ser Ser Leu Pro Gly Tyr Ser Leu Pro Gly Ser Gly Ser Met |    | 80 |
| 85                                                              | 90 | 95 |

(2) INFORMATION FOR SEQ ID NO:3017:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..90

(D) OTHER INFORMATION: / Ceres Seq. ID 1602437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3017:

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| Met Met Val Ala Ala Ala Leu Leu Ala Leu Ala Leu Ala Val Ser Thr |    |    |
| 1                                                               | 5  | 10 |
| Ala Glu Ala Arg Asn Ile Lys Thr Thr Thr Thr Xaa Lys Lys Asp Asp |    | 15 |
| 20                                                              | 25 | 30 |
| Ala Val Val Gln Pro Gln Thr Phe Pro Pro Phe Asp Arg Leu Gly Gly |    |    |
| 35                                                              | 40 | 45 |
| Gly Ala Ser Pro Ala Phe Gly Gly Leu Pro Gly Gly Ser Ile Pro Gly |    |    |
| 50                                                              | 55 | 60 |
| Ser Ser Ile Pro Gly Phe Ser Met Pro Gly Ser Gly Ser Ser Leu Pro |    |    |
| 65                                                              | 70 | 75 |
| Gly Tyr Ser Leu Pro Gly Ser Gly Ser Met                         |    | 80 |
| 85                                                              | 90 |    |

(2) INFORMATION FOR SEQ ID NO:3018:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1602438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3018:

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| Met Val Ala Ala Ala Leu Leu Ala Leu Ala Leu Ala Val Ser Thr Ala |    |    |
| 1                                                               | 5  | 10 |
| Glu Ala Arg Asn Ile Lys Thr Thr Thr Thr Xaa Lys Lys Asp Asp Ala |    | 15 |
| 20                                                              | 25 | 30 |
| Val Val Gln Pro Gln Thr Phe Pro Pro Phe Asp Arg Leu Gly Gly Gly |    |    |
| 35                                                              | 40 | 45 |
| Ala Ser Pro Ala Phe Gly Gly Leu Pro Gly Gly Ser Ile Pro Gly Ser |    |    |
| 50                                                              | 55 | 60 |
| Ser Ile Pro Gly Phe Ser Met Pro Gly Ser Gly Ser Ser Leu Pro Gly |    |    |
| 65                                                              | 70 | 75 |
| Tyr Ser Leu Pro Gly Ser Gly Ser Met                             |    | 80 |
| 85                                                              |    |    |

(2) INFORMATION FOR SEQ ID NO:3019:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 356 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..356

(D) OTHER INFORMATION: / Ceres Seq. ID 1602439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3019:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| ggcattccca  | ttcccacccg | tccatccatc | ctccgaagct | cctcggcaga | caagcagcag | 60  |
| cgagagaaaag | caagcaaggc | agaggcagtt | gtgttgctgg | tcggtccgtc | catggcgccc | 120 |
| aagagaccag  | tgctggcggc | ggcgggcgcg | gagcagccga | ggctgcgcgg | cgtgcggaag | 180 |
| cggccgtggg  | gccggtacgc | ggcggagatc | cgcgacccgg | tgcggaaggc | gcgcgtgtgg | 240 |
| ctgggcacct  | tgcacacgcc | ggagcaggcg | gcgcgggcgt | acgacgccgc | cgcgcgcaag | 300 |
| ctccgcgggc  | ccggcgccgc | caccaactac | cccgcgccgg | agccgacggc | ggaggc     |     |

(2) INFORMATION FOR SEQ ID NO:3020:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1602440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3020:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gly | Ile | Pro | Ile | Pro | Thr | Arg | Pro | Ser | Ile | Leu | Arg | Ser | Ser | Ser | Ala |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asp | Lys | Gln | Gln | Arg | Glu | Lys | Ala | Ser | Lys | Ala | Glu | Ala | Val | Val | Leu |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu | Val | Gly | Pro | Ser | Met | Ala | Pro | Lys | Arg | Pro | Val | Ser | Ala | Ala | Ala |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ala | Ala | Glu | Gln | Pro | Arg | Leu | Arg | Gly | Val | Arg | Lys | Arg | Pro | Trp | Gly |  |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Arg | Tyr | Ala | Ala | Glu | Ile | Arg | Asp | Pro | Val | Arg | Lys | Ala | Arg | Val | Trp |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Leu | Gly | Thr | Phe | Asp | Thr | Pro | Glu | Gln | Ala | Ala | Arg | Ala | Tyr | Asp | Ala |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Ala | Ala | Arg | Lys | Leu | Arg | Gly | Pro | Gly | Ala | Ala | Thr | Asn | Tyr | Pro | Ala |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Pro | Glu | Pro | Thr | Ala | Glu |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:3021:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1602441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3021:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ala | Phe | Pro | Phe | Pro | Pro | Val | His | Pro | Ser | Ser | Glu | Ala | Pro | Arg | Gln |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Thr | Ser | Ser | Ser | Glu | Arg | Lys | Gln | Ala | Arg | Gln | Arg | Gln | Leu | Cys | Cys |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Trp | Ser | Val | Arg | Pro | Trp | Arg | Pro | Arg | Asp | Gln | Cys | Arg | Arg | Arg | Arg |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Arg | Arg | Ser | Ser | Arg | Gly | Cys | Ala | Ala | Cys | Gly | Ser | Gly | Arg | Gly | Ala |  |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Gly | Thr | Arg | Arg | Arg | Ser | Ala | Thr | Arg | Cys | Gly | Arg | Arg | Ala | Cys | Gly |  |

(2) INFORMATION FOR SEQ ID NO:3022:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1602442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3022:

(2) INFORMATION FOR SEQ ID NO:3023:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 435 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..435

(D) OTHER INFORMATION: / Ceres Seq. ID 1602446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3023:

(2) INFORMATION FOR SEQ ID NO:3024:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..144
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602447
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3024:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Thr | Thr | Leu | Ala | Ser | Ser | Ser | Glu | Arg | Thr | Tyr | Val | Phe | Pro | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Ala | Ser | Tyr | Leu | Pro | Trp | Trp | Trp | Arg | Leu | Val | Tyr | Arg | Leu | Asn |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Ala | Pro | Gln | Ser | Leu | Asp | Leu | Gly | Leu | Ser | Leu | Gly | Leu | Gly | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Ala | Phe | Gln | Pro | Ser | Phe | Cys | His | Pro | Ala | Gly | Asn | Ala | Ala | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Arg | Glu | Thr | Ser | Pro | Thr | Ala | Ala | Asp | Glu | Arg | Glu | Arg | Arg | Cys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Pro | Ala | Gly | Ser | Pro | Thr | Ser | Ser | Gly | Ser | Gly | Ser | Gly | Lys | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Ala | Thr | Glu | Arg | Ser | Ala | Gly | Ser | Gly | Ser | Gly | Asp | Glu | Asp | Asp |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Gly | Gly | Ala | Arg | Lys | Lys | Leu | Arg | Leu | Ser | Lys | Asp | Gln | Ala | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Leu | Glu | Glu | Cys | Phe | Lys | Asp | Ala | Pro | His | Pro | His | Ser | Glu | Ala |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3025:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..112
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1602448
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3025:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Pro | Gln | Ser | Leu | Asp | Leu | Gly | Leu | Ser | Leu | Gly | Leu | Gly | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Ala | Phe | Gln | Pro | Ser | Phe | Cys | His | Pro | Ala | Gly | Asn | Ala | Ala | Ala |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Arg | Glu | Thr | Ser | Pro | Thr | Ala | Ala | Asp | Glu | Arg | Glu | Arg | Arg | Cys |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ser | Pro | Ala | Gly | Ser | Pro | Thr | Ser | Ser | Gly | Ser | Gly | Ser | Gly | Lys | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Ala | Thr | Glu | Arg | Ser | Ala | Gly | Ser | Gly | Ser | Gly | Asp | Glu | Asp | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Gly | Gly | Ala | Arg | Lys | Lys | Leu | Arg | Leu | Ser | Lys | Asp | Gln | Ala | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Leu | Glu | Glu | Cys | Phe | Lys | Asp | Ala | Pro | His | Pro | His | Ser | Glu | Ala |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:3026:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 84 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3026:

Met Arg Arg Arg Ser Gly Arg Pro Ala Arg Pro Arg Arg Thr Arg Gly  
1 5 10 15  
Ser Gly Gly Ala Arg Pro Pro Ala Ala Arg Arg Arg Ala Ala Ala Ala  
20 25 30  
Ala Gly Ser Ala Ser Arg Arg Arg Asp Arg Pro Ala Ala Ala Ala Ala  
35 40 45  
Thr Arg Thr Thr Thr Gly Ala Leu Ala Arg Ser Cys Gly Cys Pro Arg  
50 55 60  
Thr Arg Pro Pro Cys Ser Arg Ser Ala Ser Lys Thr His His Thr Leu  
65 70 75 80  
Thr Pro Lys Gln

(2) INFORMATION FOR SEQ ID NO:3027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..390
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3027:

atccaatacg cccaccagcc accacacatc ctctctccct cccagtccca ggagcgtggc 60  
ctcactctcc tcgtcgcatc cccctctctc atcttcgcag cgcggggcggc ggcaatggcg 120  
atggcctcca cctacgcgcc gggcggaggc gcgcggggcg tcgcgcagg tagatgcagg 180  
gtccgcggtc ccgcggggct gggtctctc ggccctcca aggccgccg cctccccgc 240  
cccctcgccc tcgccctcgc caggcggatg agcagccccg tcgcggtggg cgcaggctgc 300  
gatgcgcggc gtcgtcgctc cccgcggcgg cgcgggccgc caccggcgcc cgcttcatcc 360  
agcacaagaa ggaggccttc tggttctacc

(2) INFORMATION FOR SEQ ID NO:3028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3028:

Ile Gln Tyr Ala His Gln Pro Pro His Ile Leu Ser Pro Ser Gln Ser  
1 5 10 15  
Gln Glu Arg Gly Leu Thr Leu Leu Val Ala Ser Pro Leu Leu Ile Phe  
20 25 30  
Ala Ala Arg Ala Ala Ala Met Ala Met Ala Ser Thr Tyr Ala Pro Gly  
35 40 45  
Gly Gly Ala Arg Ala Leu Ala Gln Gly Arg Cys Arg Val Arg Gly Pro  
50 55 60  
Ala Gly Leu Gly Phe Leu Gly Pro Ser Lys Ala Ala Gly Leu Pro Arg  
65 70 75 80  
Pro Leu Ala Leu Ala Leu Ala Arg Arg Met Ser Ser Pro Val Ala Val  
85 90 95  
Gly Ala Gly Cys Asp Ala Arg Arg Arg Arg Pro Pro Arg Arg Arg Gly

100 105 110  
Pro Pro Arg Arg Arg Ala Ser Ser Thr Arg Arg Arg Pro Ser Gly  
115 120 125  
Ser Thr  
130

(2) INFORMATION FOR SEQ ID NO:3029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3029:

Ser Asn Thr Pro Thr Ser His His Thr Ser Ser Leu Pro Pro Ser Pro  
1 5 10 15  
Arg Ser Val Ala Ser Leu Ser Ser Ser His Pro Pro Ser Ser Ser  
20 25 30  
Gln Arg Gly Arg Arg Gln Trp Arg Trp Pro Pro Pro Thr Arg Arg Ala  
35 40 45  
Glu Ala Arg Gly Arg Ser Arg Arg Val Asp Ala Gly Ser Ala Val Pro  
50 55 60  
Arg Gly Trp Ala Ser Ser Ala Pro Pro Arg Pro Pro Ala Ser Pro Ala  
65 70 75 80  
Pro Ser Pro Ser Pro Ser Pro Gly Gly  
85

(2) INFORMATION FOR SEQ ID NO:3030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3030:

Met Ala Met Ala Ser Thr Tyr Ala Pro Gly Gly Gly Ala Arg Ala Leu  
1 5 10 15  
Ala Gln Gly Arg Cys Arg Val Arg Gly Pro Ala Gly Leu Gly Phe Leu  
20 25 30  
Gly Pro Ser Lys Ala Ala Gly Leu Pro Arg Pro Leu Ala Leu Ala Leu  
35 40 45  
Ala Arg Arg Met Ser Ser Pro Val Ala Val Gly Ala Gly Cys Asp Ala  
50 55 60  
Arg Arg Arg Arg Pro Pro Arg Arg Arg Gly Pro Pro Arg Arg Arg Ala  
65 70 75 80  
Ser Ser Ser Thr Arg Arg Arg Pro Ser Gly Ser Thr  
85 90

(2) INFORMATION FOR SEQ ID NO:3031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

CONFIDENTIAL

- (A) NAME/KEY: -  
(B) LOCATION: 1..504  
(D) OTHER INFORMATION: / Ceres Seq. ID 1602454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3031:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aaaccgaaac | aaacagtcac | tcattctctt | tctgtctttc | acccccgcgt | tcacgcccgc | 60  |
| ccaaacccca | aatcgcacgc | gtcatcccaa | tcccaacca  | attagtcaat | tacgacacgc | 120 |
| ctgccgccgc | acgccgccgc | aaatccggag | gggaagctcc | tcgacgacgt | agcggccagt | 180 |
| ggcagctcgg | acgatggcct | cgtccaactc | cgccgccccg | gctcccgcgc | acggggggcg | 240 |
| cgacctcgac | cagctcctcg | acagcgcgct | cgacgacttc | accaacctcg | atctctctgc | 300 |
| ctctgccgcc | ccaaaagct  | cgggcgaggc | atcggggtca | ggatcgggag | gcaaggggcc | 360 |
| agtgaagggg | ctggggctgg | ggcttcggga | ccccaaggcg | ccgaagcggc | gcgcggggaa | 420 |
| gcagccgcgc | ccgagggggc | cgtgcgcaaa | gaggcgctcg | aggagctgac | gcgcgagacg | 480 |
| cgggaggctg | tgcgcggtct | cgag       |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:3032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..120  
(D) OTHER INFORMATION: / Ceres Seq. ID 1602455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3032:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Glu | Thr | Asn | Ser | His | Ser | Ser | Ser | Phe | Cys | Leu | Ser | Pro | Pro | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Arg | Arg | Pro | Lys | Pro | Gln | Ile | Ala | Arg | Val | Ile | Pro | Ile | Pro | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Leu | Val | Asn | Tyr | Asp | Thr | Pro | Ala | Ala | Ala | Arg | Arg | Pro | Lys | Ser |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Gly | Gly | Glu | Ala | Pro | Arg | Arg | Arg | Ser | Gly | Gln | Trp | Gln | Leu | Gly | Arg |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Trp | Pro | Arg | Pro | Thr | Pro | Pro | Pro | Arg | Leu | Pro | Pro | Thr | Gly | Ala | Thr |
|     |     |     |     |     |     |     |     | 70  |     |     |     | 75  |     |     | 80  |
| Thr | Ser | Thr | Ser | Ser | Ser | Thr | Ala | Arg | Ser | Thr | Thr | Ser | Pro | Thr | Ser |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ile | Ser | Leu | Pro | Leu | Pro | Pro | Pro | Lys | Ala | Pro | Ala | Arg | His | Arg | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Gln | Asp | Arg | Glu | Ala | Arg | Gly | Gln |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..91  
(D) OTHER INFORMATION: / Ceres Seq. ID 1602456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3033:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Ser | Asn | Ser | Ala | Ala | Pro | Ala | Pro | Ala | Asp | Gly | Gly | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Leu | Asp | Gln | Leu | Leu | Asp | Ser | Ala | Leu | Asp | Asp | Phe | Thr | Asn | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Leu | Ser | Ala | Ser | Ala | Ala | Pro | Lys | Ser | Ser | Gly | Glu | Ala | Ser | Gly |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ser | Gly | Ser | Gly | Gly | Lys | Gly | Pro | Val | Lys | Gly | Leu | Gly | Leu | Gly | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |

Pro Asp Pro Lys Ala Pro Lys Arg Arg Ala Gly Lys Gln Pro Pro Pro  
65 70 75 80  
Arg Gly Ala Cys Ala Lys Arg Arg Ser Arg Ser  
85 90

(2) INFORMATION FOR SEQ ID NO:3034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..519
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3034:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gataagaaat ggtgagcagg caagcatgga gtggagtgtt tttaaatttg ggtgtcgtctg | 60  |
| tcgttgaaag cgatgggttg ctagttttac agacagacag cagcacctgc tcctccgtct  | 120 |
| ggactgactg actagtact cagctccacc cacatcccc ttcgtcgtct tctccctccc    | 180 |
| tgctagctga cctccaatcc acgataaggc aagataagct agctaggaag gcaagggatc  | 240 |
| cgatggacaa gtacgagccc gttcgcgaga tcggggcggg caacttcggg gtggccaagc  | 300 |
| tgatgggaa caaggacacg agggagctgg tggccatgaa gttcatagag cgaggaaaca   | 360 |
| ggatcgacga gaacgtgttc cgcgagatcg tgaaccaccg ctccctccgc caccccaaca  | 420 |
| tcatccggtt caaggaggtg gtgcctgack tcccacgcac cttgcgatcg tgatggagta  | 480 |
| cgctgcgggc ggggamsctg ttcgagcgca tctgcgacg                         |     |

(2) INFORMATION FOR SEQ ID NO:3035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3035:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Asp Lys Tyr Glu Pro Val Arg Glu Ile Gly Ala Gly Asn Phe Gly |  |
| 1 5 10 15                                                       |  |
| Val Ala Lys Leu Met Arg Asn Lys Asp Thr Arg Glu Leu Val Ala Met |  |
| 20 25 30                                                        |  |
| Lys Phe Ile Glu Arg Gly Asn Arg Ile Asp Glu Asn Val Phe Arg Glu |  |
| 35 40 45                                                        |  |
| Ile Val Asn His Arg Ser Leu Arg His Pro Asn Ile Ile Arg Phe Lys |  |
| 50 55 60                                                        |  |
| Glu Val Val Pro Asp Xaa Pro Arg Thr Leu Arg Ser                 |  |
| 65 70 75                                                        |  |

(2) INFORMATION FOR SEQ ID NO:3036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3036:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Arg Asn Lys Asp Thr Arg Glu Leu Val Ala Met Lys Phe Ile Glu |  |
| 1 5 10 15                                                       |  |

(2) INFORMATION FOR SEQ ID NO:3037:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3037:

(2) INFORMATION FOR SEQ ID NO:3038:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3038:

(2) INFORMATION FOR SEQ ID NO:3039:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3039:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Lys | Lys | Pro | Trp | Val | Trp | Trp | Asp | Tyr | Val | Thr | Asp | Phe | His | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Cys | Pro | Met | Lys | Glu | Lys | Lys | Tyr | Asn | Lys | Lys | Cys | Ala | Glu | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |



Val Ile Lys Ser Leu Gly Leu Asp Val Lys Lys Val Asp Lys Cys Met  
35 40 45  
Gly Asp Pro Asn Ala Asp Ser Asp His Pro Leu Leu Lys Met Glu Gln  
50 55 60  
Asp Ala Gln Ile Gly Lys Gly Ser Arg Gly Asp Val Thr Ile Leu Pro  
65 70 75 80  
Thr Leu Val Val Asn Asn Arg Gln Tyr Arg Gly Lys Leu Glu Arg Lys  
85 90 95  
Ala Val Leu Lys Ala Ile Cys Ala Gly Phe Glu Glu Thr Thr Glu Pro  
100 105 110  
Asn Val Cys Leu Ser Asp Asp Ile Glu Thr Asn Glu Cys Leu Asn Asp  
115 120 125  
Asn Gly Gly Cys Trp Gln Asp Lys Ser Ala Asn Val Thr Ala Cys Arg  
130 135 140  
Asp Thr Phe Arg Gly Arg Val Cys Glu Cys Pro Thr Phe Asn Gly Val  
145 150 155 160  
Gln Phe Lys Gly Asp  
165

(2) INFORMATION FOR SEQ ID NO:3040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3040:

Met Lys Glu Lys Lys Tyr Asn Lys Lys Cys Ala Glu Thr Val Ile Lys  
1 5 10 15  
Ser Leu Gly Leu Asp Val Lys Lys Val Asp Lys Cys Met Gly Asp Pro  
20 25 30  
Asn Ala Asp Ser Asp His Pro Leu Leu Lys Met Glu Gln Asp Ala Gln  
35 40 45  
Ile Gly Lys Gly Ser Arg Gly Asp Val Thr Ile Leu Pro Thr Leu Val  
50 55 60  
Val Asn Asn Arg Gln Tyr Arg Gly Lys Leu Glu Arg Lys Ala Val Leu  
65 70 75 80  
Lys Ala Ile Cys Ala Gly Phe Glu Glu Thr Thr Glu Pro Asn Val Cys  
85 90 95  
Leu Ser Asp Asp Ile Glu Thr Asn Glu Cys Leu Asn Asp Asn Gly Gly  
100 105 110  
Cys Trp Gln Asp Lys Ser Ala Asn Val Thr Ala Cys Arg Asp Thr Phe  
115 120 125  
Arg Gly Arg Val Cys Glu Cys Pro Thr Phe Asn Gly Val Gln Phe Lys  
130 135 140  
Gly Asp  
145

(2) INFORMATION FOR SEQ ID NO:3041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602464

OFFENSE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3041:

Met Gly Asp Pro Asn Ala Asp Ser Asp His Pro Leu Leu Lys Met Glu  
1 5 10 15  
Gln Asp Ala Gln Ile Gly Lys Gly Ser Arg Gly Asp Val Thr Ile Leu  
20 25 30  
Pro Thr Leu Val Val Asn Asn Arg Gln Tyr Arg Gly Lys Leu Glu Arg  
35 40 45  
Lys Ala Val Leu Lys Ala Ile Cys Ala Gly Phe Glu Glu Thr Thr Glu  
50 55 60  
Pro Asn Val Cys Leu Ser Asp Asp Ile Glu Thr Asn Glu Cys Leu Asn  
65 70 75 80  
Asp Asn Gly Gly Cys Trp Gln Asp Lys Ser Ala Asn Val Thr Ala Cys  
85 90 95  
Arg Asp Thr Phe Arg Gly Arg Val Cys Glu Cys Pro Thr Phe Asn Gly  
100 105 110  
Val Gln Phe Lys Gly Asp  
115

(2) INFORMATION FOR SEQ ID NO:3042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..487
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3042:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ataaaagctc cctccatct ctccctctca ctcccttctc cgccgccacg ctagagagga   | 60  |
| agagcgcgcg gagagcgaga gcccgggaga aacagcggcc ggcggcaaaa tgggtgcagcg | 120 |
| gctcacctac cggaagcgcc acagctacgc cacaaaatcc aatcagaccc gcgtggtcaa  | 180 |
| gacccttggt gggaggcttg tgtaccagta caccaagaag cgcgcgagcg gaccgaaatg  | 240 |
| cccggtcacc gggaagaaga tccaaggaat tccacacctg agacctgctg agtacaagag  | 300 |
| gtccagggtg gcaaggaacc gcaggactgt gaaccgtcca tatggtggtg ttctgtctgg  | 360 |
| taccgcagtg agagagagga tcatccgtgc ctttttggtc gaggagcaga agatcgtgaa  | 420 |
| gaaggttttg aagatccaaa aaaccaagga taaggcctcc aagaactagg cgatataggc  | 480 |
| atcttcc                                                            |     |

(2) INFORMATION FOR SEQ ID NO:3043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3043:

Lys Ser Ser Pro Pro Ser Leu Leu Leu Thr Pro Phe Ser Ala Ala Thr  
1 5 10 15  
Leu Glu Arg Lys Ser Ala Arg Arg Ala Arg Ala Arg Glu Lys Gln Arg  
20 25 30  
Pro Ala Ala Lys Trp Cys Ser Gly Ser Pro Thr Gly Ser Ala Thr Ala  
35 40 45  
Thr Pro Gln Asn Pro Ile Arg Pro Ala Trp Ser Arg Pro Leu Val Gly  
50 55 60  
Gly Leu Cys Thr Ser Thr Pro Arg Ser Ala Arg Ala Asp Arg Asn Ala  
65 70 75 80  
Arg Ser Pro Gly Arg Arg Ser Lys Glu Phe His Thr

85

90

(2) INFORMATION FOR SEQ ID NO:3044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3044:

```
Met Val Gln Arg Thr Tyr Arg Lys Arg His Ser Tyr Ala Thr Lys
1 5 10 15
Ser Asn Gln Thr Arg Val Val Lys Thr Pro Gly Gly Arg Leu Val Tyr
 20 25 30
Gln Tyr Thr Lys Lys Arg Ala Ser Gly Pro Lys Cys Pro Val Thr Gly
 35 40 45
Lys Lys Ile Gln Gly Ile Pro His Leu Arg Pro Ala Glu Tyr Lys Arg
 50 55 60
Ser Arg Leu Ala Arg Asn Arg Arg Thr Val Asn Arg Pro Tyr Gly Gly
65 70 75 80
Val Leu Ser Gly Thr Ala Val Arg Glu Arg Ile Ile Arg Ala Phe Leu
 85 90 95
Val Glu Glu Gln Lys Ile Val Lys Lys Val Leu Lys Ile Gln Lys Thr
 100 105 110
Lys Asp Lys Ala Ser Lys Asn
 115
```

(2) INFORMATION FOR SEQ ID NO:3045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..252
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3045:

```
gcagagttgt tgattgcagg gaaaccgcca attggcaagg atgaagcttg tgaccgcctt 60
cgttgtgctg ctcttttctc tctctcccgga ctogtcacc gccgaggact tcgatttctt 120
ctaccttgtc caacagtggc cgggtcgtt ctgcgacacg cggcaggggtt gctgcttccc 180
ggacggcgcg ggcaagccgg aggcggcggtt cgcatccac gggctgtggc ccaactacgc 240
caagtgccgc gg
```

(2) INFORMATION FOR SEQ ID NO:3046:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3046:

```
Ala Glu Leu Leu Ile Ala Gly Lys Pro Pro Ile Gly Lys Asp Glu Ala
1 5 10 15
Cys Asp Arg Leu Arg Cys Ala Ala Leu Phe Ser Pro Pro Arg Leu Val
```

20 25 30  
His Arg Gly Gly Leu Arg Phe Leu Leu Pro Cys Pro Thr Val Ala Gly  
35 40 45  
Leu Val Leu Arg His Ala Ala Gly Leu Leu Leu Pro Gly Arg Arg Gly  
50 55 60  
Gln Ala Gly Gly Gly Val Arg His Pro Arg Ala Val Ala Gln Leu Arg  
65 70 75 80  
Gln Val Pro Arg

(2) INFORMATION FOR SEQ ID NO:3047:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1602481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3047:

Met Lys Leu Val Thr Ala Phe Val Val Leu Leu Phe Ser Leu Leu Pro  
1 5 10 15  
Asp Ser Ser Thr Ala Glu Asp Phe Asp Phe Phe Tyr Leu Val Gln Gln  
20 25 30  
Trp Pro Gly Ser Phe Cys Asp Thr Arg Gln Gly Cys Cys Phe Pro Asp  
35 40 45  
Gly Ala Gly Lys Pro Glu Ala Ala Phe Gly Ile His Gly Leu Trp Pro  
50 55 60  
Asn Tyr Ala Lys Cys Arg  
65 70

(2) INFORMATION FOR SEQ ID NO:3048:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 460 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..460

(D) OTHER INFORMATION: / Ceres Seq. ID 1602482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3048:

aaattgccct ggtatcatta agcctgggtga gtgtaacaat tggaatcatg ccagggttaca 60  
tccacaagcc tgggcgtatt gggatcgat ctggttctgg tactttgaca tatgaagcgg 120  
tgtttcaaac aacagctgta ggattgggtc agtcaacttg ttaggcatt ggtggtgacc 180  
cgttcaacgg ccacaaattt tgttgattgc cttgaaaagt tcgttaacga cctcagaca 240  
gaaggatttg ttctcattgg tgaaattgga ggtacggctg aggaggatgc tgcgacattc 300  
atccaggaaa gcaaaacaca aaagcctggt gttgcattca ttgctggact tacggcacc 360  
ccgggcccgc gcatgggtca tgctggagct actcgtggca ggaggaaagg gtactgccca 420  
ggacaaaatc aaggcactca gagaggcagg tgtaccgttg

(2) INFORMATION FOR SEQ ID NO:3049:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..67



(B) LOCATION: 1..489

(D) OTHER INFORMATION: / Ceres Seq. ID 1602486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3052:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| atataaaaaat | cccggtaaaa | ttcccccccc | acccccgacg | cgacgcotca | aatcgctccc | 60  |
| tgcctctggt  | cacctcgctt | ccgctcccg  | ctccccctcg | gccaccaga  | catcgctcgt | 120 |
| tcgctcgcca  | agagacagga | ccggagacca | tggcggacca | gctcaccgac | gaccagatcg | 180 |
| ccgagttcaa  | ggaggccttc | agcctcttcg | acaaggacgg | cgacggttgc | atcacaacca | 240 |
| aggagctcgg  | aactgtcatg | cgatcaactg | gtcagaaccc | aaccgaggct | gagctccagg | 300 |
| acatgatcaa  | cgaggtcgat | gcggacggca | acggcaccat | cgacttcccg | gagttcctca | 360 |
| acctcatggc  | ccgcaagatg | aaggacaccg | actccgagga | ggagctcaag | gaggcggtta | 420 |
| gggtgttcga  | caaggaccag | aacggcttca | tctctgcggc | ggagctccgc | cacgtgatga | 480 |
| ccaacctcg   |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:3053:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1602487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3053:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Tyr | Lys | Asn | Pro | Gly | Lys | Ile | Pro | Pro | Pro | Pro | Pro | Thr | Arg | Arg | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |  |
| Lys | Ser | Leu | Pro | Ala | Ser | Gly | His | Leu | Ala | Ser | Ala | Pro | Gly | Ser | Pro |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Pro | Ala | Thr | Gln | Thr | Ser | Ser | Val | Arg | Ser | Pro | Arg | Asp | Arg | Thr | Gly |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asp | His | Gly | Gly | Pro | Ala | His | Arg | Arg | Pro | Asp | Arg | Arg | Val | Gln | Gly |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Gly | Leu | Gln | Pro | Leu | Arg | Gln | Gly | Arg | Arg | Arg | Leu | His | His | Asn | Gln |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Gly | Ala | Arg | Asn | Cys | His | Ala | Ile | Thr | Gly | Ser | Glu | Pro | Asn | Arg | Gly |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |

(2) INFORMATION FOR SEQ ID NO:3054:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1602488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3054:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Lys | Ile | Pro | Val | Lys | Phe | Pro | Pro | His | Pro | Arg | Arg | Asp | Ala | Ser |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asn | Arg | Ser | Leu | Pro | Leu | Val | Thr | Ser | Leu | Pro | Leu | Pro | Ala | Pro | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg | Pro | Pro | Arg | His | Arg | Pro | Phe | Ala | Arg | Gln | Glu | Thr | Gly | Pro | Glu |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Thr | Met | Ala | Asp | Gln | Leu | Thr | Asp | Asp | Gln | Ile | Ala | Glu | Phe | Lys | Glu |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ala | Phe | Ser | Leu | Phe | Asp | Lys | Asp | Gly | Asp | Gly | Cys | Ile | Thr | Thr | Lys |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Glu | Leu | Gly | Thr | Val | Met | Arg | Ser | Leu | Gly | Gln | Asn | Pro | Thr | Glu | Ala |  |

|     | 85  |     | 90  |     | 95  |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Leu | Gln | Asp | Met | Ile | Asn | Glu | Val | Asp | Ala | Asp | Gly | Asn | Gly | Thr |
|     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ile | Asp | Phe | Pro | Glu | Phe | Leu | Asn | Leu | Met | Ala | Arg | Lys | Met | Lys | Asp |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Asp | Ser | Glu | Glu | Glu | Leu | Lys | Glu | Ala | Phe | Arg | Val | Phe | Asp | Lys |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Asp | Gln | Asn | Gly | Phe | Ile | Ser | Ala | Ala | Glu | Leu | Arg | His | Val | Met | Thr |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Asn | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3055:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1602489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3055:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asp | Gln | Leu | Thr | Asp | Asp | Gln | Ile | Ala | Glu | Phe | Lys | Glu | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Phe | Ser | Leu | Phe | Asp | Lys | Asp | Gly | Asp | Gly | Cys | Ile | Thr | Thr | Lys | Glu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Leu | Gly | Thr | Val | Met | Arg | Ser | Leu | Gly | Gln | Asn | Pro | Thr | Glu | Ala | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Gln | Asp | Met | Ile | Asn | Glu | Val | Asp | Ala | Asp | Gly | Asn | Gly | Thr | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Phe | Pro | Glu | Phe | Leu | Asn | Leu | Met | Ala | Arg | Lys | Met | Lys | Asp | Thr |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asp | Ser | Glu | Glu | Glu | Leu | Lys | Glu | Ala | Phe | Arg | Val | Phe | Asp | Lys | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Asn | Gly | Phe | Ile | Ser | Ala | Ala | Glu | Leu | Arg | His | Val | Met | Thr | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3056:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 402 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..402

(D) OTHER INFORMATION: / Ceres Seq. ID 1602494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3056:

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| aaccatcgca  | attcacaagc  | aaagcaatca | gagccaagca | cccaccgtcc | tcctttcttt | 60  |
| ccttcgactc  | atcaaagcat  | gtcttgctgc | ggcggcaact | gcgcgtgcac | ctccggctgc | 120 |
| aactgcggca  | gcggatgcgg  | cggtcgcaag | atgttccttg | acgtggagac | cgccggcgtc | 180 |
| ggcggcgctga | agcccacggt  | cctcgccgcc | cccgccacca | aggcgagcgc | cggcgggttc | 240 |
| gaggcggccg  | ccgaggggcg  | cggtcgcgac | tgcaacacct | gcaactgcgg | caccagctgc | 300 |
| ggctgctcct  | gctgcagctg  | caactgagcc | acccgcgatg | acgagacaac | caccgcgcct | 360 |
| ccccccacc   | atcgctactac | aactatgtag | cggcgtctaa | at         |            |     |

(2) INFORMATION FOR SEQ ID NO:3057:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids





Ala Ser Ala Gly Gly Phe Glu Ala Ala Ala Glu Gly Gly Gly Cys Asp  
50 55 60  
Cys Asn Thr Cys Asn Cys Gly Thr Ser Cys Gly Cys Ser Cys Cys Ser  
65 70 75 80  
Cys Asn

(2) INFORMATION FOR SEQ ID NO:3060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..487
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3060:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aaagcctcgg cctctgctcc cggctccccc acggtactcc agccgctagc ctgcgattcc  | 60  |
| gccagtacgc caccaccacc gagcctggac taccgcgcgc gcccttcgcc gatatttca   | 120 |
| gcggcgaaca gcgccacca gatcccgccc ctgcgatgga gtccgtgggtg aaccggaagg  | 180 |
| cataccgcgt ggctgatgcg cagctgacga tgggtatcct cgatatcatc cagcaggccg  | 240 |
| ccaactacaa acagcttaag aagggagcga atgaagcgac gaagaccctg aataggggca  | 300 |
| tatcggagtt tgtagtgatg gcggcggaca cagagcctct cgagatcctg ctccacctcc  | 360 |
| ccttggttagc tgaggataag aacgtgccat atgtgtttgt tccatcgaag caagctcttg | 420 |
| gccgtgcttg tgggtgacga agaccggtta ttgcttgctc agtgaccagt aatgagggta  | 480 |
| gcagctg                                                            |     |

(2) INFORMATION FOR SEQ ID NO:3061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3061:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ser Leu Gly Leu Cys Ser Arg Leu Pro His Gly Thr Pro Ala Ala Ser |  |
| 1 5 10 15                                                       |  |
| Leu Arg Phe Arg Gln Tyr Ala Thr Thr Thr Glu Pro Gly Leu Pro Pro |  |
| 20 25 30                                                        |  |
| Pro Pro Phe Ala Asp Ile Phe Ser Gly Glu Gln Arg Pro Pro Asp Pro |  |
| 35 40 45                                                        |  |
| Ala Pro Ala Met Glu Ser Val Val Asn Pro Lys Ala Tyr Pro Leu Ala |  |
| 50 55 60                                                        |  |
| Asp Ala Gln Leu Thr Met Gly Ile Leu Asp Ile Ile Gln Gln Ala Ala |  |
| 65 70 75 80                                                     |  |
| Asn Tyr Lys Gln Leu Lys Lys Gly Ala Asn Glu Ala Thr Lys Thr Leu |  |
| 85 90 95                                                        |  |
| Asn Arg Gly Ile Ser Glu Phe Val Val Met Ala Ala Asp Thr Glu Pro |  |
| 100 105 110                                                     |  |
| Leu Glu Ile Leu Leu His Leu Pro Leu Leu Ala Glu Asp Lys Asn Val |  |
| 115 120 125                                                     |  |
| Pro Tyr Val Phe Val Pro Ser Lys Gln Ala Leu Gly Arg Ala Cys Gly |  |
| 130 135 140                                                     |  |
| Val Thr Arg Pro Val Ile Ala Cys Ser Val Thr Ser Asn Glu Gly Ser |  |
| 145 150 155 160                                                 |  |
| Ser                                                             |  |

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..110  
(D) OTHER INFORMATION: / Ceres Seq. ID 1602505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3062:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ser | Val | Val | Asn | Pro | Lys | Ala | Tyr | Pro | Leu | Ala | Asp | Ala | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Thr | Met | Gly | Ile | Leu | Asp | Ile | Ile | Gln | Gln | Ala | Ala | Asn | Tyr | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Leu | Lys | Lys | Gly | Ala | Asn | Glu | Ala | Thr | Lys | Thr | Leu | Asn | Arg | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ser | Glu | Phe | Val | Val | Met | Ala | Ala | Asp | Thr | Glu | Pro | Leu | Glu | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Leu | His | Leu | Pro | Leu | Leu | Ala | Glu | Asp | Lys | Asn | Val | Pro | Tyr | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Phe | Val | Pro | Ser | Lys | Gln | Ala | Leu | Gly | Arg | Ala | Cys | Gly | Val | Thr | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Val | Ile | Ala | Cys | Ser | Val | Thr | Ser | Asn | Glu | Gly | Ser | Ser |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..92  
(D) OTHER INFORMATION: / Ceres Seq. ID 1602506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3063:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ile | Leu | Asp | Ile | Ile | Gln | Gln | Ala | Ala | Asn | Tyr | Lys | Gln | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Lys | Gly | Ala | Asn | Glu | Ala | Thr | Lys | Thr | Leu | Asn | Arg | Gly | Ile | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Phe | Val | Val | Met | Ala | Ala | Asp | Thr | Glu | Pro | Leu | Glu | Ile | Leu | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Leu | Pro | Leu | Leu | Ala | Glu | Asp | Lys | Asn | Val | Pro | Tyr | Val | Phe | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Ser | Lys | Gln | Ala | Leu | Gly | Arg | Ala | Cys | Gly | Val | Thr | Arg | Pro | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Ala | Cys | Ser | Val | Thr | Ser | Asn | Glu | Gly | Ser | Ser |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..405  
(D) OTHER INFORMATION: / Ceres Seq. ID 1602514

| Table 1 |  | Table 2 |  | Table 3 |  | Table 4 |  | Table 5 |  | Table 6 |  | Table 7 |  | Table 8 |  | Table 9 |  | Table 10 |  | Table 11 |  | Table 12 |  | Table 13 |  | Table 14 |  | Table 15 |  | Table 16 |  | Table 17 |  | Table 18 |  | Table 19 |  | Table 20 |  | Table 21 |  | Table 22 |  | Table 23 |  | Table 24 |  | Table 25 |  | Table 26 |  | Table 27 |  | Table 28 |  | Table 29 |  | Table 30 |  | Table 31 |  | Table 32 |  | Table 33 |  | Table 34 |  | Table 35 |  | Table 36 |  | Table 37 |  | Table 38 |  | Table 39 |  | Table 40 |  | Table 41 |  | Table 42 |  | Table 43 |  | Table 44 |  | Table 45 |  | Table 46 |  | Table 47 |  | Table 48 |  | Table 49 |  | Table 50 |  | Table 51 |  | Table 52 |  | Table 53 |  | Table 54 |  | Table 55 |  | Table 56 |  | Table 57 |  | Table 58 |  | Table 59 |  | Table 60 |  | Table 61 |  | Table 62 |  | Table 63 |  | Table 64 |  | Table 65 |  | Table 66 |  | Table 67 |  | Table 68 |  | Table 69 |  | Table 70 |  | Table 71 |  | Table 72 |  | Table 73 |  | Table 74 |  | Table 75 |  | Table 76 |  | Table 77 |  | Table 78 |  | Table 79 |  | Table 80 |  | Table 81 |  | Table 82 |  | Table 83 |  | Table 84 |  | Table 85 |  | Table 86 |  | Table 87 |  | Table 88 |  | Table 89 |  | Table 90 |  | Table 91 |  | Table 92 |  | Table 93 |  | Table 94 |  | Table 95 |  | Table 96 |  | Table 97 |  | Table 98 |  | Table 99 |  | Table 100 |  | Table 101 |  | Table 102 |  | Table 103 |  | Table 104 |  | Table 105 |  | Table 106 |  | Table 107 |  | Table 108 |  | Table 109 |  | Table 110 |  | Table 111 |  | Table 112 |  | Table 113 |  | Table 114 |  | Table 115 |  | Table 116 |  | Table 117 |  | Table 118 |  | Table 119 |  | Table 120 |  | Table 121 |  | Table 122 |  | Table 123 |  | Table 124 |  | Table 125 |  | Table 126 |  | Table 127 |  | Table 128 |  | Table 129 |  | Table 130 |  | Table 131 |  | Table 132 |  | Table 133 |  | Table 134 |  | Table 135 |  | Table 136 |  | Table 137 |  | Table 138 |  | Table 139 |  | Table 140 |  | Table 141 |  | Table 142 |  | Table 143 |  | Table 144 |  | Table 145 |  | Table 146 |  | Table 147 |  | Table 148 |  | Table 149 |  | Table 150 |  | Table 151 |  | Table 152 |  | Table 153 |  | Table 154 |  | Table 155 |  | Table 156 |  | Table 157 |  | Table 158 |  | Table 159 |  | Table 160 |  | Table 161 |  | Table 162 |  | Table 163 |  | Table 164 |  | Table 165 |  | Table 166 |  | Table 167 |  | Table 168 |  | Table 169 |  | Table 170 |  | Table 171 |  | Table 172 |  | Table 173 |  | Table 174 |  | Table 175 |  | Table 176 |  | Table 177 |  | Table 178 |  | Table 179 |  | Table 180 |  | Table 181 |  | Table 182 |  | Table 183 |  | Table 184 |  | Table 185 |  | Table 186 |  | Table 187 |  | Table 188 |  | Table 189 |  | Table 190 |  | Table 191 |  | Table 192 |  | Table 193 |  | Table 194 |  | Table 195 |  | Table 196 |  | Table 197 |  | Table 198 |  | Table 199 |  | Table 200 |  | Table 201 |  | Table 202 |  | Table 203 |  | Table 204 |  | Table 205 |  | Table 206 |  | Table 207 |  | Table 208 |  | Table 209 |  | Table 210 |  | Table 211 |  | Table 212 |  | Table 213 |  | Table 214 |  | Table 215 |  | Table 216 |  | Table 217 |  | Table 218 |  | Table 219 |  | Table 220 |  | Table 221 |  | Table 222 |  | Table 223 |  | Table 224 |  | Table 225 |  | Table 226 |  | Table 227 |  | Table 228 |  | Table 229 |  | Table 230 |  | Table 231 |  | Table 232 |  | Table 233 |  | Table 234 |  | Table 235 |  | Table 236 |  | Table 237 |  | Table 238 |  | Table 239 |  | Table 240 |  | Table 241 |  | Table 242 |  | Table 243 |  | Table 244 |  | Table 245 |  | Table 246 |  | Table 247 |  | Table 248 |  | Table 249 |  | Table 250 |  | Table 251 |  | Table 252 |  | Table 253 |  | Table 254 |  | Table 255 |  | Table 256 |  | Table 257 |  | Table 258 |  | Table 259 |  | Table 260 |  | Table 261 |  | Table 262 |  | Table 263 |  | Table 264 |  | Table 265 |  | Table 266 |  | Table 267 |  | Table 268 |  | Table 269 |  | Table 270 |  | Table 271 |  | Table 272 |  | Table 273 |  | Table 274 |  | Table 275 |  | Table 276 |  | Table 277 |  | Table 278 |  | Table 279 |  | Table 280 |  | Table 281 |  | Table 282 |  | Table 283 |  | Table 284 |  | Table 285 |  | Table 286 |  | Table 287 |  | Table 288 |  | Table 289 |  | Table 290 |  | Table 291 |  | Table 292 |  | Table 293 |  | Table 294 |  | Table 295 |  | Table 296 |  | Table 297 |  | Table 298 |  | Table 299 |  | Table |  |
|---------|--|---------|--|---------|--|---------|--|---------|--|---------|--|---------|--|---------|--|---------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-------|--|
|---------|--|---------|--|---------|--|---------|--|---------|--|---------|--|---------|--|---------|--|---------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-------|--|

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3064:

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| actctccagt | ctccactagc | atcagtcgcc | gccgcctatc  | ctcgagcacc  | atttccatca | 60  |
| acagcatccg | cctctggaag | ctagcgtaca | ssaactcatg  | gcactccgcg  | cgctcgacaa | 120 |
| cacgatgccc | gccgcggtcg | aggagcggcc | caagaagggtg | gctaaagggtg | ggcgtccccg | 180 |
| ccgtccgccg | ccaaggycgc | cgctctcccc | tccccggga   | gtggcggcaa  | gaagaagaat | 240 |
| gggtaacgac | gagaactcgg | cgccaagggc | cacggccgcg  | gcggcggagc  | akgcgggtgg | 300 |
| agtacatctc | gtcggaggag | ctggaggcgg | cggccagccc  | caaggccaan  | gccgcggggc | 360 |
| tggtgcgcgg | acctggactc | caaggactgg | gtcaggacct  | gcgag       |            |     |

(2) INFORMATION FOR SEQ ID NO:3065:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1602515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3065:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Pro | Val | Ser | Ser | Ile | Ser | Arg | Arg | Leu | Ser | Ser | Ser | Thr |     |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |
| Ile | Ser | Ile | Asn | Ser | Ile | Arg | Leu | Trp | Lys | Leu | Ala | Tyr | Xaa | Asn |
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     | Ser |
| Trp | His | Ser | Ala | Arg | Ser | Thr | Thr | Arg | Cys | Pro | Pro | Pro | Ser | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     | Ser |
| Gly | Pro | Arg | Arg | Trp | Leu | Lys | Val | Gly | Val | Pro | Ala | Val | Arg | Arg |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     | Gln |
| Xaa | Arg | Arg | Leu | Pro | Leu | Pro | Arg | Glu | Trp | Arg | Gln | Glu | Glu | Glu |
| 65  |     |     |     |     | 70  |     |     | 75  |     |     |     |     |     | 80  |
| Val | Thr | Thr | Arg | Thr | Arg | Arg | Gln | Gly | Pro | Arg | Pro | Arg | Arg | Ser |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Xaa | Arg | Val | Glu | Tyr | Ile | Ser | Ser | Glu | Glu | Leu | Glu | Ala | Ala | Ser |
|     |     |     | 100 |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Pro | Lys | Ala | Xaa | Ala | Ala | Gly | Leu | Val | Arg | Gly | Pro | Gly | Leu | Gln |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     | Gly |
| Leu | Gly | Gln | Asp | Leu | Arg |     |     |     |     |     |     |     |     |     |
|     |     |     | 130 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3066:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1602516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3066:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Arg | Ala | Leu | Asp | Asn | Thr | Met | Pro | Ala | Ala | Val | Glu | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Arg | Pro | Lys | Lys | Val | Ala | Lys | Gly | Gly | Arg | Pro | Arg | Arg | Pro | Pro | Pro |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Arg | Xaa | Pro | Pro | Pro | Pro | Pro | Gly | Val | Ala | Ala | Arg | Arg | Arg | Met |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Gly | Asn | Asp | Glu | Asn | Ser | Ala | Pro | Arg | Ala | Thr | Ala | Ala | Ala | Ala | Glu |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Xaa | Ala | Gly | Gly | Val | His | Leu | Val | Gly | Gly | Ala | Gly | Gly | Gly | Gly | Gln |
| 65  |     |     |     |     | 70  |     |     | 75  |     |     |     |     |     | 80  |     |
| Pro | Gln | Gly | Gln | Xaa | Arg | Gly | Ala | Gly | Ala | Arg | Thr | Trp | Thr | Pro | Arg |



50

(2) INFORMATION FOR SEQ ID NO:3070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602520

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3070:

Leu Ser Glu Val Pro Asn Pro Ser Gln Ala Pro Gly Ser Asp Arg Arg  
1 5 10 15  
Thr Asp Pro Lys Cys Arg Pro Pro Ala Pro Cys Ser Pro Pro Arg Arg  
20 25 30  
Ser Pro Pro Arg Ser Gln Pro Arg Ala Ser Ala Pro Pro Pro Ser  
35 40 45  
Leu Arg Arg Ala  
50

(2) INFORMATION FOR SEQ ID NO:3071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3071:

Tyr Pro Lys Phe Arg Thr Gln Ala Lys Pro Gln Gly Pro Thr Ala Glu  
1 5 10 15  
Pro Thr Gln Asn Val Ala Arg Leu Leu His Ala His Arg Val Ala  
20 25 30  
Leu Leu Pro Ala Pro Ser Pro Ala Pro Pro Arg Arg Arg Arg Leu Arg  
35 40 45  
Ser Ala Ala Pro  
50

(2) INFORMATION FOR SEQ ID NO:3072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..455
- (D) OTHER INFORMATION: / Ceres Seq. ID 1602530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3072:

tattgttttt agaggaccaa atggagctgc tgctggagtt ggtgctcaac actcacagtg 60  
ttatgcagct tggtttgcac atgttccagg acttaagggt ctcacaccat actcttcaga 120  
agatgccga ggcttgctta aagctgctat tagggatccc gatcctgtta ttttcttgga 180  
aaatgaattg ctttatggag aatctttccc agtttctgct gaagtgcctg attctagttt 240  
ttgcctacca attggcaaag ctaagataga acgtgggggt aaagatgtta ccattactgc 300  
gttctccaag atggttggt atgctctcca ggctgcagag atactgtcca aggaaggaat 360  
cagtgcaggt gtgatcaacc ttcgatcgat cagaccactt gataaagctg ctattaatgc 420  
atctgtcagg aaaaccaacc gattggtgac tggttg

(2) INFORMATION FOR SEQ ID NO:3073:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1602531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3073:

Ile Val Phe Arg Gly Pro Asn Gly Ala Ala Gly Val Gly Ala Gln  
1 5 10 15  
His Ser Gln Cys Tyr Ala Ala Trp Phe Ala His Val Pro Gly Leu Lys  
20 25 30  
Val Leu Thr Pro Tyr Ser Ser Glu Asp Ala Arg Gly Leu Leu Lys Ala  
35 40 45  
Ala Ile Arg Asp Pro Asp Pro Val Ile Phe Leu Glu Asn Glu Leu Leu  
50 55 60  
Tyr Gly Glu Ser Phe Pro Val Ser Ala Glu Val Leu Asp Ser Ser Phe  
65 70 75 80  
Cys Leu Pro Ile Gly Lys Ala Lys Ile Glu Arg Gly Gly Lys Asp Val  
85 90 95  
Thr Ile Thr Ala Phe Ser Lys Met Val Gly Tyr Ala Leu Gln Ala Ala  
100 105 110  
Glu Ile Leu Ser Lys Glu Gly Ile Ser Ala Glu Val Ile Asn Leu Arg  
115 120 125  
Ser Ile Arg Pro Leu Asp Lys Ala Ala Ile Asn Ala Ser Val Arg Lys  
130 135 140  
Thr Asn Arg Leu Val Thr Val  
145 150

(2) INFORMATION FOR SEQ ID NO:3074:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1602532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3074:

Leu Phe Leu Glu Asp Gln Met Glu Leu Leu Leu Glu Leu Val Leu Asn  
1 5 10 15  
Thr His Ser Val Met Gln Leu Gly Leu His Met Phe Gln Asp Leu Arg  
20 25 30  
Phe Ser His His Thr Leu Gln Lys Met Pro Glu Ala Cys Leu Lys Leu  
35 40 45  
Leu Leu Gly Ile Pro Ile Leu Leu Phe Ser Trp Lys Met Asn Cys Phe  
50 55 60  
Met Glu Asn Leu Ser Gln Phe Leu Leu Lys Cys Leu Ile Leu Val Phe  
65 70 75 80  
Ala Tyr Gln Leu Ala Lys Leu Arg  
85

(2) INFORMATION FOR SEQ ID NO:3075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:



POWER OF ATTORNEY

CERES, INC.  
3007 Malibu Canyon Road  
Malibu, CA 90265

I, Richard Hamilton, Chief Financial Officer of CERES, INC. of 3007 Malibu Canyon Road, Malibu, California 90265, grant Power of Attorney and authority to empower the following attorneys to act on behalf of CERES, INC. for executing Verified Statements (Declarations) Claiming Small Entity Status to be submitted to the U.S. Patent and Trademark Office in connection with the filing of provisional or regular patent applications on behalf of CERES, INC.

Raymond C. Stewart (Reg. No. 21,066)  
Joseph A. Kolasch (Reg. No. 22,463)  
Leonard R. Svensson (Reg. No. 30,330)  
Gerald M. Murphy, Jr. (Reg. No. 28,977)  
Mark J. Nuell (Reg. No. 36,623)

This Power of Attorney is to remain in full force and effect until terminated by an official of CERES, INC.

By



Richard Hamilton

Date

9/24/98



IN THE U.S. PATENT AND TRADEMARK OFFICE

I N F O R M A T I O N   S H E E T

Applicant:        Nickolai ALEXANDROV and Vyacheslav BROVER

Appl. No.:        NEW

Filed:            October 13, 2000

For:              SEQUENCE-DETERMINED DNA FRAGMENTS AND  
CORRESPONDING       POLYPEPTIDES       ENCODED  
THEREBY

Priority Claimed:    2750-0578P    60/159,331    October 14, 1999

Send Correspondence to:

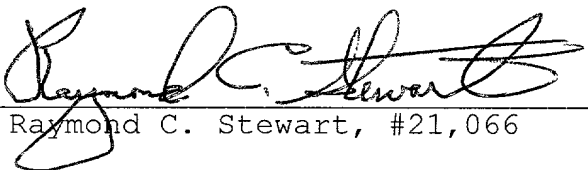
BIRCH, STEWART, KOLASCH & BIRCH, LLP    or    **CUSTOMER NO. 2292**  
P.O. Box 747  
Falls Church, VA    22040-0747  
(703) 205-8000

The above information is submitted to advise the U.S.P.T.O.  
of all relevant facts in connection with the present application.

A timely executed Declaration in accordance with 37 C.F.R.  
§ 1.64 will follow.

Respectfully submitted,

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